

From: Bunner, Bridget  
Sent: Tuesday, March 29, 2005 11:15 AM  
To: STIC-Biotech/ChemLib  
Subject: sequence search

Hi! I'd like to request a sequence search for case 09/810,796:

1. the nucleic acid sequence encoding the protein of SEQ ID NO: 5
2. the nucleic acid sequence encoding the protein of SEQ ID NO: 4
3. the nucleic acid sequence of SEQ ID NO: 1

Thanks!

Bridget Bunner

Art Unit 1647  
Rem 4C65  
(571) 272-0881  
mailbox 4C70

1 - 3071 NA  
4 - 897 AA  
5 - 888 AA

\*\*\*\*\*  
STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2- \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*  
Type of Search

NA#: \_\_\_\_\_ AA#: \_\_\_\_\_  
Interference: \_\_\_\_\_ SPDI: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure#: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*  
Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	3040.4	99.0	3137	4	US-09-590-304-1	Sequence 1, Appli
2	2890.8	94.1	3111	4	US-09-825-147-3	Sequence 3, Appli
3	2857.4	93.0	3074	4	US-09-813-148-1	Sequence 1, Appli
4	2635.4	85.8	2772	4	US-09-825-147-1	Sequence 1, Appli
5	518	16.9	2196	4	US-09-949-016-1823	Sequence 1823, Ap
6	518	16.9	2335	4	US-09-492-361-1	Sequence 1, Appli
7	517.6	16.9	2273	3	US-09-177-650-88	Sequence 88, Appl
8	511.6	16.7	2169	3	US-09-105-058C-22	Sequence 22, Appl
9	509.8	16.6	582	4	US-09-495-050A-303	Sequence 303, App
10	465.4	15.2	896	3	US-09-105-058C-1	Sequence 1, Appli
11	463.6	15.1	2814	3	US-09-177-650-90	Sequence 90, Appl
12	460.8	15.0	2565	3	US-09-105-058C-26	Sequence 26, Appl
13	460.8	15.0	2914	3	US-09-177-650-6	Sequence 6, Appli
14	452	14.7	575	4	US-09-495-050A-305	Sequence 305, App
15	425	13.8	3287	3	US-09-105-058C-19	Sequence 19, Appl
16	423.4	13.8	3232	3	US-09-177-650-1	Sequence 1, Appli
17	423.4	13.8	3237	3	US-09-177-650-95	Sequence 95, Appl
18	421.6	13.7	900	3	US-09-105-058C-3	Sequence 3, Appli
19	420.6	13.7	900	3	US-09-105-058C-5	Sequence 5, Appli
20	363.6	11.8	930	3	US-09-105-058C-17	Sequence 17, Appl
21	334.2	10.9	735	3	US-09-105-058C-7	Sequence 7, Appli
22	276.4	9.0	284	4	US-09-495-050A-304	Sequence 304, App
23	267.8	8.7	2028	4	US-09-634-920-1	Sequence 1, Appli
24	267.8	8.7	2028	4	US-09-840-125-1	Sequence 1, Appli
25	267.8	8.7	3181	3	US-09-135-021-1	Sequence 1, Appli
26	267.8	8.7	3181	3	US-09-135-020-1	Sequence 1, Appli
27	267.8	8.7	3181	3	US-09-135-010A-1	Sequence 1, Appli

Db	361	GCCTCAAGTGGCTTCTGATCCCTGAGTTCGATGATGCTGCTCTTTGGTTGGAGTTC	420	1441	CCACCCTTAAACCTGTCATTCCGAGCTATCAGAAATTATGAAATTTCATGTTGCAAAACGG	1500
Qy	430	ATCAATTCGAATCTCGTCTGCGGGTTCGTGTTCGATATAGAGAGTGGCAAGCACTG	489	1510	AAGTTTAAAGAAAARTRTHAGTCCATATGATGTAAGATGTCATTGTAACAAATATTTCTGCT	1569
Db	421	ATCAATTCGAATCTCGTCTGCGGGTTCGTGTTCGATATAGAGAGTGGCAAGCACTG	480	1501	AAGTTTAAAGAAAARTRTHAGTCCATATGATGTAAGATGTCATTGTAACAAATATTTCTGCT	1560
Qy	490	AGGTTTCTCGAAGCCCTCTGTTTATAGATACCAATGTTCTTATCGCTTCAATAGCA	549	1570	GCTCATCTGGACATGCTGTGTAGAAATTAAGAACCTTCAACACAGTGTGTGATCAAAATCTT	1629
Db	481	AGGTTTCTCGAAGCCCTCTGTTTATAGATACCAATGTTCTTATCGCTTCAATAGCA	540	1561	GCTCATCTGGACATGCTGTGTAGAAATTAAGAACCTTCAACACAGTGTGTGATCAAAATCTT	1620
Qy	550	GTTGTTCTCGAAGAACTCAGGGTAATATTTTGGCCAGCTGTGACACAGAGTCTCCGT	609	1630	GGAAAAGGGCAAAATCAATCAGATAGAAAGAGCCGAGAGAAATAACAGCAGACATGAG	1689
Db	541	GTTGTTCTCGAAGAACTCAGGGTAATATTTTGGCCAGCTGTGACACAGAGTCTCCGT	600	1621	GGAAAAGGGCAAAATCAATCAGATAGAAAGAGCCGAGAGAAATAACAGCAGACATGAG	1680
Qy	610	TTCCTACAGATCCTCGCATGCTGGATGACCGAGGGAGGACCTTGGAAATTAAGT	669	1690	ACCAAGAGAGTCTCAGATGCTCGCTCGGTGGTCAAGGTTGAAATAACAGTACAGTCC	1749
Db	601	TTCCTACAGATCCTCGCATGCTGGATGACCGAGGGAGGACCTTGGAAATTAAGT	660	1681	ACCAAGAGAGTCTCAGATGCTCGCTCGGTGGTCAAGGTTGAAATAACAGTACAGTCC	1740
Qy	670	GCTTCAGTGGTATGCTCACAGCAAGGAATTAATACAGCTTGGTACATAGGATTTTG	729	1750	ATAGAAATCAAGCTGGAGTCTTACTAGACATCTATCAACAGGTCCTTCGGAAGGCTCT	1809
Db	661	GCTTCAGTGGTATGCTCACAGCAAGGAATTAATACAGCTTGGTACATAGGATTTTG	720	1741	ATAGAAATCAAGCTGGAGTCTTACTAGACATCTATCAACAGGTCCTTCGGAAGGCTCT	1800
Qy	730	GTTCTTATTTTTCGTTCTTCTGCTATCTGCTGGAAAGGATGCCAATAAAGAGTTT	789	1810	GCCTCAGCCCTCGCTTTGGCTTCAATCCAGTTCGCCACCTTTTGAATGTGAACAGACATCT	1869
Db	721	GTTCTTATTTTTCGTTCTTCTGCTATCTGCTGGAAAGGATGCCAATAAAGAGTTT	780	1801	GCCTCAGCCCTCGCTTTGGCTTCAATCCAGTTCGCCACCTTTTGAATGTGAACAGACATCT	1860
Qy	790	TCTACATATGAGATGCTCTCTGCTGGGCAAAATTAATACAGCTTATTTGGCTATGGA	849	1870	GACTCAAAAGCCCTGTGATAGCAAGATCTTTCCGGTTCGCCACAAACAGTGGCTGC	1929
Db	781	TCTACATATGAGATGCTCTCTGCTGGGCAAAATTAATACAGCTTATTTGGCTATGGA	840	1861	GACTCAAAAGCCCTGTGATAGCAAGATCTTTCCGGTTCGCCACAAACAGTGGCTGC	1920
Qy	850	GACAAACTCCCTAACTGGCTGGAGATGCTTTCTGAGGCTTTTGGCAATTAAGATGCA	909	1930	TTATCAGATCAACTAGTGGCAACATCTCGAGAGGCTCGAGTTCATCTGACGCAAT	1989
Db	841	GACAAACTCCCTAACTGGCTGGAGATGCTTTCTGAGGCTTTTGGCAATTAAGATGCA	900	1921	TTATCAGATCAACTAGTGGCAACATCTCGAGAGGCTCGAGTTCATCTGACGCAAT	1980
Qy	910	ATTTCTTTCTTTCGCTCTCTGCTGCTCAGGTTTTCGCTTTCGCTTTCGCTTTCGCT	969	1990	GAGTTCAGTGGCCAGACTTTCTACGGCTTAGCCCTTACTATGACAGTCAAGCAACAG	2049
Db	901	ATTTCTTTCTTTCGCTCTCTGCTGCTCAGGTTTTCGCTTTCGCTTTCGCTTTCGCT	960	1981	GAGTTCAGTGGCCAGACTTTCTACGGCTTAGCCCTTACTATGACAGTCAAGCAACAG	2040
Qy	970	GAACAAACCCGCGAGAAACATTTGAGAAAGAGAAACCCAGCTGCGCACTTCAATCAG	1029	2050	GTGCCAATTAGTCAAGCGATGCTCAGAGTGGGAGCCACCAACCACTTCGCAATCCCA	2109
Db	961	GAACAAACCCGCGAGAAACATTTGAGAAAGAGAAACCCAGCTGCGCACTTCAATCAG	1020	2041	GTGCCAATTAGTCAAGCGATGCTCAGAGTGGGAGCCACCAACCACTTCGCAATCCCA	2100
Qy	1030	TGTGTTGGGCTAGTTACGAGCTGATGAGAAATCTGTTTCAATGCAACCTGGAAGCA	1089	2110	ATAAATACGCAACCCAGCGAGAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA	2169
Db	1021	TGTGTTGGGCTAGTTACGAGCTGATGAGAAATCTGTTTCAATGCAACCTGGAAGCA	1080	2101	ATAAATACGCAACCCAGCGAGAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA	2160
Qy	1090	CACCTGAAGGCTTGCACACCTGCAGCCCTTACCAAGAAAGAAACAGGGAGGATCAAGC	1149	2170	GCCATCAAGCATCTGCCAGGCGAGAACTCTGCACCTTAACCTTCAGGCTTACAGGAA	2229
Db	1081	CACCTGAAGGCTTGCACACCTGCAGCCCTTACCAAGAAAGAAACAGGGAGGATCAAGC	1140	2161	GCCATCAAGCATCTGCCAGGCGAGAACTCTGCACCTTAACCTTCAGGCTTACAGGAA	2220
Qy	1150	AGTCAGAGCTAAGTTTATAGGAGCGAGTGGCATGGCTAGCCCGAGGGGCGAGATTT	1209	2230	AGCATTTCTGACGTCACACCTGCTTGTGCTTCCAGGAAATGTTTCAAGTTCACAG	2289
Db	1141	AGTCAGAGCTAAGTTTATAGGAGCGAGTGGCATGGCTAGCCCGAGGGGCGAGATTT	1200	2221	AGCATTTCTGACGTCACACCTGCTTGTGCTTCCAGGAAATGTTTCAAGTTCACAG	2280
Qy	1210	AAGAGCGACAAAGCTCAGTAGTGACAGAGGTTCCCAAGCAGCAGATCAAGCCGAG	1269	2290	TCAAAATCTCAACAAAGGACCGTTCATGAGGAAAGCTTTCAGATGGGAGGAACTCTG	2349
Db	1201	AAGAGCGACAAAGCTCAGTAGTGACAGAGGTTCCCAAGCAGCAGATCAAGCCGAG	1260	2281	TCAAAATCTCAACAAAGGACCGTTCATGAGGAAAGCTTTCAGATGGGAGGAACTCTG	2340
Qy	1270	GGCAGTCCCAAGGCTGAGAGAGCTGAGGCTTCAACAGCCGAGCCGCTTCCGGCCC	1329	2350	TGTGCTGCTGTCTGCTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAG	2409
Db	1261	GGCAGTCCCAAGGCTGAGAGAGCTGAGGCTTCAACAGCCGAGCCGCTTCCGGCCC	1320	2341	TGTGCTGCTGTCTGCTCCAGAGGCTTCCAGAGGCTTCCAGAGGCTTCCAGAG	2400
Qy	1330	TGCTGCGCTCAAAAGTCTCAGCAAAACAGTATGATGCTGACACAGCCCTTGGC	1389	2410	ATCAGGTCGACCGAGGAACTGAATATACAACTTTTCAAGGAGTGAAGTGGCTCCAGA	2469
Db	1321	TGCTGCGCTCAAAAGTCTCAGCAAAACAGTATGATGCTGACACAGCCCTTGGC	1380	2401	ATCAGGTCGACCGAGGAACTGAATATACAACTTTTCAAGGAGTGAAGTGGCTCCAGA	2460
Qy	1390	ACTGATGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1449	2470	GGCAGCCAGATTTTTTACCCAAATGAGGAGGAAATCCAAATTTTATTAACCTGATGAGAG	2529
Db	1381	ACTGATGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1440	2461	GGCAGCCAGATTTTTTACCCAAATGAGGAGGAAATCCAAATTTTATTAACCTGATGAGAG	2520
Qy	1450	CCACCCTTAAACCTGTCATTCCGAGCTATCAGAAATTATGAAATTTCATGTTGCAAAACGG	1509	2530	GTTGGTCCGAGAGACAGACAGACACTTTTGTATGCCGACCGCAGCCTGCCAGGAA	2589
				2521	GTTGGTCCGAGAGACAGACAGACACTTTTGTATGCCGACCGCAGCCTGCCAGGAA	2580

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Qy 2590 GCTGCTTTGCAATCAGACTCTCTAAGGACTGGAAAGGTCAAGATCATCTCAGAGCAATTTGT 2649
Db 2581 GCTGCTTTTGCAATCAGACTCTCTAAGGACTGGAAAGGTCAAGATCATCTCAGAGCAATTTGT 2640
Qy 2650 AAGCGAGAGAAAGTACAGATGCGCTCAGCTTGGCTCATGTCAAACTGAAATAGTTCTT 2709
Db 2641 AAGCGAGAGAAAGTACAGATGCGCTCAGCTTGGCTCATGTCAAACTGAAATAGTTCTT 2700
Qy 2710 CATTTCTTTCCAGGCATAGCAGTTCTTTTAGCCATACATATCATTTGCAATGAATTTTCG 2769
Db 2701 CATTTCTTTCCAGGCATAGCAGTTCTTTTAGCCATACATATCATTTGCAATGAATTTTCG 2760
Qy 2770 AAAGCCCTTCAAAGTTGAAATTTGCAAGAAATCGGGAAGAACATGAAGGAGTTTATA 2829
Db 2761 AAAGCCCTTCAAAGTTGAAATTTGCAAGAAATCGGGAAGAACATGAAGGAGTTTATA 2820
Qy 2830 AGCCGGTTTACCTTTAAATTTGCATGAAATGCAATGTTTAGGGATGGCTAAATTTCCAGGT 2889
Db 2821 AGCCGGTTTACCTTTAAATTTGCATGAAATGCAATGTTTAGGGATGGCTAAATTTCCAGGT 2880
Qy 2890 GCATCGACATTAACCCACTCATTTAGTAATGTACCTTGAGTTTAAAGCCCTGAGAAACCA 2949
Db 2881 GCATCGACATTAACCCACTCATTTAGTAATGTACCTTGAGTTTAAAGCCCTGAGAAACCA 2940
Qy 2950 AACACAGCTAATGCTATGGGTGTATGAATATGTCAAGTTTAGTTCATTTAGAGATTTG 3009
Db 2941 AACACAGCTAATGCTATGGGTGTATGAATATGTCAAGTTTAGTTCATTTAGAGATTTG 3000
Qy 3010 ACACGTATTTTGAATTTATGGAGTAAACACCTTCAAAATTCA 3053
Db 3001 ACACGTATTTTGAATTTATGGAGTAAACACCTTCAAAATTCA 3044
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## RESULT 2

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US-09-825-147-3
; Sequence 3, Application US/09825147
; Patent No. 6767736
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6767736el Human Ion Channel Protein and
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; CURRENT FILING DATE: 2001-04-03
; PRIOR FILING DATE: 2001-04-03
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-3
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Query Match 94.1%; Score 2890.8; DB 4; Length 3111;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2951; Conservative 1; Mismatches 3; Indels 29; Gaps 3;

Qy 1 GGCAGCGCATGAAGGATGTGAGTCCGGCGGGGCGAGGGTCTGCTCAACTCGGCAGCC 60
Db 156 GGCAGCGCATGAAGGATGTGAGTCCGGCGGGGCGAGGGTCTGCTCAACTCGGCAGCC 215
Qy 61 GCCAGGGCGAGCGGCTGCTACTGCTGGGCAACCCCGGGCGGCACGCTTTGGTGGCGGGC 120
Db 216 GCCAGGGCGAGCGGCTGCTACTGCTGGGCAACCCCGGGCGGCACGCTCGGTGGCGGGC 275
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Qy 121 GGTGCGCTGAGGAGAGCGCCCGGGGCAAGCAGAGGGGGCCCGATGAGCTGCTGGGGAAG 180
Db 276 GGTGCGCTGAGGAGAGCGCCCGGGGCAAGCAGAGGGGGCCCGATGAGCTGCTGGGGAAG 335
Qy 181 CCGCTCTCTTACACGAGTAGCAGAGTGC CGGCGCAACGTCAGAGTCAAGTACCGCGGGTGCAG 240
Db 336 CCGCTCTCTTACACGAGTAGCAGAGTGC CGGCGCAACGTCAGAGTCAAGTACCGCGGGTGCAG 395
Qy 241 AACTACCTGTACAAACGCTGTGAGAGAGACCCCGCGGCTGGGCGTTCATCTACACGCTTTC 300
Db 396 AACTACCTGTACAAACGCTGTGAGAGAGACCCCGCGGCTGGGCGTTCATCTACACGCTTTC 455
Qy 301 GTTTTTCTCCTGTCTTTGGTTGCTTGTGTTTGTTCAGTGTGTTTCTACCATCCCTGAGCAC 360
Db 456 GTTTTTCTCCTGTCTTTGGTTGCTTGTGTTTGTTCAGTGTGTTTCTACCATCCCTGAGCAC 515
Qy 361 ACAAATTTGGGCTCAAGTTGCTCTTGATCTCGAGTTCGTCGATGATTTGTCGTTTGGT 420
Db 516 ACAAATTTGGGCTCAAGTTGCTCTTGATCTCGAGTTCGTCGATGATTTGTCGTTTGGT 575
Qy 421 TTGAGTTTCATCATTTGCAATCTGCTCTCGGGTTGCTGTTTCGATATAGAGGATGGCAA 480
Db 576 TTGAGTTTCATCATTTGCAATCTGCTCTCGGGTTGCTGTTTCGATATAGAGGATGGCAA 635
Qy 481 GGAAGACTGAGGTTGCTCGAAGCCCTTCTGTTTATAGATACCATTTGTTTCTTATCGCT 540
Db 636 GGAAGACTGAGGTTGCTCGAAGCCCTTCTGTTTATAGATACCATTTGTTTCTTATCGCT 695
Qy 541 TCAATAGCAGTTGTTTCTGCAAACTCAGGGTAAATATTTTGGCACGCTGTCACCTCAGA 600
Db 696 TCAATAGCAGTTGTTTCTGCAAACTCAGGGTAAATATTTTGGCACGCTGTCACCTCAGA 755
Qy 601 AGTCTCCGTTTCTACAGATCCTCCGATGCTGCGCATGTCGACCGAAGGGGAGGCACTTGG 660
Db 756 AGTCTCCGTTTCTACAGATCCTCCGATGCTGCGCATGTCGACCGAAGGGGAGGCACTTGG 815
Qy 661 AAATTTACTGGGTTTCAAGTGGTTTATGCTCAGCAGCAGGAAATTAATCAGAGCTTGGTACATA 720
Db 816 AAATTTACTGGGTTTCAAGTGGTTTATGCTCAGCAGCAGGAAATTAATCAGAGCTTGGTACATA 875
Qy 721 GGATTTTGGTTCCTTATTTTTCGTTCTTCTGTTCTATCTGGTGGAAAGGATGCCAAT 780
Db 876 GGATTTTGGTTCCTTATTTTTCGTTCTTCTGTTCTATCTGGTGGAAAGGATGCCAAT 935
Qy 781 AAAGAGTTTCTCATATGAGATGCTCTCTGTTGGGCAACAATTAATGACAACTAAT 840
Db 936 AAAGAGTTTCTCATATGAGATGCTCTCTGTTGGGCAACAATTAATGACAACTAAT 995
Qy 841 GGCTATGGAGACAAACTCCCTAACTTGGCTGGAGATTTGCTTCTGCAAGGCTTTGCA 900
Db 996 GGCTATGGAGACAAACTCCCTAACTTGGCTGGAGATTTGCTTCTGCAAGGCTTTGCA 1055
Qy 901 CTCCTTGGCATTTCTTTTTCGACATCTCTCCCGCATTTCTTGGCTCAGGTTTTCATTA 960
Db 1056 CTCCTTGGCATTTCTTTTTCGACATCTCTCCCGCATTTCTTGGCTCAGGTTTTCATTA 1115
Qy 961 AAAGTACAAGAACCAACCCGACAGAAACATTTTGGAGAAAGAGAACCCAGCTGCCAAC 1020
Db 1116 AAAGTACAAGAACCAACCCGACAGAAACATTTTGGAGAAAGAGAACCCAGCTGCCAAC 1175
Qy 1021 CTCATTGAGTGTGTTGGCGTAGTTTACGACAGTGTAGTGAATCTGTTTCCATTGCAACC 1080
Db 1176 CTCATTGAGTGTGTTGGCGTAGTTTACGACAGTGTAGTGAATCTGTTTCCATTGCAACC 1235
Qy 1081 TGGAGGCGCACACTTTGAAGCCCTTCACACCTGACGCCCTTACCAAGAAAGAACCAAGGGAA 1140
Db 1236 TGGAGGCGCACACTTTGAAGCCCTTCGACACCTGACGCCCTTACCAAGAAAGAACCAAGGGAA 1279
Qy 1141 GCATCAAGCAGTCAAGAGCTTAAGTTTAAAGAGCGAGTGCAGTGGCTAGCCCGAGGGC 1200
Db 1280 -----TCAGAGCTAAGTTTAAAGAGCGAGTGCAGTGGCTAGCCCGAGGGC 1328
Qy 1201 CAGAGTATTAGAGCGCGACAGCCCTCAGTAGTGCAGGAGGTCCCCAAGCACCGACATC 1260
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Query Match				93.0%; Score 2857.4; DB 4; Length 3074;			
Best Local Similarity				99.7%; Pred. No. 0;			
Matches 2861; Conservative 1; Mismatches 7; Indels 0; Gaps 0;							
Qy	1	GGCAGCGCATGAGGATGGAGTGGAGTGGGCGGGCGGCGAGGGTGGCTGCTGAACTCCGCGAGCC	60				
Db	206	GGCAGCGCATGAGGATGGAGTGGAGTGGGCGGGCGGCGAGGGTGGCTGCTGAACTCCGCGAGCC	265				
Qy	61	GCCAGGGCGGAGCGGCTGCTACTGCTGGGCGACCCGCGCGGCGACGCTTGGTGGGCGGCGGC	120				
Db	266	GCCAGGGCGGAGCGGCTGCTACTGCTGGGCGACCCGCGCGGCGACGCTTGGTGGGCGGCGGC	325				
Qy	121	GGTGGCTTGAGGGAGAGCGCGCGGGCAAGCAGAGGGGGCCCGGATGAGCCTGCTGGGGAG	180				
Db	326	GGTGGCTTGAGGGAGAGCGCGCGGGCAAGCAGAGGGGGCCCGGATGAGCCTGCTGGGAAGC	385				
Qy	181	CCGCTCTCTTACAGAGTAGCAGAGCTGCGGGCGCAACGTCAGTAGCCGGGGGTGCAG	240				
Db	386	CGCTCTCTTACAGAGTAGCAGAGCTGCGGGCGCAACGTCAGTAGCCGGGGGTGCAG	445				
Qy	241	AACTACCTGTACAGCTGCTGGAGAGACCCCGCGGCTGGGGTTCATCTACAGCGCTTTC	300				
Db	446	AACTACCTGTACAGCTGCTGGAGAGACCCCGCGGCTGGGGTTCATCTACAGCGCTTTC	505				
Qy	301	GTTTTCTCTTGTCTTGGTGTGATTTTGTGCTGAGTGTTCATCCCTGAGCAC	360				
Db	506	GTTTTCTCTTGTCTTGGTGTGATTTTGTGCTGAGTGTTCATCCCTGAGCAC	565				
Qy	361	ACAAATTTGGCTCAAGTGTCTCTTGATCTGGAGTTCGFGATGATGTCGTCTTGGT	420				
Db	566	ACAAATTTGGCTCAAGTGTCTCTTGATCTGGAGTTCGFGATGATGTCGTCTTGGT	625				
Qy	421	TTGGAGTTTCATTCGAATCTGGTCTCGGGTGTCTGTTGCGATATAGAGGATGGCAA	480				
Db	626	TTGGAGTTTCATTCGAATCTGGTCTCGGGTGTCTGTTGCGATATAGAGGATGGCAA	685				
Qy	481	GGAGAGCTGAGGTTTGTCTGAAAGCCCTTCTGTGTATAGATACATTTGTTCTTATCGCT	540				
Db	686	GGAGAGCTGAGGTTTGTCTGAAAGCCCTTCTGTGTATAGATACATTTGTTCTTATCGCT	745				
Qy	541	TCAATAGCAGTTGTTCTGCAAAACTCAGGGTATATTTTGGCCAGCTGCACTCAGA	600				
Db	746	TCAATAGCAGTTGTTCTGCAAAACTCAGGGTATATTTTGGCCAGCTGCACTCAGA	805				
Qy	601	AGTCTCCGTTTCTACAGATCCTCGCATGGTGGCGATGGACCGAAGGGGAGGCACTTGG	660				
Db	806	AGTCTCCGTTTCTACAGATCCTCGCATGGTGGCGATGGACCGAAGGGGAGGCACTTGG	865				
Qy	661	AAATTAATCTGGGTTGAGTGGTTATGCTCACAGCAAGGAATTAATCAGCTTGGTACATA	720				
Db	866	AAATTAATCTGGGTTGAGTGGTTATGCTCACAGCAAGGAATTAATCAGCTTGGTACATA	925				
Qy	721	GGATTTTGGTTCATTTTTCGTTCTTCTGCTGCTATCTGTTGGTGGAAAGGATGCCAAT	780				
Db	926	GGATTTTGGTTCATTTTTCGTTCTTCTGCTGCTATCTGTTGGTGGAAAGGATGCCAAT	985				
Qy	781	AAAGAGTTTTCTACATATGCAATGCTCTCGTGGGGCGACAAATTAATTGACAACTATT	840				
Db	986	AAAGAGTTTTCTACATATGCAATGCTCTCGTGGGGCGACAAATTAATTGACAACTATT	1045				
Qy	841	GGCTATGAGACAAACTCCCTTAATCTTGGCTGGGAAGATTGCTTTCGAGGCTTTGCA	900				
Db	1046	GGCTATGAGACAAACTCCCTTAATCTTGGCTGGGAAGATTGCTTTCGAGGCTTTGCA	1105				
Qy	901	CTCCTTGGCATTTCTTTTGGCTCTTCTCGCGCATTTCTTGGCTCAGGTTTGCATTA	960				
Db	1106	CTCCTTGGCATTTCTTTTGGCTCTTCTCGCGCATTTCTTGGCTCAGGTTTGCATTA	1165				
Qy	961	AAAGTACAGAAACACACCGGCAGAAACATTTTGAGAAAGAGAAACCCAGCTGCCAAC	1020				
Db	1166	AAAGTACAGAAACACACCGGCAGAAACATTTTGAGAAAGAGAAACCCAGCTGCCAAC	1225				

Qy	1021	CTCATTCAGTGTGTTTGGCGTAGTTTACGACGCTGATGAGAAATCTGTTTCAATTCGAACC	1080
Db	1226	CTCATTCAGTGTGTTTGGCGTAGTTTACGACGCTGATGAGAAATCTGTTTCAATTCGAACC	1285
Qy	1081	TGGAAGCCACACTTTGAAGGCTTCACACCTGCGAGCCTTACCAAGAAAGAACAGGGGAA	1140
Db	1286	TGGAAGCCACACTTTGAAGGCTTCACACCTGCGAGCCTTACCAAGAAAGAACAGGGGAA	1345
Qy	1141	GCATCAAGCAGTCAAGAGCTAAAGTTTAAAGGAGCGAGTGGCGATGGCTAGCCCGAGGGC	1200
Db	1346	GCATCAAGCAGTCAAGAGCTAAAGTTTAAAGGAGCGAGTGGCGATGGCTAGCCCGAGGGC	1405
Qy	1201	CAGAGTATTAAGACCCAGAACCTCAGTAGTGCAGAGGAGTCCCGAGCACCGACATC	1260
Db	1406	CAGAGTATTAAGACCCAGAACCTCAGTAGTGCAGAGGAGTCCCGAGCACCGACATC	1465
Qy	1261	ACAGCCGAGGCGAGTCCACCCAAAGTGCAGAAAGAGTGGAGCTTCAACGACCGAACCCGC	1320
Db	1466	ACAGCCGAGGCGAGTCCACCCAAAGTGCAGAAAGAGTGGAGCTTCAACGACCGAACCCGC	1525
Qy	1321	TTCCGGCCCTCGCTGCGCTCAAAGTTCTCAGGCCAAACCCAGTGATAGTGTGACACA	1380
Db	1526	TTCCGGCCCTCGCTGCGCTCAAAGTTCTCAGGCCAAACCCAGTGATAGTGTGACACA	1585
Qy	1381	GCCCTTGGCACTGATGATGATATATGATGAAAGAGTGCAGTGTGATGATGATGAGTGA	1440
Db	1586	GCCCTTGGCACTGATGATGATATATGATGAAAGAGTGCAGTGTGATGATGATGAGTGA	1645
Qy	1441	GACCTACCCCGACACTTAAACCTGCTATTCGAGCTATCAGAAATTTGAAATTTTCATGTT	1500
Db	1646	GACCTACCCCGACACTTAAACCTGCTATTCGAGCTATCAGAAATTTGAAATTTTCATGTT	1705
Qy	1501	GCAAAACGGAAGTTTAAAGGAAACRTTACGTCATATGATGTAAGAGTGTGATTTGAACAA	1560
Db	1706	GCAAAACGGAAGTTTAAAGGAAACRTTACGTCATATGATGTAAGAGTGTGATTTGAACAA	1765
Qy	1561	TATTCCTGCTGCTCATCTGGACATGTTGTGTAGAAATTAAGAGCTTCAACAGCGTTGAT	1620
Db	1766	TATTCCTGCTGCTCATCTGGACATGTTGTGTAGAAATTAAGAGCTTCAACAGCGTTGAT	1825
Qy	1621	CAAAATTCCTGGAAGGGCAAAATCACATCAGATGAAGAGAGCCGAGAGAAATTAACAGCA	1680
Db	1826	CAAAATTCCTGGAAGGGCAAAATCACATCAGATGAAGAGAGCCGAGAGAAATTAACAGCA	1885
Qy	1681	GAAATGAGAGCCACAGACGATCTCAGTATGCTCGGTGCGGTGGTCAAGGTTGAAAAACAG	1740
Db	1886	GAAATGAGAGCCACAGACGATCTCAGTATGCTCGGTGCGGTGGTCAAGGTTGAAAAACAG	1945
Qy	1741	GTACAGTCCATAGAAATCCAGCTGGACTGCTACTAGACATCTATCAACAGGTCCTTCGG	1800
Db	1946	GTACAGTCCATAGAAATCCAGCTGGACTGCTACTAGACATCTATCAACAGGTCCTTCGG	2005
Qy	1801	AAAGGCTCTGCTCAGCCCTCGCTTTCGCTTTCATTCAGATTTCCACCTTTTGAATGTCAA	1860
Db	2006	AAAGGCTCTGCTCAGCCCTCGCTTTCGCTTTCATTCAGATTTCCACCTTTTGAATGTCAA	2065
Qy	1861	CAGACATCTGACTATCAAGGCTTGGATAGCAAGAGATCTTTCGGGTTCCGCAAAAAC	1920
Db	2066	CAGACATCTGACTATCAAGGCTTGGATAGCAAGAGATCTTTCGGGTTCCGCAAAAAC	2125
Qy	1921	AGTGGCTGCTTATCCAGATCAACTAGTGCACCAATCTCGAGAGGCTGCGAGTTCATTCG	1980
Db	2126	AGTGGCTGCTTATCCAGATCAACTAGTGCACCAATCTCGAGAGGCTGCGAGTTCATTCG	2185
Qy	1981	ACGCCAAATGAGTTTCAGTGGCCAGACTTTCATCGCGCTTAGCCCTACTATGACAGTCAA	2040
Db	2186	ACGCCAAATGAGTTTCAGTGGCCAGACTTTCATCGCGCTTAGCCCTACTATGACAGTCAA	2245
Qy	2041	GCAACACAGGTGCGAATTAAGTCAAAGCGATGGCTCAGCAGTGGCGGACCAACCAACAT	2100
Db	2246	GCAACACAGGTGCGAATTAAGTCAAAGCGATGGCTCAGCAGTGGCGGACCAACCAACAT	2305
Qy	2101	GCAAAACCAATTAATACGGCACCCAGCGACGCCCAACAACTTTTACAGATCCACCT	2160

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Db 2306 GCAACCAAAATAATACGGACCCACAGCCAGCCCAACAACTTTACAGATCCCACT 2365
Qy 2161 CCTCTCCAGCATCAAGCATCTGCCAGGCGAGAAACTCTGCAACCCCTAACCCCTGCAGGC 2220
Db 2366 CCTCTCCAGCATCAAGCATCTGCCAGGCGAGAAACTCTGCAACCCCTAACCCCTGCAGGC 2425
Qy 2221 TTACAGGAAGCATTTCTGAGCTCACCACCTGCTTGTGCTTCCCAAGGAATGTTTCAG 2280
Db 2426 TTACAGGAAGCATTTCTGAGCTCACCACCTGCTTGTGCTTCCCAAGGAATGTTTCAG 2485
Qy 2281 GTTGACAGTCAAAATCTCACCAGGACCGTCTCTATGAGGAAAGCTTTGACATCGGAGGA 2340
Db 2486 GTTGACAGTCAAAATCTCACCAGGACCGTCTCTATGAGGAAAGCTTTGACATCGGAGGA 2545
Qy 2341 GAAACTCTGTTGTCTGTCTGCCATGTCAGGAGGAGCTTTGGGCAAACTTTTCTGTGTG 2400
Db 2546 GAAACTCTGTTGTCTGTCTGCCATGTCAGGAGGAGCTTTGGGCAAACTTTTCTGTGTG 2605
Qy 2401 CAAAACCTGATCAGGTGCGACCGAGGAAGTGAATACAACTTTTCCAGGAGTGAGTCAAGT 2460
Db 2606 CAAAACCTGATCAGGTGCGACCGAGGAAGTGAATACAACTTTTCCAGGAGTGAGTCAAGT 2665
Qy 2461 GGCTCCAGAGGCGCAAGATTTTACCCCAATGAGGGAATCCAAATTTGTTTAACT 2520
Db 2666 GGCTCCAGAGGCGCAAGATTTTACCCCAATGAGGGAATCCAAATTTGTTTAACT 2725
Qy 2521 GATGAAGAGTGGTCCGAGAGAGACAGACACTTTTGTATGCGGACCCAGCCT 2580
Db 2726 GATGAAGAGTGGTCCGAGAGAGACAGACACTTTTGTATGCGGACCCAGCCT 2785
Qy 2581 GCCAGGAGTGGTCCGAGAGAGACAGACACTTTTGTATGCGGACCCAGCCT 2640
Db 2786 GCCAGGAGTGGTCCGAGAGAGACAGACACTTTTGTATGCGGACCCAGCCT 2845
Qy 2641 AGCATTTGTAAGGCGAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAA 2700
Db 2846 AGCATTTGTAAGGCGAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAA 2905
Qy 2701 TAAGTCTTTCATTTCTTCAGGATAGCAGTCTTTAGGCATACATATCATTTGCATGA 2760
Db 2906 TAAGTCTTTCATTTCTTCAGGATAGCAGTCTTTAGGCATACATATCATTTGCATGA 2965
Qy 2761 ACTATTTCCGAAGCCCTTCTAAAAGTTGAAATTCGAAGATCGGGAAGACATGAAAGG 2820
Db 2966 ACTATTTCCGAAGCCCTTCTAAAAGTTGAAATTCGAAGATCGGGAAGACATGAAAGG 3025
Qy 2821 CAGTTTATAAGCCCGTTACCTTTTAAATTCGATGAAATGCAATGTTTAGG 2869
Db 3026 CAGTTTATAAGCCCGTTACCTTTTAAATTCGATGAAATGCAATGTTTAGG 3074
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RESULT 4

US-09-825-147-1

; Sequence 1, Application US/09825147

; Patent No. 6767736

; GENERAL INFORMATION:

; APPLICANT: Hu, Yi

; APPLICANT: Kieke, James Alvin

; APPLICANT: Turner, C. Alexander Jr.

; APPLICANT: Nehls, Michael C.

; APPLICANT: Friedrich, Glenn

; APPLICANT: Zambowicz, Brian

; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: No. 6767736el Human Ion Channel Protein and

; FILE REFERENCE: Polynucleotides Encoding the Same

; CURRENT APPLICATION NUMBER: US/09/825,147

; CURRENT FILING DATE: 2001-04-03

; PRIOR APPLICATION NUMBER: US 60/194,255

; PRIOR FILING DATE: 2000-04-03

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1  
; LENGTH: 2772  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-825-147-1

Query Match 85.8%; Score 2635.4; DB 4; Length 2772;

Best Local Similarity 98.9%; Pred. No. 0;

Matches 2673; Conservative 1; Mismatches 2; Indels 27; Gaps 1;

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Qy 1 GG CAG CGG CAT GAA GAT G T G A G T C G G C C G G G C A G G G T G C T G C T G A C T C G G C A G C C 60
Db 97 G G C A G C G G C A T G A A G G A T G T G A G T C G G C C G G G C A G G G T G C T G T G A A C T C G G C A G C C 156
Qy 61 G C C A G G G C G A C C G C C T G C T A C T G C T G G C C A C C C G C G C C A C G C T T G G T G G C G G C G G C 120
Db 157 G C C A G G G C G A C C G C C T G C T A C T G C T G G G C A C C C G C G C C A C G C T C G G T G G C G G C G G C 216
Qy 121 G G T G G C C T C A G G G A G A G C C G C G G G C A A G C A G G G G C C C G G A T G A G C C T G C T G G G G A A G 180
Db 217 G G T G G C C T C A G G G A G A G C C G C G G G C A A G C A G G G G C C C G G A T G A G C C T G C T G G G G A A G 276
Qy 181 C C G C T C T T T A C A C G A G T A C C A G A C T G C C G G G C C A A C G T C A A G T A C C G G C G G T G C A G 240
Db 277 C C G C T C T T T A C A C G A G T A C C A G A C T G C C G G G C C A A C G T C A A G T A C C G G C G G T G C A G 336
Qy 241 A A C T A C C T G T A C A C G T G C T G G A G A G A C C C C G G G C T T G G C G T T C A T C T A C C A C G C T T T C 300
Db 337 A A C T A C C T G T A C A C G T G C T G G A G A G A C C C C G G C T T G G C G T T C A T C T A C C A C G C T T T C 396
Qy 301 G T T T T T C C T T G T C T T T G G T T G C T G A T T T T G T C A G T T T T T T T T T T T T T T T T T T T T T T T 360
Db 397 G T T T T T C C T T G T C T T T G G T T G C T G A T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T 456
Qy 361 A C A A A T T G G C C T C A G T T G C C T T G A T C C T G S A G T T C G T G A T G A T T G C T C T T T G G T 420
Db 457 A C A A A T T G G C C T C A G T T G C C T T G A T C C T G S A G T T C G T G A T G A T T G C T C T T T G G T 516
Qy 421 T T G A G T T C A T C A T T C G A A T C T G S A G T T G C G G G T T G C T T G T T G C A T A T A G A G A G A T G C A A 480
Db 517 T T G A G T T C A T C A T T C G A A T C T G S A G T T G C G G G T T G C T T G T T G C A T A T A G A G A G A T G C A A 576
Qy 481 G G A A G A C T G A G T T T G C T C G A A A G C C C T T C T G T G T T A T A G A T A C C A T T G T T C T T A T C G C T 540
Db 577 G G A A G A C T G A G T T T G C T C G A A A G C C C T T C T G T G T T A T A G A T A C C A T T G T T C T T A T C G C T 636
Qy 541 T C A A T A G C A G T T G T T C T G C A A A A A C T C A G G G T A A T A T T T T T G C C A C G T C T G C A C T C A G A 600
Db 637 T C A A T A G C A G T T G T T C T G C A A A A A C T C A G G G T A A T A T T T T T G C C A C G T C T G C A C T C A G A 696
Qy 601 A G T C C C G T T T C C T A C A G A T C C T C C G C A T G G T G C G A T G G A C C G A G G G G A G G C A C T T G G 660
Db 697 A G T C C C G T T T C C T A C A G A T C C T C C G C A T G G A C C G A G G G G A G G C A C T T G G 756
Qy 720 A A A T T A C T G G G T T C A G T G G T T A T G C T C A C A G C A A G A A T T A A T C A C A G C T T G T T A C A T A 720
Db 757 A A A T T A C T G G G T T C A G T G G T T A T G C T C A C A G C A A G A A T T A A T C A C A G C T T G T T A C A T A 816
Qy 721 G G A T T T T G G T T C T T A T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T 780
Db 817 G G A T T T T G G T T C T T A T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T 876
Qy 781 A A A G A G T T T T C A T A T G A G A T G C T C T C T G T G G G G C A C A A T T A C A T T G A C A A C T A T T 840
Db 877 A A A G A G T T T T C A T A T G A G A T G C T C T C T G T G G G G C A C A A T T A C A T T G A C A A C T A T T 936
Qy 841 G G C T A T G G A G A C A A A C T C C C C T A A C T T G G C T G G A A G A T T G C T T C T G C A G G C T T T G C A 900
Db 937 G G C T A T G G A G A C A A A C T C C C C T A A C T T G G C T G G A A G A T T G C T T C T G C A G G C T T T G C A 996
Qy 901 C T C C T T G G C A T T T C T T T T T T G C A T T C C T C C C G G C A T T C T T G G C T C A G G T T T T T G C A T T A 960
Db 997 C T C C T T G G C A T T T C T T T T T T G C A T T C C T C C C G G C A T T C T T G G C T C A G G T T T T T G C A T T A 1056
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QY 961 AAAGTACAGAAACAAACCGCCGAGAAACATTTTGAAGAAAGAAAGAACCCAGCTGCCAAC 1020  
DB 1057 AAAGTACAGAAACAAACCGCCGAGAAACATTTTGAAGAAAGAAAGAACCCAGCTGCCAAC 1116  
QY 1021 CTCAATTCAGTCTGTTTGGCGTAGTTAGCGAGCTCATGAGAAATCTGTTTCCATTTGCAACC 1080  
DB 1117 CTCAATTCAGTCTGTTTGGCGTAGTTAGCGAGCTCATGAGAAATCTGTTTCCATTTGCAACC 1176  
QY 1081 TGAAGCCACACTTTGAAGCCCTTGACACCTGCGAGCCCTACCAAGAAAGAAACAAAGGGGAA 1140  
DB 1177 TGAAGCCACACTTTGAAGCCCTTGACACCTGCGAGCCCTACCAAGAAAGAAACAAAGGGGAA 1220  
QY 1141 GCATCAAGCAGTCAAGAGCTTAAGTTTAAAGAGCGAGTGGCGCATGGCTAGCCCCAGGGGC 1200  
DB 1221 -----TCAGAAGCTAAGTTTAAAGAGCGAGTGGCGCATGGCTAGCCCCAGGGGC 1269  
QY 1201 CAGAGTATTAAGAGCCGACAGCTCAGTAGGTGACAGAGGCTCCCAAGCACCGACATC 1260  
DB 1270 CAGAGTATTAAGAGCCGACAGCTCAGTAGGTGACAGAGGCTCCCAAGCACCGACATC 1329  
QY 1261 ACAGCCGAGGCGAGTCCCAACAAAGTGCAGAGAGCTGGAGCTTCAACGACCGAACCCGC 1320  
DB 1330 ACAGCCGAGGCGAGTCCCAACAAAGTGCAGAGAGCTGGAGCTTCAACGACCGAACCCGC 1389  
QY 1321 TTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCCAAAACCAAGTATGATGCTGACACA 1380  
DB 1390 TTCCGGCCCTCGCTGCGCCTCAAAAGTTCTCAGCCCAAAACCAAGTATGATGCTGACACA 1449  
QY 1381 GCCCTTGGCAGTATGATATGATGATAAGAGATGCCAGTCTGATGATCATAGTGGAA 1440  
DB 1450 GCCCTTGGCAGTATGATATGATGATAAGAGATGCCAGTCTGATGATCATAGTGGAA 1509  
QY 1441 GACCTCACCCCAACACTTCAAAAGTCTCATTCGAGCTATCAGAAATTAAGAAATTTTCATGTT 1500  
DB 1510 GACCTCACCCCAACACTTCAAAAGTCTCATTCGAGCTATCAGAAATTAAGAAATTTTCATGTT 1569  
QY 1501 GCAAAACGGAAGTTAAGAAACCTTACGTCCATATGATGATAAGATGATCATTTGAACAA 1560  
DB 1570 GCAAAACGGAAGTTAAGAAACCTTACGTCCATATGATGATAAGATGATCATTTGAACAA 1629  
QY 1561 TATTCGCTGCTCATCTGGACATGTTGTTAGAAATTAAGCCCTTCAACACGCTGTTGAT 1620  
DB 1630 TATTCGCTGCTCATCTGGACATGTTGTTAGAAATTAAGCCCTTCAACACGCTGTTGAT 1689  
QY 1621 CAAATTTCTGAAAGGCGCAATCACATCAGATGAAGAGCCGAGAGAAATTAACAGCA 1680  
DB 1690 CAAATTTCTGAAAGGCGCAATCACATCAGATGAAGAGCCGAGAGAAATTAACAGCA 1749  
QY 1681 GAAATGAGACCAAGAGATCTCAGTATGCTCGGTGCGGTGCTCAAGGTTGAAAGAACAG 1740  
DB 1750 GAAATGAGACCAAGAGATCTCAGTATGCTCGGTGCGGTGCTCAAGGTTGAAAGAACAG 1809  
QY 1741 GTACAGTCCATAGAAATCCAGCTGAGCTGCTTACTAGACATCTATCAACAGGCTCTTCGG 1800  
DB 1810 GTACAGTCCATAGAAATCCAGCTGAGCTGCTTACTAGACATCTATCAACAGGCTCTTCGG 1869  
QY 1801 AAAGGCTCTGCTCAGCCCTCGCTTGGCTTCAATTCAGATTCACACCTTTTGAATGTGAA 1860  
DB 1870 AAAGGCTCTGCTCAGCCCTCGCTTGGCTTCAATTCAGATTCACACCTTTTGAATGTGAA 1929  
QY 1861 CAGACATCTGACTATCAAGCCCTGTGATAGCAAGAAATCTTTGGGTTCCGCAACAAAC 1920  
DB 1930 CAGACATCTGACTATCAAGCCCTGTGATAGCAAGAAATCTTTGGGTTCCGCAACAAAC 1989  
QY 1921 AGTGGCTCTTATCCAGATCAACTAGTGCACATCTCGAGGCGCTGAGTCTTCTCTG 1980  
DB 1990 AGTGGCTCTTATCCAGATCAACTAGTGCACATCTCGAGGCGCTGAGTCTTCTCTG 2049  
QY 1981 ACGCCAAATGAGTTTCAAGTCCAGACTTTCTACGCGCTTAGCCCTTACTATGACAGTCAA 2040  
DB 2050 ACGCCAAATGAGTTTCAAGTCCAGACTTTCTACGCGCTTAGCCCTTACTATGACAGTCAA 2109

QY 2041 GCAACACAGGTGCCAATTTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACCAATTT 2100  
DB 2110 GCAACACAGGTGCCAATTTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACCAATTT 2169  
QY 2101 GCAACCAAAATAATACCGCACCCCAAGCCAGCAGCCCAACAACTTTTACAGATCCACCT 2160  
DB 2170 GCAACCAAAATAATACCGCACCCCAAGCCAGCAGCCCAACAACTTTTACAGATCCACCT 2229  
QY 2161 CCTCTCCAGCCATCAAGCATCTGCCAGGCCAGAAACTCTGCAACCTTAAACCTTGCAGG 2220  
DB 2230 CCTCTCCAGCCATCAAGCATCTGCCAGGCCAGAAACTCTGCAACCTTAAACCTTGCAGG 2289  
QY 2221 TTACAGAAAGCATTTCTGAGCTCACCACCTGCTTGGCTTGCCTCAAGGAAATGTTTCAG 2280  
DB 2290 TTACAGAAAGCATTTCTGAGCTCACCACCTGCTTGGCTTGCCTCAAGGAAATGTTTCAG 2349  
QY 2281 GTTGCACAGTCAAAATCTCACCAAGGAGCGTTCTATGAGGAAAGCTTTGACATGGGAGGA 2340  
DB 2350 GTTGCACAGTCAAAATCTCACCAAGGAGCGTTCTATGAGGAAAGCTTTGACATGGGAGGA 2409  
QY 2341 GAAACTCTGTTGCTGCTGCTCCATGCTGCCAGGAGCTTTGGCAAAATCTTTGCTGTG 2400  
DB 2410 GAAACTCTGTTGCTGCTGCTCCATGCTGCCAGGAGCTTTGGCAAAATCTTTGCTGTG 2469  
QY 2401 CAAAACCTGATCAGCTCGACCGAGGAATCAATATACAACTTTTTCAGGAGTGAAGTCAAGT 2460  
DB 2470 CAAAACCTGATCAGCTCGACCGAGGAATCAATATACAACTTTTTCAGGAGTGAAGTCAAGT 2529  
QY 2461 GGCTCCAGAGGCGCCCAAGATTTTTTACCCAAATGGAGGGAATCCAAATTTGTTTATACT 2520  
DB 2530 GGCTCCAGAGGCGCCCAAGATTTTTTACCCAAATGGAGGGAATCCAAATTTGTTTATACT 2589  
QY 2521 GATGAAGAGGTGGGTCCTCCGAGGAGACAGACAGACTTTTGTATGCCGCAACCGAGCCT 2580  
DB 2590 GATGAAGAGGTGGGTCCTCCGAGGAGACAGACAGACTTTTGTATGCCGCAACCGAGCCT 2649  
QY 2581 GCCAGGAAGCTGCTTTGATCAGACTCTCTAAGGAGTGAAGTCAAGTCAATCTCAG 2640  
DB 2650 GCCAGGAAGCTGCTTTGATCAGACTCTCTAAGGAGTGAAGTCAAGTCAATCTCAG 2709  
QY 2641 AGCAATTTGAAGGCGAGGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAA 2700  
DB 2710 AGCAATTTGAAGGCGAGGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAA 2769  
QY 2701 TAA 2703  
DB 2770 TAA 2772

## RESULT 5

US-09-949-016-1823  
; Sequence 1823, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1823  
; LENGTH: 2196  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-1823







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; ORGANISM: Homo sapiens
;
; FEATURE:
;
; NAME/KEY: gene
; LOCATION: (1)..(2335)
;
; NAME/KEY: CDS
; LOCATION: (83)..(2170)
US-09-492-361-1

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Query Match 16.9%; Score 518; DB 4; Length 2335;  
Best Local Similarity 60.1%; Pred. NO. 5.3e-145;  
Matches 1102; Conservative 1; Mismatches 566; Indels 165; Gaps 8;

QY	226	TACCGGGGGTGCAGAACTACCTGTACAAACGTGTGTGAGAGACCCCGCGGTGCGGCTTC	285
DB	320	TACCGCGCCTGCAGAACTGGGTCTACAAACGTGTGTGAGCGCGCCCGCGGTGCGGCTTC	379
QY	286	ATCTACACACGCTTTTCGTTTTTCTCCTTGTCTTTTCGTTGCTTGTATTTTGTTCAGTGTCTTCT	345
DB	380	GTCTACACAGTCTTCATATTTTTCGCTGTCTTCACTGCTGCTGTGTCTGTCTGTCTTC	439
QY	346	ACCATCCTGAGCACACAAAATTTGGCCTCAAGTTTGCCTCTTTGATCTCTGGAGTTCGTGATG	405
DB	440	ACTATCAGGAGCACACGGAATTCGCCAACGAGTGTCTCCTCATCTTGGAAATTCGTGATG	499
QY	406	ATTGTCTCTTTTGGTTTGGAGTTTCATCATTCGAAATCTGGTCTCGGGTGTCTGTGTTCGACG	465
DB	500	ATCGTGGTTTTTGGGTTTGGAGTACATCGTCCGGTCTGGTCCGCGCGAGTGTCTGTCGCCG	559
QY	466	TATAGAGATGGCAAGGAAGACTCAGGTTTTCCTCGAAGCCCTCTCTGTGTATAGATACC	525
DB	560	TACGAGATGGCAGGTGCGTCTCCGTTTTCGCAAGAGCCCTCTCTGTCTATCAGCTTC	619
QY	526	ATTGTTCTTATCGCTTCAATAGCAGTTGTTTCTCAAAAACCTCAGGGTAAATATTTTTCGCC	585
DB	620	ATCGTGTTCGTGGCTCGTGGCCGTTCATCGCCGCGGGTACCCAGAGGCACATCTTCGCC	679
QY	586	ACGCTGCACCTCAGAAGTCTCCGTTTCTACAGATCTCCGATCGGTGGCGATCGACCGA	645
DB	680	ACGTCGCGCTCGCAGCATCGCTTCTCTGCAGATCTCGCGATGTGTGGCATGTGACCGC	739
QY	646	AGGGAGGCATTTGGAATTTACTTGGTTTCACTGGTGTATGCTCTACAGCAGGAAATTAATC	705
DB	740	CGCGCGCGCACCTTGAAGAGTCTCGGGCTCAGTGGTCTACGCGCATACGAAGGAGCTGATC	799
QY	706	ACAGCTGTGTACATAGGATTTTGGTCTCTATATTTTTCGTCTTTCCTTGTCTATCTCGTG	765
DB	800	ACCGCTGTGTACATCGGGTTCCTGGTGTCTCATCTTCGGCTCTTCTCTGTTCTACTCGCC	859
QY	766	GAAGAAGATGCCAATAAGAGTTTTTACATATGCAGATGCTCTCTGGTGGGGCACAAATT	825
DB	860	GAGAAGACGCCAACTCCGACTTCTCTCTCTACGCCGACTCGCTCTGTTGGGGACGATT	919
QY	826	ACATTGACAACTATTGGCTATGGAGACAAAACCTCCCTTAATTGGCTGGGAGAAATTCGTT	885
DB	920	ACATTGCAACCATCGGCTATGGTGTACAAGACACCGCACATGGCTGGCGAGGCTCCGT	979
QY	886	TCTGCAGCTTTGCACCTCTTGGCATTTCTTTTTCACATTCTCTCGCGGCATCTTTCGGC	945
DB	980	GTCTCGCTTCGCTTACTTGGGCATCTCTTTCTTTCGCCCTGCTCGCGGCATCTTAGGC	1039
QY	946	TCAGGTTTTTGCATTTAAAGTACAAGAACAAACACCGCCAGAAACACTTTTGAGAAAAGAGG	1005
DB	1040	TCGGCTTTTGCCTTGAAGTCCAGGACGACGACCGCAGAGCACTTCGAGAAGCGGAGG	1099
QY	1006	AACCCAGCTGCAACCTCATTTCACTGTGTGTGGGTAGTTTACGCAGCTGTAGAGAAATCT	1065
DB	1100	ATGCGCGCAGCAACCTCATCCAGGCTGCTTGGCGCTGTACTCCACCGCATATGAGCGCG	1159
QY	1066	GTCTCCATTCGAACCTTGAAGCCACATTGGAAGCCCTTGCACTCTGACAGTATCTTCCAG	1116
DB	1160	GCCTACTGTGACAGCCACTGTACTATATGACAGTATCTTCCCATCTCTCAGAGAGCTG	1219
QY	1117	CCTACCAAGAAAGAAACGAGGGAAGCATCAAGCAGTCAAGAGCTA-----	1161

## RESULT 7

US-09-177-650-88

US-09-177-030-88  
; Sequence 88. Application US/09177650

: : Patent No. 6413719  
; sequence 88; Appl.; PATENT NO. 6413719  
; GENERAL INFORMATION:

; GENERAL INFORMATION: Mark F.

APPLICANT: Leppert, Mark F.  
APPLICANT: Singh, Nanda

; APPLICANT: Singh, Nanda  
: APPLICANT: Charlier, Carole

APPLICANT: Charlier, Carole  
TITLE OF INVENTION: KCNO2 AND KCNO3 - POTASSIUM CHANNEL GENES WHICH ARE

;; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)  
;; TITLE OF INVENTION: AND OTHER EPILEPSIES  
;; FILE REFERENCE: 2323-134  
;; CURRENT APPLICATION NUMBER: US/09/177,650  
;; CURRENT FILING DATE: 1998-10-23

;; EARLIER APPLICATION NUMBER: 60/063,147  
;; EARLIER FILING DATE: 1997-10-24  
;; NUMBER OF SEQ ID NOS: 129  
;; SOFTWARE: PatentIn Ver. 2.0

;; SEQ ID NO 88

;; LENGTH: 2273

;; TYPE: DNA

;; ORGANISM: Mus musculus

;; FEATURE:

;; NAME/KEY: CDS

;; LOCATION: (1)..(2271)

US-09-177-650-88

Query Match 16.9%; Score 517.6; DB 3; Length 2273;

Best Local Similarity 57.7%; Pred. No. 6.8e-145;

Matches 1031; Conservative 2; Mismatches 683; Indels 72; Gaps 4;

Qy	73	GGCTGTCTACTGCTGGGACCCGCGCCACAGCTTGGTGGCGGGGGTGGCTCAGG	132
Db	67	GGCTTGTGGGGCTGGACCCCGCGGCGCCGANTCCACGCGACGCGNCTACTATC	126
Qy	133	GAGAGCGCGCGGCAAGCAGCGGGCGCGGATGAGCTGTGGGGAAGCGCTCTCTTAC	192
Db	127	GCGGGCTCCGAGGCCCCAGCGGGGCGGNCNNTTGGCAAGCGCGGCGGGCGGCG	186
Qy	193	ACGAGTAGCAGAGCTGCGCGCGCAAGCTCAAGTACCGGGGGTGCAGAACTACTGTAC	252
Db	187	GGANCCGGGAAGCCCNANCGCAAGCCCTTACCGCAAGCTGCAGAAATTCCTCTAC	246
Qy	253	AACGTGTGGAGACCCCGCGGTGGCGTTCATCTACACGCTTTCGTTTTCTCTTT	312
Db	247	AACGTGTAGAGCGCGCGCGGTGCGGTTCATCTACCAAGCTACGTTCTCTCTG	306
Qy	313	GTCTTTGGTCTGTTGATTTGTGAGTGTCTTACCATCCCTGAGCACACAAAATTGGCC	372
Db	307	GTCTTCTCTGCTTGTCTTCTGTGTTTCCACCATCAAGAGTAGGAGAGCTCT	366
Qy	373	TCAAGTTCCTCTTGAATCCTGAGTTCGTGATGATGTCGTTTTGTTGGAGTTCATC	432
Db	367	GAGGGGCGCTCTACATCTTGAATCTGACTATCGTGGTATTCGGTGTGAGTACTTT	426
Qy	433	ATTGCAATCTGCTGCGGTGCTGTGTCGATATAGAGATGCAAGAGACTGAGG	492
Db	427	GTGAGGATCTGGGCTGAGGCTGCTGTTGCGGGTATCGAGGCTGGAGGGGAGGCTCAAG	486
Qy	493	TTTGCTCGAAAGCCCTCTGTTGATATAGATACCATGTTCTTATCGCTTCAATAGCAGTT	552
Db	487	TTTGCCAGGAGCGTCTGTGATGATATCATGTTGCTGATGCTCCTCAATGCTGTG	546
Qy	553	GTCTTCGCAAAAATCAGGGTAATATTTTCCACGCTGTCACAGAGTCTCCGTTTC	612
Db	547	CTGGCTGCTGTTCCAGGGCAATGTCTTTCGCAATCTGGGCTTCGAGCTTCGGGTT	606
Qy	613	CTACAGATCTCCGCTGCTGCGCATGCAACGGAAGGGGAGGACCTTGGAAATTAAGT	672
Db	607	TGCAAAATCTTCCGATGATCCGTATGAGACCGGAGGGGTGGACCTGGAAGCTTTGGGA	666
Qy	673	TCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTATATAGGATTTTGGTT	732
Db	667	TCGTTAGTCTACGCTCACAGCAAGGAGCTGGTGTGACTGCTGTATATGCTTCTCTGC	726
Qy	733	CTTATTTTTCCTCTTCTCTGCTCTATCTGTGGAAGAGTGCATTAAGAGTTTCT	792
Db	727	CTCATCTCTGGCTCATTTCTGGTGTACTTGGCAGAAAAGGGTGAAGATGACCACTTTGAC	786
Qy	793	ACATATCAGATGCTCTCTGTTGGGCGACATTAATTCATTCAGCACTTATGCTGAGAC	852
Db	787	ACCTACGAGATGCACTCTGTTGGGGTCTGATCACCTTGACGACCATTTGGCTACGGGAC	846

Qy	853	AAAACCTCCCTAACTTGGCTGGGAAGATTGCTTTCTGACGGCTTTCACCTCTTGGCAAT	912
Db	847	AAGTACCCTCAGACCTTGAACGGGAGGCTGCTGGCAGGACCTTTACCTCATTTGGTGTG	906
Qy	913	TCCTTTCTTTGACATCTCTGCGGCAATCTTCTGGCTCAGGTTTTCGATTTAAAGTACAGAA	972
Db	907	TCGTTCTTTGCTCTCTTCCGGCTGGCATTTTGGGATTCGGCTTTCGCTTGAAGTCAAGAG	966
Qy	973	CAACACCGCCAGAAACACTTTTGAAGAAAGAAACCCAGCTGCAACCTCATTCAGTGT	1032
Db	967	CAGCATCGGCAAAAACACTTTTGAAGAAAGGAAACCTTGGGAGGCTCTGATCCAGTCT	1026
Qy	1033	GTITGGCTAGTTTACGCGAGCTGAT-----	1056
Db	1027	GCCTGGAGATTCTATGCTACTAACTCTCAGCAGCGAGCTGCACTCCAGTGGCAGTAC	1086
Qy	1057	---GAGAAATCTGTTTCCATTGCAACCTGGAAGCACACTTGAAGGCTTGCACACTGC	1113
Db	1087	TACGAGCGNACAGTCACTGTCCCATGTACAGCTTCAAAACTCAAACTATGGGGCTCC	1146
Qy	1114	AG-----CCCTACCAAGAAAGAACAGGGAAGCATCAAGCAGTCAGAAGCTAAGTTTA	1168
Db	1147	AGACTCATCCACTCTGAAACAGCTGAGCTGTGAGGAATCTCAAGAGCAATCTGGA	1206
Qy	1169	AGGAGCGAGTGGCGCATGGCTAGCCCCAGGGGCCAGAGTATTAAGAGCCGCAAGCCTCAG	1228
Db	1207	CTCACCTTTCAGGAAGGAGCCACAGCCAGAGCCATCACAAGCCCCGAGGCGATGGCTGCC	1266
Qy	1229	TAGTGTACAGAGGTCCCAAGCACCGACATCAAGC-----	1265
Db	1267	AAGGAAAGGGGTCTCCCGAGGCCAGACGCTCCGCGGCTCCCGAGTGGGATCAGAGT	1326
Qy	1266	--CGAGGGCAGTCCCAAGTGCAGAGAGCTTGAAGCTTCAACAGCCGAAACCGCTTC	1323
Db	1327	CTTGATACAGCCCGAGCAAGGTGCCCAAGAGCTTGGTGAACCGCAGCCGACACA	1386
Qy	1324	CGGCGCTCGCTGGCGCTCAAAAAGTTCTCAGCCCAAAACAGTGTATGCTGCACACAGCC	1383
Db	1387	CGCCAGGCTTTCGCGCATCAAGGGTGTGCTATCCCGGAGAAATTCAGAAGAAAGCGCTC	1446
Qy	1384	CTTGGCAGCTGATGATGATATGATGAAAGAGTGCAGAGTGTGATGATCAGTGGAGAGAC	1443
Db	1447	CCTGGGAGGACATCGTAGAGGACACAGAGCTGTAACTGCGAGTTTGTGACTGGAAGAT	1506
Qy	1444	CTCACCCACACACTTAAACTGTCTATTCGAGCTATCAGAAATTAATAATTTCAATGTTGCA	1503
Db	1507	CTTACCCCTGGCTCAAGTYAGCATCAGAGCCGTGTGTGTATGCGGTTCTTGTGTATCT	1566
Qy	1504	AAACGGAAGTTTAAAGGAACRTTACGTTCCATATGATGTAAGAGATGTCATTGAAACAATAT	1563
Db	1567	AAGCAAGTTTCAAGAGAGTCTGCGCCCATATGATGTATGAGAGCTCATCGAACAGTAC	1626
Qy	1564	TCGTGCTCATCTGGACATGTTGTGTAGATTAAGAGCCCTTCAACACGCTGTTGATCAA	1623
Db	1627	TCGCTTGGACACTTGGATATGTTGTCCCGCATCAAGAGCTTGCAGACAGAGTGGACAG	1686
Qy	1624	ATTCTCGAAAGGGCAAAATCACATCAGATAAGAGAGCCGAGAGAAATAACAGCAGAA	1683
Db	1687	ATTGTGGGGGGGCCCAACATACCGGATAGGA---TCGACCAAGGCCGAGCGGAA	1743
Qy	1684	CATGAGACCAAGACAGTCTCAGTATGCTCGGTGGGTGTCAGAGTTGAAAAACAGGTA	1743
Db	1744	ACGAGCTGCGCGAAGACCCAGCATGATGGAGCGGCTTGGAAAGGTGGAGAAACAGGTC	1803
Qy	1744	CAGTCCATAGAAUCCAGCTGGAGTGCCTACTAGACATCTATCAACAG	1791
Db	1804	TTGTCCATGGAAGAAAGCTCGACTTCTTGGTGGAGCATCTATACACAG	1851

RESULT 8

US-09-105-058C-22

; Sequence 22, Application US/09105058C

Patent No. 6403360  
; GENERAL INFORMATION:  
; APPLICANT: Blonar, Michael A.  
; APPLICANT: Dworetzky, Steven  
; APPLICANT: Gribkoff, Valentin K.  
; APPLICANT: Levesque, Paul C.  
; APPLICANT: Little, Wayne A.  
; APPLICANT: Neubauer, Michael G.  
; APPLICANT: Yang, Wen-Pin  
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME  
; FILE REFERENCE: 3053-4052  
; CURRENT APPLICATION NUMBER: US/09/105,058C  
; CURRENT FILING DATE: 1998-06-26  
; PRIOR APPLICATION NUMBER: US 60/055,599  
; PRIOR FILING DATE: 1997-08-12  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 2169  
; TYPE: DNA  
; ORGANISM: mouse  
US-09-105-058C-22

Query Match 16.7%; Score 511.6; DB 3; Length 2169;  
Best Local Similarity 58.2%; Pred. No. 4.3e-143;  
Matches 1044; Conservative 0; Mismatches 669; Indels 81; Gaps 5;  
  
Qy 73 GGCCTGCTACTGCTGGGACCCGGCGGCCACGCTTGGTGGCGGGCGGTGGCTGAGG 132  
Db |||||  
Db 67 GGCCTGCTGGGCTGGACCCCGCGCGCCGACCTCCACACGGGCGGCGCTACTCATC 126  
Qy 133 GAGAGCCCGCGGGCAAGACAGGGGCGCGGATGAGCTGCTGGGGAAGCCGCTCTCTTAC 192  
Db |||||  
Db 127 GCGGCTCCGAGGCGCCCAAGCGCGCAGCGCTTTTGAGCAAGCGCGACGGGGCGCG 186  
Qy 193 ACAGTAGCCAGAGCTGCGCGGCAAGCTCAAGTACCGCGGGTGCAGAACTACTGTAC 252  
Db |||||  
Db 187 GGAGCGGGGAAGCCCGGAAGCGCAACGCCCTTCTACCGCAAGCTGCAGAACTTCTCTAC 246  
Qy 253 AACGTGCTGGAGAGACCCCGGGCTGGCGGCTTCTATACCAAGCTTCTGTTTTCTCTCTT 312  
Db |||||  
Db 247 AACGTGCTAGAGCGGCCCGCGGCTGGCGGCTTCTATACCAAGCTTCTCTTTTA 306  
Qy 313 GCTTTGCTGCTGATTTGCTAGTGTGCTTCTACCATCCCTGAGACACAAAATTTGGCC 372  
Db |||||  
Db 307 GCTTTCTCTGCTGCTTCTGCTTTTCCACCATCAAGGAGTACGAGAAGAGCTCT 366  
Qy 373 TCAAGTTCCCTTGATCCTCGAGTTCTGATGATGTTGCTTGTGGTGTGAGTACTATC 432  
Db |||||  
Db 367 GAGGGGCGCTTACATCTTGGAAATCGTACTATCGTGGTATTCGGTGTGAGTACTTT 426  
Qy 433 ATTGAAATCTGCTGCGGGTGTGTTGTCGATATAGAGATGCGAAGGAAGACTGAGG 492  
Db |||||  
Db 427 GTGAGATCTGGCTGCAAGCTGCTGTTGCGGATATCGAGCTGGAGGGCAGGCTCAAG 486  
Qy 493 TTGCTCGAAGCCCTTCTGTTTATAGATACCAATGTTCTTATGCTTCAATAGCAGTT 552  
Db |||||  
Db 487 TTGCGCAGAGCCGCTTCTGTTGATTTGATATCATGTTGCTGATTCCTCCATGCTGTG 546  
Qy 553 GTTCTGCAAAAATCTCAGGTAATATTTTCCAGCTCTGCACCTCAGAGTCTCGTTTC 612  
Db |||||  
Db 547 CTGGCTGTGTTCCAGGGCAATGCTTTTGCACATCTGGCTTCGGAGCTTGGGTTTC 606  
Qy 613 CTACAGATCTCTCGGCTGGTGGACCGAAGGGGAGGCACTTGGAAATTTACTGGGT 672  
Db |||||  
Db 607 TTGCAAAATCTTGGGATGATCCGATAGACCGGAGGGTGGCACTGGAAGCTCTTGGGA 666  
Qy 673 TCAGTGGTTTATGCTCACAGCAAGGAATTAATACAGCTTGGTACATAGGATTTTGGTT 732  
Db |||||  
Db 667 TCGGTAGTCTACGCTCACAGCAAGAGCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 726  
Qy 733 CTTATTTTCTGCTCTTCTGCTCTATCTGTTGGAAAGGATGCGCAATAAAGAGTTTCT 792  
Db |||||

Db 727 CTCAATCTGGCCTCATTTCTGGTGTACTTGGCAGAAAGGGTGAGATGACCACTTTGAC 786  
Qy 793 ACATATGCAGATGCTCTCTGGTGGGACCAATATACATTTGAACAATTTGGCTATGGAGAC 852  
Db |||||  
Db 787 ACCTACGCAGATGCACCTCTGGTGGGTCTGATCACCCCTGACGACCAATTTGGCTACGGGAC 846  
Qy 853 AAAACTCCCTAAGTCTGGCTGGGAAGATTGCTTTCTGAGGCTTTGCACTCTCTGGCAAT 912  
Db |||||  
Db 847 AAGTACCTCAGACCTCGAAACGGGAGGCTGCTGCGCAGGACCTTTTACCTCATTTGGTCTC 906  
Qy 913 TCTTTCTTTGACATCTCTGCGGCAATCTTGGCTCAGGTTTGCATTTAAAGTACCAAGAA 972  
Db |||||  
Db 907 TCGTTCTTTGCTCTCTGCTGGCATTTTGGATTCGGCTTTGCGCTGAAAGTCCAAGAG 966  
Qy 973 CAACACCCCGCAGAAACACTTTGAGAAAGAAAGAACCCAGCTGCAACCTCATTCAGTGT 1032  
Db |||||  
Db 967 CAGCATCGGCAAAAACACTTTGAGAAACGGCGGAACCTCGCGCAGGCTCTGATCCAGTCT 1026  
Qy 1033 GTTTGGGCTAGTTAGCAGCTGATGAGAAAT----- 1063  
Db |||||  
Db 1027 GCCTGGAGATTCTATGCTACTTAACCTCTCAGCACCGACCTGCACTCCACGTGGCAGTAC 1086  
Qy 1064 -----CTGTTTCCATTGCAACCTGGGAAGCCACACTTTGAAGGCTTTGCAC 1107  
Db |||||  
Db 1087 TACGAGCGGACAGTCACTGTCCCATGTACAGACTATCCCATCTCTGAAACAGCTGGAG 1146  
Qy 1108 ACCTGACGCCCTCAAGA-----AAGAAACAAGGGAA 1140  
Db |||||  
Db 1147 CTGCTGAGGAATCTCAAGAGCAAAATCTGGACTCACCTTCAGGAAGAGGCCACAGCCAG 1206  
Qy 1141 GCATCAAGCAGTCAAGAGCTAAGTTTAAAGAGGAG-----TGCGCATGGCTAGCCCCAGG 1197  
Db |||||  
Db 1207 CCATCACAAGTCAAGAGGTCAGTTTGAAGATCTGTCTTCTCAGCCCCCGAGGCAATG 1266  
Qy 1198 GGCCAGAGATTAAGAGCCGACAAAGCTCAGTAGTGACAGAGGTGCTCCCAAGCACCGAC 1257  
Db |||||  
Db 1267 GCTGCCAAGGAAGGGTCTCCAGCCGACAGGCTCGGCGGTCCCCAGTGGGAT 1326  
Qy 1258 ATCAAGCCGAGGCGAGTCCACCAAAAGTCAGAGAGCTGAGGCTTCAACGACCGAACC 1317  
Db |||||  
Db 1327 CAGAGCTTTGATGACAGCCGAGCAAGGTGCCCAAGAGCTGGAGCTTTGGTGACCGCAGC 1386  
Qy 1318 CGCTTCGGCCTCGCTGCGGCTCAAAAGTTCTCAGCCAAACAGCTGATGATGATGCTGAC 1377  
Db |||||  
Db 1387 CGCACGCCAGGCTTTCCGCATCAAGGGTCTGCATCCCGGACAGAAATTCAGAAAGCAAGC 1446  
Qy 1378 ACAGCCCTTGGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1437  
Db |||||  
Db 1447 C---TCCTGGGAGGACATGATAGAGCAACAGAGCTGTAAGTGGAGTGTGACT 1503  
Qy 1438 GAAGACCTCACCCACCACTTAAAACTGTCTATTCGAGCTATCAGAAATTTGAAATTTCAAT 1497  
Db |||||  
Db 1504 GAAGATCTTACCCCTGGCCTCAAAAGTTAGCATCAGAGCTGTGTGTGTGTGTGTGTGTGTG 1563  
Qy 1498 GTTCCAAAACGGAAGTTTAAAGAAACRTTACGCTCCATATGATGTAAGAAAGTGTCAATGAA 1557  
Db |||||  
Db 1564 GTATCTAAGCGAAAAGTTCAAGAGAGAGTCTGCGCCCATATGATGATGATGATGATGATGAT 1623  
Qy 1558 CAATATTCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1617  
Db |||||  
Db 1624 CAGTACTCGGCTGACACTTGGATATGTTGTCCGCATCAAGAGCTGAGCTGAGTCCAGAGTG 1683  
Qy 1618 GATCAAAATTTTGAAGAGGCAATCAATCAGTATGAGAGAGAGCCGAGAGAAATAACA 1677  
Db |||||  
Db 1684 GACCAGATTGTTGGGCGGGGCGCCCAACATAACGATTAAGGA---TCGCACCAAGGCCCA 1740  
Qy 1678 GCAGAAATGAGACCAAGAGCATCTCAGTATGCTCGTTCGGTGGTCAAGTTTGAAGAAA 1737  
Db |||||  
Db 1741 GCGGAAACGGAGCTGCGCCGAGACCCAGCAGTATGATGGAGCGGCTTGGGAAGGTGGAGAAA 1800  
Qy 1738 CAGGTACAGTCCATAGAAATCCAAGCTGACCTGCTACTAGACATCTATCAACAG 1791  
Db |||||  
Db 1801 CAGGCTTTGCTCCATGGAAAAGAGCTGACCTTCTTGGTGGACATCTATACAG 1854

## RESULT 9

US-09-495-050A-303  
; Sequence 303, Application US/09495050A  
; Patent No. 6492505  
; GENERAL INFORMATION:  
; APPLICANT: Roopa, Reddy  
; APPLICANT: Guesler, Karl, J.  
; APPLICANT: Au-Young, Janice  
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED P  
; FILE REFERENCE: PA-0013 US  
; CURRENT APPLICATION NUMBER: US/09/495,050A  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: 60/118,318  
; PRIOR FILING DATE: February 1, 1999  
; NUMBER OF SEQ ID NOS: 305  
; SOFTWARE: PERL Program  
; SEQ ID NO 303  
; LENGTH: 582  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. 6492505 4970006CT1  
US-09-495-050A-303

Query Match 16.6%; Score 509.8; DB 4; Length 582;  
Best Local Similarity 99.4%; Pred. No. 5.4e-143;  
Matches 522; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
Qy 1630 GGAAGGGGCAATACATACATAGATGAAGAGCGAGAGAAATAACAGACAGACATGAG 1689  
Db 1 GGAAGGGGCAATACATACATAGATGAAGAGCGAGAGAAATAACAGACAGACATGAG 60  
Qy 1690 ACCACAGACATCTCAGTATGCTCGGTGGGTGCTCAAGGTTGAAAAACAGGTACAGTCC 1749  
Db 61 ACCACAGACATCTCAGTATGCTCGGTGGGTGCTCAAGGTTGAAAAACAGGTACAGTCC 120  
Qy 1750 ATGAATCCAGCTGGAGTCTACTAGACATCTATCAACAGGTCCTTCGGAAGGCTCT 1809  
Db 121 ATGAATCCAGCTGGAGTCTACTAGACATCTATCAACAGGTCCTTCGGAAGGCTCT 180  
Qy 1810 GCCTCAGCCCTCGCTTTGGCTTCATTCAGTTCGCCACCTTTTGAATGTGAACAGACATCT 1869  
Db 181 GCCTCAGCCCTCGCTTTGGCTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT 240  
Qy 1870 GACTATCAAGCCCTGTGGATAGCAAGATCTTTCCGGTTCGCCACAAACAGTGGTGC 1929  
Db 241 GACTATCAAGCCCTGTGGATAGCAAGATCTTTCCGGTTCGCCACAAACAGTGGTGC 300  
Qy 1930 TTATCCAGATCAACTAGTGCCAACTCTCGAGAGCCCTGCAATCTCTGACGCCAAT 1989  
Db 301 TTATCCAGATCAACTAGTGCCAACTCTCGAGAGCCCTGCAATCTCTGACGCCAAT 360  
Qy 1990 GAGTTCAGTGCCAGACTTCTACGCGCTTAGCCCTACTATGACAGTCAAGCAACACAG 2049  
Db 361 GAGTTCAGTGCCAGACTTCTACGCGCTTAGCCCTACTATGACAGTCAAGCAACACAG 420  
Qy 2050 GTGCCAATTAGTCAAGCGATGGTTCAGAGTGGGAGCCACCAACATTTGCAAAACAA 2109  
Db 421 GTGCCAATTAGTCAAGCGATGGTTCAGAGTGGGAGCCACCAACATTTGCAAAACAA 480  
Qy 2110 ATAAATAGGCAACCAAGCCAGAGCCCAACAACTTTACAGATC 2154  
Db 481 ATAAATAGGCAACCAAGCCAGAG-CCCAACAACTTTACAGATC 524

## RESULT 10

US-09-105-058C-1  
; Sequence 1, Application US/09105058C  
; Patent No. 6403360  
; GENERAL INFORMATION:  
; APPLICANT: Blonar, Michael A.  
; APPLICANT: Dworetzky, Steven  
; APPLICANT: Gribkoff, Valentin K.  
; APPLICANT: Levesque, Paul C.  
; APPLICANT: Little, Wayne A.  
; APPLICANT: Neubauber, Michael G.  
; APPLICANT: Yang, Wen-Pin  
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME  
; FILE REFERENCE: 3053-4052  
; CURRENT APPLICATION NUMBER: US/09/105,058C  
; CURRENT FILING DATE: 1998-06-26  
; PRIOR APPLICATION NUMBER: US 60/055,599  
; PRIOR FILING DATE: 1997-08-12  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 896  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Consensus  
; OTHER INFORMATION: nucleotide sequence as shown in Fig. 16A-16D  
; OTHER INFORMATION: y=c or t; f=a or g; m=a or c; k=g or t; s=g or c;  
; OTHER INFORMATION: w=a or t; h=a, c, or t; b=g, t, or c; v=g, c, or a  
US-09-105-058C-1

Query Match 15.2%; Score 465.4; DB 3; Length 896;  
Best Local Similarity 53.7%; Pred. No. 1.9e-129;  
Matches 460; Conservative 231; Mismatches 162; Indels 4; Gaps 2;  
Qy 199 AGCCAGAGCTGCCGGCCCAACAGTACCGGGGGTGCAGAACTACCTGTACAACGTG 258  
Db 13 RGSNRSCCMSYSAAAGMGMAACGCCWSTACCGSMRSMTCARAMTTTSMCTACRAGYS 72  
Qy 259 CTGGAGAGACCCCGCGCTGGGGTTCATCTACACGCTTTGTTTTCTCTCTGCTTT 318  
Db 73 CTRGAGMGRCSCGGCTGGGGTSMYTTACACGCTWSGTGTTCTCTBHTDGTYS 132  
Qy 319 GGTTCGTGATTTTGTTCAGTGTTCCTACCATCCTCGACACACAAATTTGGCCTCAAGT 378  
Db 133 KSSTGCTYBTKCTGCTGHS-YKCCACMWTCAAGAGTAYGAGAMKRYTCBGRGRS 191  
Qy 379 TGCTCTTGATCTCTGGAGTTCTGATGATTTGCTTTGTTGGAGTTTCATCATTCGA 438  
Db 192 KSSCTYWSMTWTGGARAYMKRCVATYKTSRTVTYGGHGYBGAGTWYKYKTCWGR 251  
Qy 439 ATCTGCTCGGGTTCCTGCTGTCGATATAGAGATGGCAAGAACTGAGTTTCT 498  
Db 252 ATCTGGCYCGWGMTYTSYTCGCRATCMRWGGCTGGMGSGMGRCTSAAGTTTGCC 311  
Qy 499 CGAAAGCCCTTCTGTGTTATAGATACCATTTGTTCTTCAATAGCAGTTGTTCT 558  
Db 312 MGGAARCCVTSYRTGTGTGAYATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 371  
Qy 559 GCAAAAACCTCAGGTAATATTTTGGCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 618  
Db 372 GYBGHMMCCAGCAAYGVYTKGVACVCTY---CTBCGRAGCYTGGSTTCVTRCAR 428  
Qy 619 ATCTCCGATGTGCGCATGGACCGAAGGGAGGCACTTGGAAATTTACTGGGTTCTAGT 678  
Db 429 ATYTRCGATGTTSCGBATGGACCGMGHGGCACTTGGAAAGCTBYTGGGTCGTYV 488  
Qy 679 GTTTATCTCACAGAGGAATTAATCACAGCTTGGTACATAGATTTTGGTTCTTATT 738  
Db 489 RTCTRYGCYACAGCAARGARTSRTSACKGCTGGTGTACATYGGYTTCTBWSHCTCATC 548  
Qy 739 TTTTCTGCTTTCTCTGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 798  
Db 549 CTCKCYTCRTYCTKGTSTACTYGGYGAARSSDGAAGRWBGAYSMTTYGASACCTAY 608  
Qy 799 GCAGATCTCTCTGGTGGGCAATTTACATTCAGCACTATTGCTGCTGCTGCTGCTGCTGCT 858  
Db 609 GCRGATGCTSTGTTGGGCTGATCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 668



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Db      1707  TGACWTCTCTCATTTGAGACATGATCCCTCCCTTAAAGGCTGCCATCCGAGCTGTCAGAAT 1766
QY      1485  TATGAAATTTTCATGTTGCGAAACCGAAGTTTAAAGGAAACRRTTACGTCCATCATGATGTAAA 1544
Db      1767  TCTACAGTTCCTGCTATATATAAAAAAGTTCAAGGAGACGCTTGAGGCCCTTATGATGTGAA 1826
QY      1545  AGATGTCATTGAACAATATTCTGCTGGTCTCATCTGGACATGTTGTGTAGAATTTAAAGCCT 1604
Db      1827  AGATGTGATTGAGCAGTATTTCGGCCGACATCTTGACATGCTTTCCAGGATAAAGTACCT 1886
QY      1605  TCAACACAGCTGTTGATCAAAATCT 1628
Db      1887  ACAGACAAGAAATAGATGATTTT 1910

RESULT 12
US-09-105-058C-26
; Sequence 26, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blanz, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Grikoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-pin
; TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 2565
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-105-058C-26

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QY	433	ATTGGAATCTGCTGCGGTTGCTGTCTCAATATAGAGGATGGCAAGAACTGTGAG	492
DB	463	TTGAGGATCTGGGCTGCTGGATGTTTGTCTCCGATACAAAGGCTGGCGGGCCGACTGAAG	522
QY	493	TTTGTCTGAAAGCCCTTCTGTGTTATAGATACCATTTGTTCTTATCGCTTCAATAGCAGTT	552
DB	523	TTTGGCAGGAAGCCCTGTGCATGTTGGACATCTTTGTCTGATTTGCCCTCTGTGCCAGTG	582
QY	553	GTTTCTGCAAAACTCAGGGTAATATTTTTTGGCAGCTGTGCACCTCAGAAAGTCTCGGTTTC	612
DB	583	GTTTGTCTGGGAAACCAAGGCAATGTTCTTGGCCACCT---CCCTGCGAAAGCCCTGCGCTTC	639
QY	613	CTACAGATCCTCGCATGTGCGCATGGAACCGAAGGGAGGCACCTTGGAAAATTACTGGGT	672
DB	640	CTGCAGATCCTCGGCATGCTCGGATGGACCGAGAGGTGGCACCTGGAAAGCTTCTGGGC	699
QY	673	TCAGTGTGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGATATTTTGGTT	732
DB	700	TCAGCCATCTGTGCCACAGCAAGAACTCATCAGGCCGTGGTACATCGGTTTTCTTGACA	759
QY	733	CTTAATTTTTTGGTCTTCTGTCTATCTGGTGGAAAAGGATGCC-----	777
DB	760	CTCATCTTCTTCTCAATTTCTGTCTACTCTGGTTGAAAGACGCTCCAGAGGTGGATGCA	819
QY	778	-----AATAAGAGTTTTCTACATATGCAGATGCTCTCTGTGTGGGGCAC	822
DB	820	CAAGGAGAGGAGTGAAGAGGAGTTTGAGACTATGCAGATGCCCTGTGTGTGGGCCCTG	879
QY	823	ATTACATTCACAACTATTGGCTATGGAGCAAAATCTCCCTTAATCTTGGCTGGGAAGATTG	882
DB	880	ATCACACTGGCCACCATTTGGCTATGGAGCAAGACACCCAAACCGTGGGAAGCCCTCTG	939
QY	883	CTTTCTGCAAGCTTTGCACCTCTTGGCATTTCTTCTTTGGCACTTCTCTCCCGCATCTT	942
DB	940	ATTGCCCGCACCTTTTCTTAATTTGGCGTCTCTTTTTTGGCCCTTCCAGGGGCATCCTG	999
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QY	1003	AGGAACCCAGCTGCGAAACCTCATTAGTGTGTTTGGGTAGTTATCGCAGCTGATGAGAA	1062
DB	1060	AGGAAGCCAGCTGCTGAGCTCAATTCAGGTGCGCTGGAGGATATATGCTACCAACCCCAAC	1119
QY	1063	TCTGTTTTCATTGCAACCTGGAAGCCACACTTGAAGGCCTTGACACCTGCAAGCCCTACC	1122
DB	1120	AGGATTGACCTGGTGGGACATGGAGATTTATGAATCAGTCGTCTCTTTTCTTTCTTCT	1179
QY	1123	AAGAAAGAACAGGGGAAGCATCAAGCAGTTCAGAGACTAAGTTTAAAGGAGCGAGTGGCG	1182
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Qy	1483	ATTATGAAATTTCAATGTTGCAAAACCGGAAGTTTAAAGAAACRTTTCGTCCATATGATGTA	1542
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Db	1576	AAGGATGTGATTGACGAGTATTTCTCGCGGGCATCTCGACATGCTTTCCAGGATAAAGTAC	1635
Qy	1603	CTTCAAACACGTGTTGATCAAAATTCCT	1628
Db	1636	CTTCAGACGAGAAATAGATATGATTTT	1661

## RESULT 13

```

US-09-177-650-6
; Sequence 6, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCNO2 AND KCNO3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; TITLE OF INVENTION: AND OTHER EPILEPSIES
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 2914
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)..(2634)
; FEATURE:
; NAME/KEY: allele
; LOCATION: (840)
; OTHER INFORMATION: The polymorphism of a T to a C at this position
; OTHER INFORMATION: has appeared in one individual.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (947)
; OTHER INFORMATION: The missense mutation from a G to a T occurs at
; OTHER INFORMATION: this position in a BFNC family.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (678)
; OTHER INFORMATION: This position is polymorphic for C or T.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (750)
; OTHER INFORMATION: This position is polymorphic for T or C.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1089)
; OTHER INFORMATION: This position is polymorphic for G or C.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (2598)
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US-09-177-650-6

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	Query Match	15.08;	Score 460.8;	DB 3;	Length 2914;
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DB	712	CTGCAGATCTGGCATGTGCGGATGGACCGGAGAGTGGACCTTGGAAAGTCTCTGGGC	771
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DB	772	TCAGCCATCTGTGCCACAGCAAGAACTCATACGGCTGGTACATCGGTTTCTTGACA	831
QY	733	CTTAATTTTTCGTTTCTTCTGTCTATCTGGTGGAAGATGCC-----	777
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QY	778	-----AATAAGAGTTTCTACATATGCAGATGCTCTCTGTGGGGCACA	822
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

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Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 4: gb\_on.\*
- 5: gb\_ov.\*
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- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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13	2635.4	85.8	2772	6	AX565635 Sequence
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ALIGNMENTS

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DEFINITION Sequence 1 from patent US 6649371.  
ACCESSION AR430568  
VERSION AR430568.1 GI:40191384  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 3137)  
AUTHORS Jentsch, T.J.  
TITLE Potassium channel KCNQ5 and sequences encoding the same  
JOURNAL Patent: US 6649371-A 1 18-NOV-2003;  
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Location/Qualifiers  
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Db 1981 GAGTTTCAGTCCCGCAGACTTTTCTACGGCTTACGCCCTTATGCAAGTCAAGCAACAG 2040  
Qy 2050 GTGCCAATTAAGTCAAAAGCGATGCTCAGCAGTGGCAGCCACCAACACCTTTCGCAACCAA 2109  
Db 2041 GTGCCAATTAAGTCAAAAGCGATGCTCAGCAGTGGCAGCCACCAACACCTTTCGCAACCAA 2100  
Qy 2110 ATAAATACGCGCACCCAGCCAGAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA 2169  
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Db 2161 GCCATCAAGCATCTGCCAGGCGAGAACTCTGCACTTAACTTACCTTCAGGCTTACAGGAA 2220  
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Db 2221 AGCATTTCTGACGTCACCACTGCTTGTTCCTTCCAAAGGAAATTTTCAAGTTGCAACAG 2280  
Qy 2290 TCAATCTCACAAGGACCGTTCTATGAGGAAAGCTTTCATGCGGAGGAGAACTCTG 2349  
Db 2281 TCAATCTCACAAGGACCGTTCTATGAGGAAAGCTTTCATGCGGAGGAGAACTCTG 2340  
Qy 2350 TTGCTGCTGCTGCTCCATGCTCCGAGACTTGGGCAAACTTTTGTGCTGTGCAAAACCTG 2409  
Db 2341 TTGCTGCTGCTGCTCCATGCTCCGAGGACTTGGGCAAACTTTTGTGCTGTGCAAAACCTG 2400  
Qy 2410 ATCAGGTGCAAGGAGAACTGAATATACAACTTTTCAAGGAGTGAAGTCAAGTGGCTCCAGA 2469  
Db 2401 ATCAGGTGCAAGGAGAACTGAATATACAACTTTTCAAGGAGTGAAGTCAAGTGGCTCCAGA 2460



QY 850 GACAAAACCTCCCTAACTTGGCTGGGAAGATTGCTTTCTCGAGCCTTTGCACTCCTTGGC 909  
DB 841 GACAAAACCTCCCTAACTTGGCTGGGAAGATTGCTTTCTCGAGCCTTTGCACTCCTTGGC 900  
QY 910 ATTTCTTTCTTTGACATCTTCTGCGGCACTTTCTGGCTCAGGTTTTCATTAAGTACAA 969  
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QY 970 GAAACAACCCCGCAGAACACTTTGAGAAAAGAGAACCCAGCTGCGCAACCTCATTCAG 1029  
DB 961 GAAACAACCCCGCAGAACACTTTGAGAAAAGAGAACCCAGCTGCGCAACCTCATTCAG 1020  
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QY 1330 TCGCTGGCGCTCAAAAGTTCTCAGCCAAAACAGTATAGTGTATCAGTGGAAAGCCTCACC 1389  
DB 1321 TCGCTGGCGCTCAAAAGTTCTCAGCCAAAACAGTATAGTGTATCAGTGGAAAGCCTCACC 1380  
QY 1390 ACTGATGATGATATGATGAAAAGAGTGCAGTGTGATGTATCAGTGGAAAGCCTCACC 1449  
DB 1381 ACTGATGATGATATGATGAAAAGAGTGCAGTGTGATGTATCAGTGGAAAGCCTCACC 1440  
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QY 1690 ACCACAGACCATCTCAGTATGCTCGGTGCGGTGGTCAAGGTTGAAAGGTAAGTACAGTCC 1749  
DB 1681 ACCACAGACCATCTCAGTATGCTCGGTGCGGTGGTCAAGGTTGAAAGGTAAGTACAGTCC 1740  
QY 1750 ATGAAATCCAGCTGGAGCTGCTACTAGACATCTATCAACAGTCTTCCGAAAGGCTCT 1809  
DB 1741 ATGAAATCCAGCTGGAGCTGCTACTAGACATCTATCAACAGTCTTCCGAAAGGCTCT 1800  
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QY 1870 GACTATCAAGCCCTGTTGGATAGCAAGATCTTTGGGTTCCGCAACAAACAGTGGCTGC 1929  
DB 1861 GACTATCAAGCCCTGTTGGATAGCAAGATCTTTGGGTTCCGCAACAAACAGTGGCTGC 1920  
QY 1930 TTATCCAGATCAACTAGTGGCAACATCTCGAGAGGCGCTGCGAGTTCTTCTGCGCCAAAT 1989

DB 1921 TTATCCAGATCAACTAGTGGCAACATCTCGAGAGGCGCTGCGAGTTCAATCTGCGCCAAAT 1980  
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QY 2290 TCAATCTCACCAAGCAGCTTCTATGAGGAAAGCTTTGACATGGAGGAGAACTCTG 2349  
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QY 2350 TTGCTGCTGCTGCCATGCTGCGAAGGACTTTGGGCAATCTTTGCTGTCGCAAACTCTG 2409  
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DB 2461 GGCAGCCAGATTTTACCCCAATGAGGAGTCCAAATGTTGTTATATACTGATGAAGAG 2520  
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DB 2521 GTGGGTCGCCAAGAGACAGAGACACACTTTTGTGATGCGCGCACCGAGCCTGCGAGGAA 2580  
QY 2590 GCTGCTTTGCTGATCAGACTCTTAAGGAGTGAAGGTCAGATCATCTCAGAGCATTTGT 2649  
DB 2581 GCTGCTTTGCTGATCAGACTCTTAAGGAGTGAAGGTCAGATCATCTCAGAGCATTTGT 2640  
QY 2650 AAGCAGGAGAAAGTACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2709  
DB 2641 AAGCAGGAGAAAGTACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700  
QY 2710 CATTTTCTTCCAGGATAGCTTCTTATAGCCATACATATCATTCATGCACTATTTTCG 2769  
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QY 2770 AAAGCCCTTCTAAAGAGTTGAAATTCAGAAATTCGGAAGAAATGAAAGGCGAGTTTATA 2829  
DB 2761 AAAGCCCTTCTAAAGAGTTGAAATTCAGAAATTCGGAAGAAATGAAAGGCGAGTTTATA 2820  
QY 2830 AGCCCGTTACCTTTTAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 2889  
DB 2821 AGCCCGTTACCTTTTAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 2880  
QY 2890 GCATCGCATTAACCCACTCATTTAGTAACTGAGTTTAAAGGCTGAGAAACCA 2949  
DB 2881 GCATCGCATTAACCCACTCATTTAGTAACTGAGTTTAAAGGCTGAGAAACCA 2940  
QY 2950 AACACAGCTAATGCTATGGGTGATGAATGATGAATGATGAATGATGAATGATGAATGATGA 3009  
DB 2941 AACACAGCTAATGCTATGGGTGATGAATGATGAATGATGAATGATGAATGATGAATGATGA 3000  
QY 3010 ACACGTATTTTGAATTTATGGGATGAACACCTTCAATTTCA 3053

Db	3001	ACACTGTATTGAAATTATGGAGTAAACACCTTCAAAATTCA	3044	Db	61	GACGCGCTGCTACTGCTGGGCAACCGCGCGGCACGCTCGGTGGCGGGGGTGGCGCTG	120
RESULT 3	AF202977			Qy	130	AGGAGAGCCGCGCGGGCAAGCAGCGGGCCCGGATGAGCCCTGCTGGGGAAGCCGCTCTCT	189
LOCUS	AF202977	3137 bp mRNA linear PRI 01-AUG-2000		Db	121	AGGAGAGCCGCGCGGGCAAGCAGCGGGCCCGGATGAGCCCTGCTGGGGAAGCCGCTCTCT	180
DEFINITION	AF202977	Homo sapiens potassium voltage-gated channel, KQT-like subfamily, member 5 (KCNQ5) mRNA, complete cds.		Qy	190	TACAGGATAGCAGAGCTGCCGGCGCAACGCTCAAGTACCGCGGGTGCAGAACTACCTG	249
ACCESSION	AF202977			Db	181	TACAGGATAGCAGAGCTGCCGGCGCAACGCTCAAGTACCGCGGGTGCAGAACTACCTG	240
VERSION	AF202977.1	GI:7798695		Qy	250	TACAACTGCTGGAGAGACCCCGGCTGGGCGTTTCATCTACCAACGCTTTCGTTTTCTC	309
KEYWORDS				Db	241	TACAACTGCTGGAGAGACCCCGGCTGGGCGTTTCATCTACCAACGCTTTCGTTTTCTC	300
SOURCE				Qy	310	CTTGCTTTGGTTCCTTTGATTTTCTCAGTGTGTTTCTACCATCCCTGAGCAGACAAAATTG	369
ORGANISM				Db	301	CTTGCTTTGGTTCCTTTGATTTTCTCAGTGTGTTTCTACCATCCCTGAGCAGACAAAATTG	360
				Qy	370	GCCTCAAGTTGCCTTCTGATCTCTGAGTTCGTGATGATTCGTCTTTTGGTTTGGAGTTC	429
REFERENCE				Db	361	GCCTCAAGTTGCCTTCTGATCTCTGAGTTCGTGATGATTCGTCTTTTGGTTTGGAGTTC	420
AUTHORS				Qy	430	ATCATTCGAATCTCGTCTGCGGGTTCGTGTTGTCGATATAGAGGATGCAAGGAAGACTG	489
				Db	421	ATCATTCGAATCTCGTCTGCGGGTTCGTGTTGTCGATATAGAGGATGCAAGGAAGACTG	480
TITLE				Qy	490	AGSTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCAATGTTTCTTATCGCTTCAATAGCA	549
JOURNAL				Db	481	AGSTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCAATGTTTCTTATCGCTTCAATAGCA	540
MEDLINE				Qy	550	GTGTTTCTCGAAAACTCAGGGTAATATTTTTCGACGCTGCACTCAGAGTCTCCGT	609
PUBMED				Db	541	GTGTTTCTCGAAAACTCAGGGTAATATTTTTCGACGCTGCACTCAGAGTCTCCGT	600
REFERENCE				Qy	610	TTCTACAGATCTCTCCGATGTCGCGATGACCGAAGGGGAGGACCTTGGAAATTTACTG	669
AUTHORS				Db	601	TTCTACAGATCTCTCCGATGTCGCGATGACCGAAGGGGAGGACCTTGGAAATTTACTG	660
				Qy	670	GGTTCAGTGTGTTATGCTCAGCAAGGAAATTAATCAAGCTGCTGATACATAGGATTTTGG	729
				Db	661	GGTTCAGTGTGTTATGCTCAGCAAGGAAATTAATCAAGCTGCTGATACATAGGATTTTGG	720
FEATURES				Qy	730	GTTCCTATTTTTCGTCCTTCTGCTATCTGCTGGGAAAGGATGCCAATAAGAGTTT	789
source				Db	721	GTTCCTATTTTTCGTCCTTCTGCTATCTGCTGGGAAAGGATGCCAATAAGAGTTT	780
gene				Qy	790	TCTACATATGAGATGCTCTCTGCTGGGCAATTAATCAATGACAACTATTGGCTATGGA	849
CDS				Db	781	TCTACATATGAGATGCTCTCTGCTGGGCAATTAATCAATGACAACTATTGGCTATGGA	840
				Qy	850	GACAAAACCTCCCTAACTTGGCTGGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC	909
				Db	841	GACAAAACCTCCCTAACTTGGCTGGGGAAGATTGCTTTCTGCAGGCTTTGCACTCCTTGGC	900
				Qy	910	ATTTCTTTTTCGCTCTGCGGCAATTCCTTGGCTCAGGCTTTTGCATTTAAAGTACAA	969
				Db	901	ATTTCTTTTTCGCTCTGCGGCAATTCCTTGGCTCAGGCTTTTGCATTTAAAGTACAA	960
				Qy	970	GAACAACACCGCCAGAAACACTTTTGAGAAAAGAGGAACCCAGCTGCCAACCTCATTCAG	1029
				Db	961	GAACAACACCGCCAGAAACACTTTTGAGAAAAGAGGAACCCAGCTGCCAACCTCATTCAG	1020
ORIGIN				Qy	1030	TGTGTTTGGCGTAGTTACGAGCTGATGAGAAATCTGTTTTCATTTGCAACTGGAAGCCA	1089
				Db	1021	TGTGTTTGGCGTAGTTACGAGCTGATGAGAAATCTGTTTTCATTTGCAACTGGAAGCCA	1080
				Qy	1090	CATTGGAAGGCTTGACACCTGCGAGCCCTACCAAGAAAGAACCAAGGGAGGATCAAGC	1149
				Db	1081	CATTGGAAGGCTTGACACCTGCGAGCCCTACCAAGAAAGAACCAAGGGAGGATCAAGC	1140
				Qy	1150	AGTCAGAGCTTAAGTCTTTTAAAGGAGCGAGTGGCGATGCTAGCCCCAGGGGCGAGTATT	1209
				Db	1141	AGTCAGAGCTTAAGTCTTTTAAAGGAGCGAGTGGCGATGCTAGCCCCAGGGGCGAGTATT	1200

QY	2290	TCAAA	TCTCACC	AGGACCG	TTCTATG	AGGAAAA	AGCTTTG	ACATGGG	AGAGAA	ACTCTG	2349
DB	2281	TCAAA	TCTCACC	AGGACCG	TTCTATG	AGGAAAA	AGCTTTG	ACATGGG	AGAGAA	ACTCTG	2340
QY	2350	TTGTCTG	TCTGTCC	ATGGTCCG	GAAGACTT	GGCAAA	TCTTTGT	CTGTG	CAAAAC	CTG	2409
DB	2341	TTGTCTG	TCTGTCC	ATGGTCCG	GAAGACTT	GGCAAA	TCTTTGT	CTGTG	CAAAAC	CTG	2400
QY	2410	ATCAG	TGTCAG	CCGAGG	ACTGAAT	ATACAA	CTTTTC	CAGGAG	TGAGTCA	AGTGG	2469
DB	2401	ATCAG	TGTCAG	CCGAGG	ACTGAAT	ATACAA	CTTTTC	CAGGAG	TGAGTCA	AGTGG	2460
QY	2470	GGCAG	CAAGA	ATTTTTC	CCCCAA	ATGGAG	GGAATCC	CAAA	TGTTTAT	AACATGA	2529
DB	2461	GGCAG	CAAGA	ATTTTTC	CCCCAA	ATGGAG	GGAATCC	CAAA	TGTTTAT	AACATGA	2520
QY	2530	GTGGT	CTCCG	AGAGAC	AGAGAC	GAGAC	CTTTTGT	ATGCG	CACCG	ACGCTGC	2589
DB	2521	GTGGT	CTCCG	AGAGAC	AGAGAC	GAGAC	CTTTTGT	ATGCG	CACCG	ACGCTGC	2580
QY	2590	GCTGC	CTTTGC	ATCAG	ACTCTTA	AGGACTG	GGAAGT	TCAG	ATCA	TCTCAG	2649
DB	2581	GCTGC	CTTTGC	ATCAG	ACTCTTA	AGGACTG	GGAAGT	TCAG	ATCA	TCTCAG	2640
QY	2650	AAGC	GAGG	AGAA	AGTAC	AGTGC	CTCAT	GTCAA	ACTG	AAATAG	2709
DB	2641	AAGC	GAGG	AGAA	AGTAC	AGTGC	CTCAT	GTCAA	ACTG	AAATAG	2700
QY	2710	CATTTT	CTTTC	CAGG	CATAC	AGTCT	CTTTAG	CCAT	ACATAT	CATTG	2769
DB	2701	CATTTT	CTTTC	CAGG	CATAC	AGTCT	CTTTAG	CCAT	ACATAT	CATTG	2760
QY	2770	AAAG	CCCTTCT	AAAA	GTGAA	ATTG	CAAA	ATGCG	GAAG	ACATGA	2829
DB	2761	AAAG	CCCTTCT	AAAA	GTGAA	ATTG	CAAA	ATGCG	GAAG	ACATGA	2820
QY	2830	AGCC	GGTTA	CTTTTAA	TTCAT	GCAAA	TGCTTT	AGG	GATGG	CTTAAAA	2889
DB	2821	AGCC	GGTTA	CTTTTAA	TTCAT	GCAAA	TGCTTT	AGG	GATGG	CTTAAAA	2880
QY	2890	GCAT	CGAC	ATTAA	CCCA	CTCAT	TTAG	TAA	TGTACT	TTAGAT	2949
DB	2881	GCAT	CGAC	ATTAA	CCCA	CTCAT	TTAG	TAA	TGTACT	TTAGAT	2940
QY	2950	AA	CACAG	CTTA	TGCTAT	GGGG	TGAT	TGA	ATAT	TGTCA	3009
DB	2941	AA	CACAG	CTTA	TGCTAT	GGGG	TGAT	TGA	ATAT	TGTCA	3000
QY	3010	ACA	CTGTAT	TTGAA	TTAT	TGG	AGTAA	CA	ACCTT	CAAA	3053
DB	3001	ACA	CTGTAT	TTGAA	TTAT	TGG	AGTAA	CA	ACCTT	CAAA	3044

RESULT 4  
BD275572  
LOCUS ..... 3718 bp DNA linear  
BD275572 ..... Vectors-Cloned Potassium Channel. PAT 17-JUL-2003

ACCESSION	BD275572	GI:33085340
ACCESSION	BD275572.1	

VERSION  
KEYWORDS

REVIEWED	SOURCE	Homo sapiens (human)

ORGANISM      Homo sapiens

Eukaryota; Metazoa;  
Mammalia; Eutheria;

REFERENCE 1 (bases 1 to 3718)  
Mammalia; Eutheria;

REFERENCE  
AUTHORS  
I (bases 1 to 3718)  
Metzker, M.L.; Li, W.

AUTHORS	MECHANISM, n.d.	Novel Human Voltage-
TITLE		

JOURNAL Patent: JP 200254370

Merck and Co Inc

COMMENT	OS	Homo Sapiens
	OS	ID 2002E43768-

PN JF 2002543/68-1  
24-DEC-2002

PD	24-DEC-2002	
PF	10-APR-2000	JP

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QY	1270	GGCAGTCCCAACCAAGTGCAGAAGAGTGGAGCTTCAACGACCGAACCCGCTTCGGGCC	1329
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DB	1321	TGCGTCGGCCTCAAAAGTTCTCAGCCCAAAACAGTGTAGTGTGACACAGCCCTTGGC	1380
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QY	1810	GCCTCAGCCCTCGCTTGGCTTCATCCAGTCCCACTTTTGAATGTGAACAGACATCT	1869
DB	1801	GCCTCAGCCCTCGCTTGGCTTCATCCAGTCCCACTTTTGAATGTGAACAGACATCT	1860
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DB	1861	GACTATCAAGCCCTGTGGATAGCAAAAGATCTTTTCGGGTTTCGCACAAAACAGTGGCTGC	1920
QY	1930	TTATCCAGATCAACTAGTGTGCCAAATCTCGAGAGCCTGCAGTTCAATCTGACGCCAAT	1989
DB	1921	TTATCCAGATCAACTAGTGTGCCAAATCTCGAGAGCCTGCAGTTCAATCTGACGCCAAT	1980
QY	1990	GAGTTCAGTGGCCGACATTTCTACGCGTTAGCCCTACTATGACACAGTCAAGCAACACAG	2049
DB	1981	GAGTTCAGTGGCCGACATTTCTACGCGTTAGCCCTACTATGACACAGTCAAGCAACACAG	2040
QY	2050	GTGCCAAATAGTCAAGCGATGGCTCAGCAGTGGAGCGCAACCAACCAATTCGAACCAA	2109
DB	2041	GTGCCAAATAGTCAAGCGATGGCTCAGCAGTGGAGCGCAACCAACCAATTCGAACCAA	2100
QY	2110	ATAAATACGGCACCCBAAGCCAGCGCCCAACACTTTTACAGATCCCACTCTCTCCCA	2169
DB	2101	ATAAATACGGCACCCBAAGCCAGCGCCCAACACTTTTACAGATCCCACTCTCTCCCA	2160
QY	2170	GCCATCAAGCATCTGCCAGGCGAGAACTCTGCAACCTTAAACCTGACGGTTACAGAA	2229
DB	2161	GCCATCAAGCATCTGCCAGGCGAGAACTCTGCAACCTTAAACCTGACGGTTACAGAA	2220
QY	2230	AGCAATTCGACGTGACCACTGCTTGTGCTTCCAAAGGAAATGTTTCAGTTGACACAG	2289
DB	2221	AGCAATTCGACGTGACCACTGCTTGTGCTTCCAAAGGAAATGTTTCAGTTGACACAG	2280



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FEATURES	source	Location/Qualifiers
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Query Match		
Best Local Similarity 95.6%; Score 2936.2; DB 6; Length 3718;		
Matches 2941; Conservative 1; Mismatches 9; Indels 0; Gaps 0;		
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Db	78	ACTGCTGAGNACTCGCGCGGTGGCGCTGAGGGAGAGCCGCCGGGGCAAGCAGGGGGCCCCGG 137
Qy	163	ATGAGCTGCTGGGGAAGCCGCCTCTTTACACGAGTAGCCAGAGCTGCCCGCGCAACGTC 222
Db	138	ATGAGCTGCTGGGGAAGCCGCCTCTTTACACGAGTAGCCAGAGCTGCCCGCGCAACGTC 197
Qy	223	AAGTACC GGCGGTGCAGAACTACTGTACAACGTGCTGGAGAGACCCC CGCGCTGGCGC 282
Db	198	AAGTACC GGCGGTGCAGAACTACTGTACAACGTGCTGGAGAGACCCC CGCGCTGGCGC 257
Qy	283	TTCATCTACCACGCTTTTCGTTTTTCTCCTTGCTTTTGTGTTGCTTGATTTTGTCAGTGT 342
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Qy	343	TCTACCATCCCTGAGCACACAAAATTGGCCTCAAAGTTGCCTCTTCATCTCGAGTTCGTG 402
Db	318	TCTACCATCCCTGAGCACACAAAATTGGCCTCAAAGTTGCCTCTTCATCTCGAGTTCGTG 377
Qy	403	ATGATTGTCGTCCTTTGGTTTGGAGTTCATCATTCGAAATCTGGTCTGCGGGTTCGTGTG 462
Db	378	ATGATTGTCGTCCTTTGGTTTGGAGTTCATCATTCGAAATCTGGTCTGCGGGTTCGTGTG 437
Qy	463	CGATATAGAGATGCGCAGGAAGACTGAGGTTTCGTCGAAAGCCCTCTCTGTGTTATAGAT 522
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Qy	583	GCCAAGTCTGCACTCAGAAGTCTCCGTTTTCCTACAGATCTCTCCGCATGGTCGCATGGAC 642
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Db	858	CTTTCTGAGGCTTTTGCACTCTCTTGGCACTTTCTTTCTTTGTCAC TTTCTGCGGCATCTT 917
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ACCESSION AR393778
VERSION AR393778.1 GI:40120748
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3074)
AUTHORS Steinmeyer,K., Lerche,C., Scherer,C., Seebom,G. and Busch,A.E.
TITLE Nucleic acid molecule encoding the potassium channel protein, KCNQ5
JOURNAL Patent: US 6617131-A 1 09-SEP-2003;
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AUTHORS	1		
TITLE	Lerche, C., Scherer, C., Seebohm, G., Busch, A. and Steimmeyer, K.		
JOURNAL	Potassium channel protein knnds, a target for diseases of central nervous system and cardiovascular system		
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE 1			
AUTHORS Argentieri,T.M. and Sheldon,J.H.			
TITLE Methods of selecting compounds for modulation of bladder function			
JOURNAL Patent: US 0232960-A 5 25-APR-2002;			
Wyeth (US)			
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Matches 2861; Conservative 1; Mismatches 7; Indels 0; Gaps 0;			
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Db	206	GGCAGCGGCATGAAGATGTGGAGTCTGGCCGGGCGAGGTCGTCTGAACTCGGCAGCC	265
QY	61	GCCAGGGCGCACGGCCTGCTACTCTGGGCACCCGGGCGGCCACCGTTGGTGGCGCGGC	120
Db	266	GCCAGGGCGCACGGCCTGCTACTCTGGGCACCCGGGCGGCCACCGTTGGTGGCGCGGC	325
QY	121	GCTGGCCTGAGGGAGAGCCCGCGGGCAAGCAGGGGGCCGGATGACCTGCTGGGGGAAG	180
Db	326	GCTGGCCTGAGGGAGAGCCCGCGGGCAAGCAGGGGGCCGGATGACCTGCTGGGGGAAG	385
QY	181	CGCTCTCTTACAGATGACGAGCTGCCGGCGCAAACGCTCAAGTACC GGCGGGTGCAG	240
Db	386	CGCTCTCTTACAGATGACGAGCTGCCGGCGCAAACGCTCAAGTACC GGCGGGTGCAG	445
QY	241	AAC TACCTGTACAACGCTGCTGGAGAGACCCCGGGCTGGGGCTTCATCACCAGCTTTC	300
Db	446	AAC TACCTGTACAACGCTGCTGGAGAGACCCCGGGCTGGGGCTTCATCACCAGCTTTC	505
QY	301	GT TTTTCTCTTGCTTTTGGTTCGTGATTTTGTTCAGTGT TTTCTACCATCCCTGAGCAC	360
Db	506	GT TTTTCTCTTGCTTTTGGTTCGTGATTTTGTTCAGTGT TTTCTACCATCCCTGAGCAC	565
QY	361	ACAAAATTGG CCTCAAGTTGCCTCTTGATCTCTGGAGTTGCTGATGATGCTCTTTGGT	420
Db	566	ACAAAATTGG CCTCAAGTTGCCTCTTGATCTCTGGAGTTGCTGATGATGCTCTTTGGT	625
QY	421	TTCGAGTTTCATTCGAAATCTGGTCTCGGGGTCCTGCTCTCGATATAGAGGATGGCAA	480
Db	626	TTGGAGTTTCATTCGAAATCTGGTCTCGGGGTCCTGCTCTCGATATAGAGGATGGCAA	685



Qy 481 GGAAGACGTAGGTTGCTCGAAGCCCTTCTGTGTATAGATACATTTGTTCTTATCGCT 540  
Db 686 GGAAGACGTAGGTTGCTCGAAGCCCTTCTGTGTATAGATACATTTGTTCTTATCGCT 745  
Qy 541 TCAATAGCAGTTGTTCTGCAAAACCTCAGGTAATATTTTGGCCAGCTCTGCACTCAGA 600  
Db 746 TCAATAGCAGTTGTTCTGCAAAACCTCAGGTAATATTTTGGCCAGCTCTGCACTCAGA 805  
Qy 601 AGTCTCGGTTTCTACAGATCCTCGCATGTTGGCGATGAGCCGAAGGGAGGCACTTGG 660  
Db 806 AGTCTCGGTTTCTACAGATCCTCGCATGTTGGCGATGAGCCGAAGGGAGGCACTTGG 865  
Qy 661 AAATACTGGGTTTATGCTTATGCTCAGAGAGGAAATTAATACAGCTTGTGATACATA 720  
Db 866 AAATACTGGGTTTATGCTTATGCTCAGAGAGGAAATTAATACAGCTTGTGATACATA 925  
Qy 721 GGATTTTGGGTTTATTTTTCGTTCTTCTGTCTATCTGTGGAAGGATGCCAAT 780  
Db 926 GGATTTTGGGTTTATTTTTCGTTCTTCTGTCTATCTGTGGAAGGATGCCAAT 985  
Qy 781 AAAGAGTTTCTACATATGCAATGCTCTCTGTGGGCAAAATTTACATTTGCAAACTATT 840  
Db 986 AAAGAGTTTCTACATATGCAATGCTCTCTGTGGGGCAAAATTTACATTTGCAAACTATT 1045  
Qy 841 GGCTATGGAGCAAACTCCCTTAACCTTGGCTGGGAAGATTGCTTTCTGCAAGGCTTTGCA 900  
Db 1046 GGCTATGGAGCAAACTCCCTTAACCTTGGCTGGGAAGATTGCTTTCTGCAAGGCTTTGCA 1105  
Qy 901 CTCCTTGGCAATTTCTTTCTTGGCACTTCTCCCGCATTTCTTGGCTCAGGTTTTCGATTA 960  
Db 1106 CTCCTTGGCAATTTCTTTCTTGGCACTTCTCCCGCATTTCTTGGCTCAGGTTTTCGATTA 1165  
Qy 961 AAAGTACAAAGAACCAACCGCCAGAAACATTTTGGAAAAAGAGAACCCAGCTGCCAAC 1020  
Db 1166 AAAGTACAAAGAACCAACCGCCAGAAACATTTTGGAAAAAGAGAACCCAGCTGCCAAC 1225  
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Db 1226 CTCAATCAGTGTGTTGGCGTAGTTACGCACTGATGAGAAATCTGTTTCATTTGCAACC 1285  
Qy 1081 TGAAGCCACACTTGAAGCGCTTCACACCTGACGCCCTTACCAAGAAAGAACAGGGGAA 1140  
Db 1286 TGAAGCCACACTTGAAGCGCTTCGACACCTTGCAGCCCTTACCAAGAAAGAACAGGGGAA 1345  
Qy 1141 GCATCAAGCAGTCAGAAGCTAAAGTTTAAAGAGCGAGTGCATGGCTAGCCCGAGGGGC 1200  
Db 1346 GCATCAAGCAGTCAGAAGCTAAAGTTTAAAGAGCGAGTGCATGGCTAGCCCGAGGGGC 1405  
Qy 1201 CAGAGTATTAAAGCGGCAAGCCTCAGTAGGTGACAGGAGGTCCCAAGCACCGACATC 1260  
Db 1406 CAGAGTATTAAAGCGGCAAGCCTCAGTAGGTGACAGGAGGTCCCAAGCACCGACATC 1465  
Qy 1261 ACAGCGAGGCGAGTCCCAACCAAGTGACAGAGCTGAGCTTCAACGACCGAACCCGC 1320  
Db 1466 ACAGCGAGGCGAGTCCCAACCAAGTGACAGAGCTGAGCTTCAACGACCGAACCCGC 1525  
Qy 1321 TTCCGGCCCTCGCTCGCGCTCAAAAGTTTCTCAGCCCAAAACCAAGTATGATGCTGACACA 1380  
Db 1526 TTCCGGCCCTCGCTCGCGCTCAAAAGTTTCTCAGCCCAAAACCAAGTATGATGCTGACACA 1585  
Qy 1381 GCCCTTGGCACTGATGATATGATGAAAGGATGCGAGTGTGATGATGATGATGATGATG 1440  
Db 1586 GCCCTTGGCACTGATGATATGATGAAAGGATGCGAGTGTGATGATGATGATGATGATG 1645  
Qy 1441 GACCTCACCCCAACCTTAAACCTGCTATTCGAGCTATCAGAAATTTATGAAATTTTCATGTT 1500  
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Qy 1501 GCAAAACGGAAGTTTAAAGAAACRTTACGCTCCATATGATGTAAGAGATGTCATTTGAAACA 1560  
Db 1706 GCAAAACGGAAGTTTAAAGAAACRTTACGCTCCATATGATGTAAGAGATGTCATTTGAAACA 1765  
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Db 1766 TATTCTGCTGTCATCTGGAACATGTTGTGTAGAAATTTAAAGCCCTTCAAAACGCTGTTGAT 1825  
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Qy 1741 GTACAGTCCATAGAAATCCAAGCTGGAATCTAGACATCTATCAACAGGCTCTTCGG 1800  
Db 1946 GTACAGTCCATAGAAATCCAAGCTGGAATCTAGACATCTATCAACAGGCTCTTCGG 2005  
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Qy 1921 AGTGGCTGCTTATCCAGATCAACTAGTGCACCAATCTCGAGAGCCCTGCAGTTCATTTCTG 1980  
Db 2126 AGTGGCTGCTTATCCAGATCAACTAGTGCACCAATCTCGAGAGCCCTGCAGTTCATTTCTG 2185  
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Db 2186 ACGCCAAATGAGTTTCACTGCGCCAGACTTCTACCGGCTTAGCCCTTACTATGACAGTCAA 2245  
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Db 2366 CCTCTCCAGCCATCAAGCATCTGCCAGGCGCAAACTCTGCACCCCTTAAACCTTGCAGGC 2425  
Qy 2221 TTACAGAAAGCAGTTTCTGAGCTCACCCTGCTTCTGTGCTTCAAGGAAAAATGTTTCAAG 2280  
Db 2426 TTACAGAAAGCAGTTTCTGAGCTCACCCTGCTTCTGTGCTTCAAGGAAAAATGTTTCAAG 2485  
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Qy 2341 GAAACTCTGTTGCTGCTGCTCCATGCTGCGGAGGACTTTGGGCAAAATCTTTTGTCTGTG 2400  
Db 2546 GAAACTCTGTTGCTGCTGCTCCATGCTGCGGAGGACTTTGGGCAAAATCTTTTGTCTGTG 2605  
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Db 2606 CAAACCTCTGATCAGGTGCAAGGAACTGAATATACAACTTTTCAAGGAGTGAAGTCAAGT 2665  
Qy 2461 GGCTCCAGAGGCGCAGGAAATTTTACCCAAATGAGGGAATCCAAATTTGTTTATAACT 2520  
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Qy 2521 GATGAAGAGGTGGGTCCCGAAGAGACAGACAGACACTTTTGTATGCGCAGCCGAGCCT 2580  
Db 2726 GATGAAGAGGTGGGTCCCGAAGAGACAGACAGACACTTTTGTATGCGCAGCCGAGCCT 2785  
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Db 2786 GCCAGGAAGCTGCTTTTGCATCAGACTCTCTTAAGGACTGGAAGGTACAGATCATCTCAG 2845  
Qy 2641 AGCATTTGTAGGAGGAGGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCATCTCAATCTGAAA 2700

[illegible]

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Db	1226	CTCA	TT	CAGTGTGTTTGGCGTAGTTACG	AGCTGATGAGAAATCTGTTTCCAT	TGCAACC	1285		
		TTGA	AGCCACACTTGA	AGGCTTGCACAC	CTGAGAAATCTGTTTCCAT	TGCAACC	1345		
Qy	1081	TG	AA	AGCCACACTTGA	AGGCTTGCACAC	CTGAGAAATCTGTTTCCAT	TGCAACC	1140	
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Qy	1141	GC	AT	CAAGCAGTCA	GAAGCTAAAGTTTAA	GGAGCGAGTGGCGATGCTAG	CCCCCAGGGC	1200	
Db	1346	GC	AT	CAAGCAGTCA	GAAGCTAAAGTTTAA	GGAGCGAGTGGCGATGCTAG	CCCCCAGGGC	1405	
Qy	1201	CAG	AGTATTAAG	AGCCGACAAAGCCTC	AGTATGTCAGAGGTC	CCCAAGCACCGACATC	1260		
Db	1406	CAG	AGTATTAAG	AGCCGACAAAGCCTC	AGTATGTCAGAGGTC	CCCAAGCACCGACATC	1465		
Qy	1261	AC	AGCCGAGGAGTCC	CAACCAAGTCG	ACAGAGCTTCACAGCCG	ACCAACCCGC	1320		
Db	1466	AC	AGCCGAGGAGTCC	CAACCAAGTCG	ACAGAGCTTCACAGCCG	ACCAACCCGC	1525		
Qy	1321	TT	CGGCGCTCG	CTCGCCCTCA	AAAGTTCTCAG	CAAAAC	CCAGTGATGCTGACACA	1380	
Db	1526	TT	CGGCGCTCG	CTCGCCCTCA	AAAGTTCTCAG	CAAAAC	CCAGTGATGCTGACACA	1585	
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Qy	1441	GAC	CTCACC	CCACACACTTAA	ACCTGTCATTCG	AGCTATCAGAA	TATGAAATTTTCATGTT	1500	
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Qy	1741	GT	CAGTCCAT	TAGAAATCA	AGCTGGACTG	CTACTAGACATCTAT	CAACAGGTCCTTCGG	1800	
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Db	2066	CAG	ACATCTG	ACTATCAA	AGCCCTGTGGAT	AGCAAGATCTTTC	GGGTTCCGACAAAC	2125	
Qy	1921	AG	TGGCTGCTTAT	CCAGATCA	ACTAGTGC	CAACATCTC	GAGAGCCCTG	CAGTTTCATTTCTG	1980
Db	2126	AG	TGGCTGCTTAT	CCAGATCA	ACTAGTGC	CAACATCTC	GAGAGCCCTG	CAGTTTCATTTCTG	2185
Qy	1981	AC	GCAAAATG	AGTTT	CAGTGGCC	CAGACTTTCTAC	GGCTTTAGCCCTACTATG	CAAGTCAA	2040
Db	2186	AC	GCAAAATG	AGTTT	CAGTGGCC	CAGACTTTCTAC	GGCTTTAGCCCTACTATG	CAAGTCAA	2245
Qy	2041	GCA	ACAG	GTGCCAAT	TAGTCAA	AGCGATGGCTC	AGTGGCAGCCACCA	CCACTT	2100
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Db	2306	GC	AAACCAAAATAATACGGCACCCAGCAGAGAGCCCAACAACATTTTACAGATCCCACT	2365
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Db	2426	TT	TACAGAAAGCATTTCTGACGTCACACACCTGCTGTTTGTGCTTCCAAGGAAAAATGTTT	2485
Qy	2281	GT	TGCACAGTCAAAATCTCAACAAGACCGTTTATAGAGGAAAGCTTTGACATGGAGGA	2340
Db	2486	GT	TGCACAGTCAAAATCTCAACAAGACCGTTTATAGAGGAAAGCTTTGACATGGAGGA	2545
Qy	2341	GA	AACTCTGTGTCGTCTGCTGCCCATGGTGCAGAGGACTTTGGGCAAACTCTTTGCTGTG	2400
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Qy	2401	CA	AAACCTGATCAGGTGCGACCGAGGAACCTGAAATATACAACTTTTCAGGAGTGAAGT	2460
Db	2606	CA	AAACCTGATCAGGTGCGACCGAGGAACCTGAAATATACAACTTTTCAGGAGTGAAGT	2665
Qy	2461	GG	CTCAGAGGCAAGAAATTTTACCCCAATGAGAGGAATCCAAATTTGTTTATAACT	2520
Db	2666	GG	CTCAGAGGCAAGAAATTTTACCCCAATGAGAGGAATCCAAATTTGTTTATAACT	2725
Qy	2521	GAT	GAAGAGTGGTCCGAGAGACAGACAGACACTTTTTCATGCCGACCGCAGCT	2580
Db	2726	GAT	GAAGAGTGGTCCGAGAGACAGACAGACACTTTTTCATGCCGACCGCAGCT	2785
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Db	2786	GC	CAGGAAGCTGCCTTTTGATCAGACTCTCTAAGACTGGAAGGTCACGATCATCTCAG	2845
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Qy	2761	ACT	ATTTCGAAAGCCCTCTTAAAAAGTTGAAATTCGAAAGTCCGGAAGAACATGAAAG	2820
Db	2966	ACT	ATTTCGAAAGCCCTCTTAAAAAGTTGAAATTCGAAAGTCCGGAAGAACATGAAAG	3025
Qy	2821	CAG	TTTATAAGCCGTTTACCTTTTAAATTCATGAAATGCAATGTTTAGG	2869
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RESULT 11				
LOCUS	AF263835		2832 bp	linear
DEFINITION	Homo sapiens voltage-gated potassium channel KCNQ5 (KCNQ5) mRNA, partial cds.			
ACCESSION	AF263835			
VERSION	AF263835.1	GI:8132996		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	Kniazeva,M. and Han,M.			
TITLE	A new gene of the voltage-gated potassium channel KCNQ family, KCNQ5, is a candidate gene for retinal disorders			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 2832)			
AUTHORS	Kniazeva,M. and Han,M.			
TITLE	Direct Submission			

JOURNAL	Submitted (04-MAY-2000) MCDB, University of Colorado at Boulder,
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ORIGIN	
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	Best Local Similarity 99.6%; Pred. No. 0;
	Matches 2822; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
Qy	118 GCGCGTGGCTTGAGGGAGAGCCGCCGGGCAAGCAGCGGGGCCGGATGAGCCTCTCGGG 177
Db	1 GCGCGTGGCTTGAGGGAGAGCCGCCGGGCAAGCAGGGGGCCGGATGAGCCTCTCGGG 60
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AX322509
LOCUS AX322509 2694 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 1 from Patent WO0192526.
ACCESSION AX322509
VERSION AX322509.1 GI:18093555
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Dworesky, S.I., Ramanathan, C.S., Trojnecki, J.T., Boissard, C.G. and
Gribkoff, V.K.
Human kcnq5 potassium channel, methods and compositions thereof
Patent: WO 0192526-A 1 06-DEC-2001;
Bristol-Myers Squibb Company (US)
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1. 2694
/organism="Homo sapiens"
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Best Local Similarity 99.9%; Pred. No. 0;
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DEFINITION	Sequence 1 from patent US 6767736.		
ACCESSION	AR565635		
VERSION	AR565635.1	GI:53981668	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 2772)		
AUTHORS	Hu, Y., Kieke, J.A., Turner, C.A. Jr., Nehls, M.C., Friedrich, G.,		
TITLE	Zambrowicz, B. and Sands, A.T.		
JOURNAL	Human ion channel protein and polynucleotides encoding the same		
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RESULT 15

AF263836

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

3108 bp mRNA linear ROD 01-JUN-2000  
Mus musculus voltage-gated potassium channel KCNQ5 (Kcnq5) mRNA,  
partial cds.  
AF263836  
AF263836.1 GI:8132998  
Mus musculus (house mouse)

REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
AUTHORS	Kniazeva, M. and Han, M.
TITLE	A new gene of the voltage-gated potassium channel KCNQ family, KCNQ5, is a candidate gene for retinal disorders
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 3108)
AUTHORS	Kniazeva, M. and Han, M.
TITLE	Direct Submission
JOURNAL	Submitted (04-MAY-2000) MCDB, University of Colorado at Boulder, Porter Biosciences Bldg., Boulder, CO 80309, USA
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Db	361	ACAAAATTTGGCTCAAGTGTGCTCTTGATCCTGGAGTTCTGTGATGATTTGTCTTGTGT	420
QY	421	TTGGAGTTCATCATTCGAATCTGTCTGGGGTGTCTGTTGTCGATATAGAGATGGCAA	480
Db	421	TTGGAGTTCATCATTCGAATCTGTCTGGGGTGTCTGTTGTCGATATAGAGATGGCAA	480
QY	481	GGAGACTGAGCTTGTCTCGAAGCCCTCTGTCTTATAGATACCATTTGTTCTTATCGCT	540
Db	481	GGAGACTGAGCTTGTCTCGAAGCCCTCTGTCTTATAGATACCATTTGTTCTTATCGCT	540
QY	541	TCAATPAGCAGTGTCTTGCAGAACTCAGGGTAATATTTTGGCAGCTGTGCACTCAGA	600
Db	541	TCAATPAGCAGTGTCTTGCAGAACTCAGGGTAATATTTTGGCAGCTGTGCACTCAGA	600
QY	601	AGTCTCCGTTCTTACAGATCCTCGCATGCTGGCGATGGAACGAGGGAGGCACTTGG	660
Db	601	AGTCTCCGTTCTTACAGATCCTCGCATGCTGGCGATGGAACGAGGGAGGCACTTGG	660
QY	661	AAATTTACTGGGTTCAAGTGTATGCTCAGCAGAGGAATTAATCAGAGCTTGTGATATA	720
Db	661	AAATTTACTGGGTTCAAGTGTATGCTCAGCAGAGGAATTAATCAGAGCTTGTGATATA	720
QY	721	GGATTTTGGTCTTATTTTTCGTTCTTCTGCTATCTGCTGGAAGAGATGCCAAT	780
Db	721	GGATTTTGGTCTTATTTTTCGTTCTTCTGCTATCTGCTGGAAGAGATGCCAAT	780
QY	781	AAAGAGTTTCTACATATGACATGCTCTCTGGTGGGCGACAAATTTACATTTGACAACTAT	840
Db	781	AAAGAGTTTCTACATATGACATGCTCTCTGGTGGGCGACAAATTTACATTTGACAACTAT	840
QY	841	GGCTATGGAGACAAACCTCCCTAACTTGGCTGGGAAGATTTGCTTCTGCAAGGCTTTGCA	900
Db	841	GGCTATGGAGACAAACCTCCCTAACTTGGCTGGGAAGATTTGCTTCTGCAAGGCTTTGCA	900
QY	901	CTCCTTGGCATTTCTTCTTGGCTTCTGCTGCGGCTTCTGCTCAGGTTTGTCAATTA	960
Db	901	CTCCTTGGCATTTCTTCTTGGCTTCTGCTGCGGCTTCTGCTCAGGTTTGTCAATTA	960
QY	961	AAAGTACAAAGAACACACCGCGAGAAACATTTTGAGAAAGAGAAACCGAGCTGCCAAC	1020
Db	961	AAAGTACAAAGAACACACCGCGAGAAACATTTTGAGAAAGAGAAACCGAGCTGCCAAC	1020
QY	1021	CTCATTCAGTGTGTGGGCTAGTTACGAGCTGTGATGAAATCTGTTTCCATTTCCAACT	1080
Db	1021	CTCATTCAGTGTGTGGGCTAGTTACGAGCTGTGATGAAATCTGTTTCCATTTCCAACT	1080
QY	1081	TGGAAGCCACACTTGAAGGCTTGGCAGCTGAGCCCTTACCAAGAAAGAAACAGGGGAA	1140
Db	1081	TGGAAGCCACACTTGAAGGCTTGGCAGCTGAGCCCTTACCAAGAAAGAAACAGGGGAA	1140
QY	1141	GCATCAAGCAGTCAGAGCTAAAGTTTAAAGAGAGAGTGGCGATGGCTAGCCCCAGGGGC	1200
Db	1141	GCATCAAGCAGTCAGAGCTAAAGTTTAAAGAGAGAGTGGCGATGGCTAGCCCCAGGGGC	1200
QY	1201	CAGAGTATTAAGAGCCGACAAAGCCTCAGTGTGACAGGAGTCCCAAGCAGCAGCATC	1260
Db	1201	CAGAGTATTAAGAGCCGACAAAGCCTCAGTGTGACAGGAGTCCCAAGCAGCAGCATC	1260
QY	1261	ACAGCCGAGGAGTCCCAACCAAGTGCAGAGAGTGGAGCTTCAACAGCCGAAACCCGC	1320
Db	1261	ACAGCCGAGGAGTCCCAACCAAGTGCAGAGAGTGGAGCTTCAACAGCCGAAACCCGC	1320
QY	1321	TTCCGGCCCTCGCTCGGCTCAAAAGTTCTCAGCCAAACCCAGTATAGATGCTGACACA	1380
Db	1321	TTCCGGCCCTCGCTCGGCTCAAAAGTTCTCAGCCAAACCCAGTATAGATGCTGACACA	1380
QY	1381	GCCCTTGGCAGTGTATATGATGAAAAAGATGCCAGTGTGATGATGATGATGATGATGAT	1440
Db	1381	GCCCTTGGCAGTGTATATGATGAAAAAGATGCCAGTGTGATGATGATGATGATGATGAT	1440
QY	1441	GACCTCACCCACCACTTAAAGCTGTCTGAGCTATCAGAAATTTATGAAATTTTCACTGT	1500
Db	1441	GACCTCACCCACCACTTAAAGCTGTCTGAGCTATCAGAAATTTATGAAATTTTCACTGT	1500
QY	1501	GCAAAACGGAAGTTTAAAGAAACRTTACGTCATATGATGATGATGATGATGATGATGAT	1560
Db	1501	GCAAAACGGAAGTTTAAAGAAACRTTACGTCATATGATGATGATGATGATGATGATGAT	1560
QY	1561	TATTCGTGGTTCATCTGGACATGTTGTGAGATTTAAAGCTTCAACACAGTGTGAT	1620
Db	1561	TATTCGTGGTTCATCTGGACATGTTGTGAGATTTAAAGCTTCAACACAGTGTGAT	1620
QY	1621	CAAAATTTTGGAAAAAGGGCAATTCATCAGATATGAGAGCCGAGAGAAAAATACAGCA	1680
Db	1621	CAAAATTTTGGAAAAAGGGCAATTCATCAGATATGAGAGCCGAGAGAAAAATACAGCA	1680
QY	1681	GAACTGAGACACACAGACGATCTCAGTATGCTCGGTGGGTGCTCAAGTTCGAAAAACAG	1740
Db	1681	GAACTGAGACACACAGACGATCTCAGTATGCTCGGTGGGTGCTCAAGTTCGAAAAACAG	1740
QY	1741	GTACAGTCCATAGAAATCCAAAGCTGGAGTCCCTACTAGACATCTATCAACAGGTCCTCGG	1800
Db	1741	GTACAGTCCATAGAAATCCAAAGCTGGAGTCCCTACTAGACATCTATCAACAGGTCCTCGG	1800
QY	1801	AAAGGCTCTGCTCAGCCCTCGCTTGGCTTCAATCCAGTTCCTCCAGTTCCTGTA	1860
Db	1801	AAAGGCTCTGCTCAGCCCTCGCTTGGCTTCAATCCAGTTCCTCCAGTTCCTGTA	1860
QY	1861	CAGACATCTGACTATCAAAAGCCCTGGATAGCAAAAGATCTTTTCGGGTTCCGCAAAAC	1920
Db	1861	CAGACATCTGACTATCAAAAGCCCTGGATAGCAAAAGATCTTTTCGGGTTCCGCAAAAC	1920
QY	1921	AGTGGCTGCTTATCCAGATCAACTAGTGCCAAATCTCAGAGGCTCGAGTTCATCTG	1980
Db	1921	AGTGGCTGCTTATCCAGATCAACTAGTGCCAAATCTCAGAGGCTCGAGTTCATCTG	1980
QY	1981	ACGCCAAATCAGTTCAGTCCCGAGATTTCTAGCGCTTAGCCCTACTATGACAGTCAA	2040
Db	1981	ACGCCAAATCAGTTCAGTCCCGAGATTTCTAGCGCTTAGCCCTACTATGACAGTCAA	2040
QY	2041	GCAACACAGTGGCAATTTAGTCAAAAGCGATGGCTCAGAGTGGAGCCACCAACCAT	2100
Db	2041	GCAACACAGTGGCAATTTAGTCAAAAGCGATGGCTCAGAGTGGAGCCACCAACCAT	2100
QY	2101	GCAACCAAAATTAATACGGCACCCAGCAGGAGCCCAACACTTTTACAGATCCCACT	2160
Db	2101	GCAACCAAAATTAATACGGCACCCAGCAGGAGCCCAACACTTTTACAGATCCCACT	2160
QY	2161	CCTCTCCAGCATCAAGCATCTGCCAGGCGCAAAACTCTGCACCCCTAAACCTGACGC	2220
Db	2161	CCTCTCCAGCATCAAGCATCTGCCAGGCGCAAAACTCTGCACCCCTAAACCTGACGC	2220
QY	2221	TTACAGGAAAGCAATTTCTGAGCTCCACCTGCTGCTTGTGCTTCCAGGAAATGTTTCA	2280



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Db 2221 TTACAGGAACATTTCTGACGTCACCACTGCTTGTGCTCCAAAGGAAATGTTTCAG 2280  
Qy 2281 GTTGCACAGTCAAAATCTCACCAAGACCGTCTCTATGAGGAAAGCTTTGACATGGGAGGA 2340  
Db 2281 GTTGCACAGTCAAAATCTCACCAAGACCGTCTCTATGAGGAAAGCTTTGACATGGGAGGA 2340  
Qy 2341 GAAACTCTGTGTCTGTCTGTCCTCATGTCGCGAAGACCTTGGGCAAAATCTTTGCTGTG 2400  
Db 2341 GAAACTCTGTGTCTGTCTGTCCTCATGTCGCGAAGACCTTGGGCAAAATCTTTGCTGTG 2400  
Qy 2401 CAAACCTGTATCAGTGCAGCGGAACTGAATATACAACTTTTCAGGAGTGAAGTCAAGT 2460  
Db 2401 CAAACCTGTATCAGTGCAGCGGAACTGAATATACAACTTTTCAGGAGTGAAGTCAAGT 2460  
Qy 2461 GGCTCCAGAGCGACCAAGATTTTACCCAAATGGAGGGAATCCAAATGTTTATAACT 2520  
Db 2461 GGCTCCAGAGCGACCAAGATTTTACCCAAATGGAGGGAATCCAAATGTTTATAACT 2520  
Qy 2521 GATGAAGAGTGGTCCGGAAGACAGACAGACACTTTTGTATGCCGACCGACGCT 2580  
Db 2521 GATGAAGAGTGGTCCGGAAGACAGACAGACACTTTTGTATGCCGACCGACGCT 2580  
Qy 2581 GCCAGGAGTGCCTTTGCATCAGACTCTTAAGGACTGGAAGTCAAGTCAATCTCAG 2640  
Db 2581 GCCAGGAGTGCCTTTGCATCAGACTCTTAAGGACTGGAAGTCAAGTCAATCTCAG 2640  
Qy 2641 AGCAATTTGAAGCAGGAGAAAGTACAGATCCCTCAGCTTGCCTCATGTCAAACTGAAA 2700  
Db 2641 AGCAATTTGAAGCAGGAGAAAGTACAGATCCCTCAGCTTGCCTCATGTCAAACTGAAA 2700  
Qy 2701 TAAGTTCTTCAATTTCTTCCAGCATAGCAGTTCTTTAGCCATACATATCATTTGCATGA 2760  
Db 2701 TAAGTTCTTCAATTTCTTCCAGCATAGCAGTTCTTTAGCCATACATATCATTTGCATGA 2760  
Qy 2761 ACTATTTGGAAGCCCTCTAAAGTTGAAATGCAAGATCGGAGAACATGAAGG 2820  
Db 2761 ACTATTTGGAAGCCCTCTAAAGTTGAAATGCAAGATCGGAGAACATGAAGG 2820  
Qy 2821 CAGTTTATAGCCGCTTACCTTTTAAATGCAATGAAATGCAATGTTAGGAGTGCCTAAAA 2880  
Db 2821 CAGTTTATAGCCGCTTACCTTTTAAATGCAATGAAATGCAATGTTAGGAGTGCCTAAAA 2880  
Qy 2881 TTCAAAGTGTCATCGACATTAACCCACTCAATTTAGTAAATGTAAGTCAATTTGAGTCAATTTA 2940  
Db 2881 TTCAAAGTGTCATCGACATTAACCCACTCAATTTAGTAAATGTAAGTCAATTTGAGTCAATTTA 2940  
Qy 2941 GAGAAACCAACACAGCTAATGCTATGGGTGATGAATATGTCAGTTTGAAGTCAATTTA 3000  
Db 2941 GAGAAACCAACACAGCTAATGCTATGGGTGATGAATATGTCAGTTTGAAGTCAATTTA 3000  
Qy 3001 GAAGATTTGACACTGTATTTTGAATATGGAATATGGAAGTAAACACCTTCAAAATTTCAAAAAA 3060  
Db 3001 GAAGATTTGACACTGTATTTTGAATATGGAATATGGAAGTAAACACCTTCAAAATTTCAAAAAA 3060  
Qy 3061 AAAAAA 3071  
Db 3061 AAAAAA 3071

RESULT 2  
US-10-661-629-1  
; Sequence 1, Application US/10661629  
; Publication No. US20040180405A1  
; GENERAL INFORMATION:  
; APPLICANT: JENTSCH, Thomas  
; FILE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNELS  
; TITLE REFERENCE: 2815-0236P  
; CURRENT APPLICATION NUMBER: US/10/661,629  
; CURRENT FILING DATE: 2003-09-15  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1

LENGTH: 3137  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(2691)  
US-10-661-629-1  
Query Match 99.0%; Score 3040.4; DB 18; Length 3137;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3041; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Qy 10 ATGAAGATGTGAGTTCGGGCCGGGCGCAGGGTGTCTGTGAATCTGGGAGCGCCGACGGGC 69  
Db 1 ATGAAGATGTGAGTTCGGGCCGGGCGCAGGGTGTCTGTGAATCTGGGAGCGCCGACGGGC 60  
Qy 70 GAGGCTGTCTACTGTCTGGGCAACCGCGCGGCCACGCTGTGTGGCGGCGGGTGGCTG 129  
Db 61 GAGGCTGTCTACTGTCTGGGCAACCGCGCGGCCACGCTGTGTGGCGGCGGGTGGCTG 120  
Qy 130 AGGAGAGCCGCGGGGCAAGCAGGCGGCCCGATGAGCCTGTCTGGGGAAGCCGCTCTCT 189  
Db 121 AGGAGAGCCGCGGGGCAAGCAGGCGGCCCGATGAGCCTGTCTGGGGAAGCCGCTCTCT 180  
Qy 190 TACACGATGACGAGTGTCCGGCGCAACGTCAGTACCGCGGGTGCAGAACTACCTG 249  
Db 181 TACACGATGACGAGTGTCCGGCGCAACGTCAGTACCGCGGGTGCAGAACTACCTG 240  
Qy 250 TACAACTGTCTGGAGAGACCCCGGCTGGCGCTTCACTACCAACGCTTTCGTTTCTC 309  
Db 241 TACAACTGTCTGGAGAGACCCCGGCTGGCGCTTCACTACCAACGCTTTCGTTTCTC 300  
Qy 310 CTGTCTTCTGTTGCTTGTGATTTTGTCAAGTGTCTTACCATCCCTGAGCACAAAAATTG 369  
Db 301 CTGTCTTCTGTTGCTTGTGATTTTGTCAAGTGTCTTACCATCCCTGAGCACAAAAATTG 360  
Qy 370 GCCTCAAGTGTCTTGTATCTCGAGTTCGTGATGATGTCTGCTTGTGTTGGAGTTC 429  
Db 361 GCCTCAAGTGTCTTGTATCTCGAGTTCGTGATGATGTCTGCTTGTGTTGGAGTTC 420  
Qy 430 ATCAATTCGAATCTGTCTGCGGGTGTCTGTCGATATAGAGATGCAAGGAAAGACTG 489  
Db 421 ATCAATTCGAATCTGTCTGCGGGTGTCTGTCGATATAGAGATGCAAGGAAAGACTG 480  
Qy 490 AGGTTTCTCGAAGGCCCTTCTGTGTTATAGATACCAATGTTCTTATCGCTTCAATAGCA 549  
Db 481 AGGTTTCTCGAAGGCCCTTCTGTGTTATAGATACCAATGTTCTTATCGCTTCAATAGCA 540  
Qy 550 GTTGTTCGCAAAACCTCAGGGTAATATTTTGGCAGCTGTGCACTCAGAACTCTCGGT 609  
Db 541 GTTGTTCGCAAAACCTCAGGGTAATATTTTGGCAGCTGTGCACTCAGAACTCTCGGT 600  
Qy 610 TTCTACAGATCTCCGATGTGCGCATGACCGAAGGGAGGACCTTGGAAATTTACTG 669  
Db 601 TTCTACAGATCTCCGATGTGCGCATGACCGAAGGGAGGACCTTGGAAATTTACTG 660  
Qy 670 GGTTCAAGTGTATGCTCAGCAGCAAGAAATTAATCAAGCTTGTGATAGGATTTTGT 729  
Db 661 GGTTCAAGTGTATGCTCAGCAGCAAGAAATTAATCAAGCTTGTGATAGGATTTTGT 720  
Qy 730 GTTCTTATTTTTCGCTTCTTCTATCTGTGGGAAAGGATGCCAATAAAGAGTTT 789  
Db 721 GTTCTTATTTTTCGCTTCTTCTATCTGTGGGAAAGGATGCCAATAAAGAGAGTTT 780  
Qy 790 TCTACATATCAGATGCTCTCTGTGGGCAACATTAATGACAACTATTGGCTATGGA 849  
Db 781 TCTACATATCAGATGCTCTCTGTGGGCAACATTAATGACAACTATTGGCTATGGA 840  
Qy 850 GACAAAACTCCCTTAATCTTGGCTGGGAAAGATGCTTCTGCAAGCTTTTGCACCTCTTGGC 909  
Db 841 GACAAAACTCCCTTAATCTTGGCTGGGAAAGATGCTTCTGCAAGCTTTTGCACCTCTTGGC 900  
Qy 910 ATTTCTTTTTCGCACTTCTCTCGGCGCAATCTTGGCTCAGGTTTGTGCAATTAAGATACA 969

1981	GAGTTGAGTCCCGAGCTTTCTACGGCTTAGCCCTACTATGACAGTCAAGCAACACAG	2040
2050	GTGCAATTAAGTCAAGCGATGCTCAGCAGTGGCGAGCCACCAACACCACTTGCACCAACAA	2109
2041	GTGCAATTAAGTCAAGCGATGCTCAGCAGTGGCGAGCCACCAACCACTTGCACCAACAA	2100
2110	ATAAATACGGCACCACCAAGCCAGCAGCCCAACCACTTTACAGATCCCACTCTCTCCCA	2169
2101	ATAAATACGGCACCACCAAGCCAGCAGCCCAACCACTTTACAGATCCCACTCTCTCCCA	2160
2170	GCCATCAAGCATCTGCGCAGCCAGCAAACTCTGCAACCTTAACCTCGAGGCTTACAGGAA	2229
2161	GCCATCAAGCATCTGCGCAGCCAGCAAACTCTGCAACCTTAACCTCGAGGCTTACAGGAA	2220
2230	AGCATTTCTGACGTCACCACTGCTTGTTCCTTCAAGGAAATGTTCAAGTTGACAG	2289
2221	AGCATTTCTGACGTCACCACTGCTTGTTCCTTCAAGGAAATGTTCAAGTTGACAG	2280
2290	TCAAATCTCACCAAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG	2349
2281	TCAAATCTCACCAAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG	2340
2350	TTGCTCTGCTCTGCTCCATGCTCGAAGGACTTGGGCAAACTCTTGTCTGTGCAAAACCTG	2409
2341	TTGCTCTGCTCTGCTCCATGCTCGAAGGACTTGGGCAAACTCTTGTCTGTGCAAAACCTG	2400
2410	ATCAGGTCCGACGAGGAACTCAATATACAACTTTTCAAGGAGTGAATCAAGTGGCTCCAGA	2469
2401	ATCAGGTCCGACGAGGAACTCAATATACAACTTTTCAAGGAGTGAATCAAGTGGCTCCAGA	2460
2470	GGCAGCGAAGATTTTACCCCAATGGAGGAACTCAAAATGTTTATAAATGATGAAGAG	2529
2461	GGCAGCGAAGATTTTACCCCAATGGAGGAACTCAAAATGTTTATAAATGATGAAGAG	2520
2530	GTGGGTCCCGAAGACAGACAGACACTTTTGAATCCGCAACCGCAGCTTCCAGGAA	2589
2521	GTGGGTCCCGAAGACAGACAGACACTTTTGAATCCGCAACCGCAGCTTCCAGGAA	2580
2590	GCTGCTTTGCAATCAGACTCTTAAGGCTGGAAGTCCAGATCATCTCAGAGCATTTGT	2649
2581	GCTGCTTTGCAATCAGACTCTTAAGGCTGGAAGTCCAGATCATCTCAGAGCATTTGT	2640
2650	AAGGAGGAGAAAGTACAGATGCTTCAAGTTCCTCATGTCAAACTGAAATTAAGTTCTT	2709
2641	AAGGAGGAGAAAGTACAGATGCTTCAAGTTCCTCATGTCAAACTGAAATTAAGTTCTT	2700
2710	CATTTCTTTCCAGGATAGCAGTTCTTTAGGCATACATCATCTGCAATGAACTTTTCG	2769
2701	CATTTCTTTCCAGGATAGCAGTTCTTTAGGCATACATCATCTGCAATGAACTTTTCG	2760
2770	AAAGCCCTTCTAAAAAGTTGAAATTCGAAGATCGGAAAGAACATGAAAGGAGTTTATA	2829
2761	AAAGCCCTTCTAAAAAGTTGAAATTCGAAGATCGGAAAGAACATGAAAGGAGTTTATA	2820
2830	AGCCCGTTACCTTTTAAATGCAATGCAATGCTGTTAGGGATGCTTAAATTTCAAGGT	2889
2821	AGCCCGTTACCTTTTAAATGCAATGCAATGCTGTTAGGGATGCTTAAATTTCAAGGT	2880
2890	GCATCGCATTAACCACTCATTTAGTATGATGCTTGAATGAAAGGCTTGAAGAACCA	2949
2881	GCATCGCATTAACCACTCATTTAGTATGATGCTTGAATGAAAGGCTTGAAGAACCA	2940
2950	AACACAGCTAATGCTAGGGGTGTATGAATATGCTAAGTTTAGTCTATTTAGAGATTG	3009
2941	AACACAGCTAATGCTAGGGGTGTATGAATATGCTAAGTTTAGTCTATTTAGAGATTG	3000
3010	ACACTGTATTTTGAATTTATGGGAGTAAACACCTTCAAAATTTCA	3053
3001	ACACTGTATTTTGAATTTATGGGAGTAAACACCTTCAAAATTTCA	3044







Qy	2641	AGCATTGTAAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAA	2700	241	AACTACCTGTACAACTGCTGGAGAGACCCCGGGCTGGCGTTCTATCTACCAAGCTTTC	300
Db	2769	AGCAATTTGTAAGGAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAA	2828	446	AACTACCTGTACAACTGCTGGAGAGACCCCGGGCTGGCGTTCTATCTACCAAGCTTTC	505
Qy	2701	TAACTGCTTCATTTCTTTCCAGCATAGCAGTCTTTAGCCATACATATCATGTGATGA	2760	301	GTTTTTCTCCTGTCTTTGGTGTGATTTTGTAGTGTCTTCTACCATCCCTGAGCAC	360
Db	2829	TAACTGCTTCATTTCTTTCCAGCATAGCAGTCTTTAGCCATACATATCATGTGATGA	2888	506	GTTTTTCTCCTGTCTTTGGTGTGATTTTGTAGTGTCTTCTACCATCCCTGAGCAC	565
Qy	2761	ACTATTTTCGAAGCCCTTCTAAAGTTGAAATTTGCAAGAAATCGGAAGAACATGAAAGG	2820	361	ACAAATTTGGCTCAAGTTGCTCTTCATCTCTGAGTTCGTGATGATTTGCTGCTTTGGT	420
Db	2889	ACTATTTTCGAAGCCCTTCTAAAGTTGAAATTTGCAAGAAATCGGAAGAACATGAAAGG	2948	566	ACAAATTTGGCTCAAGTTGCTCTTCATCTCTGAGTTCGTGATGATTTGCTGCTTTGGT	625
Qy	2821	CAGTTTATAAGCCCGTTACCTTTTAAATTCGATGAAATGATGTTAGGATCGCTTAAA	2880	421	TTGAGATTCATCATTCGAATCTGCTGCGGTTGCTGTTGTGATATAGAGATGCGAA	480
Db	2949	CAGTTTATAAGCCCGTTACCTTTTAAATTCGATGAAATGATGTTAGGATCGCTTAAA	3008	626	TTGAGATTCATCATTCGAATCTGCTGCGGTTGCTGTTGTGATATAGAGATGCGAA	685
Qy	2881	TTCCAAAGTGCATGACATTAACCCACTCATTTAGTAATGACCTTGAGTTTAAAGCCCT	2940	481	GGAGACTGAGGTTTGTCTCGAAAGCCCTTCTGTATATAGATACCATTTGTTTATCGCT	540
Db	3009	TTCCAAAGTGCATGACATTAACCCACTCATTTAGTAATGACCTTGAGTTTAAAGCCCT	3067	686	GGAGACTGAGGTTTGTCTCGAAAGCCCTTCTGTATATAGATACCATTTGTTTATCGCT	745
Qy	2941	GAGAAACCAACACAGCTTAATGCTATGGGGGTGATGAATATGT	2983	541	TCAATAGCAGTTGTTTCTGCAAAAATCTCAGGGTAAATATTTTGGCATCTGCACTCAGA	600
Db	3068	GAGAAACCAACACAGCTTAATGCTATGGGGGTGATGAATATGT	3111	746	TCAATAGCAGTTGTTTCTGCAAAAATCTCAGGGTAAATATTTTGGCATCTGCACTCAGA	805
RESULT 5						
US-09-813-148-1						
; Sequence 1. Application US/09813148						
; Patent No. US20020076809A1						
; GENERAL INFORMATION:						
; APPLICANT: STEINMEYER, Klaus						
; APPLICANT: LERCHE, Christian						
; APPLICANT: SCHERER, Constanze						
; APPLICANT: SEEBOHM, Guisard						
; APPLICANT: BUSCH, Andreas E.						
; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CEN						
; TITLE OF INVENTION: NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM						
; FILE REFERENCE: 38005-119						
; CURRENT APPLICATION NUMBER: US/09/813,148						
; CURRENT FILING DATE: 2001-03-21						
; PRIOR APPLICATION NUMBER: DE 100 13 732.6						
; PRIOR FILING DATE: 2000-03-21						
; PRIOR APPLICATION NUMBER: US 60/194,041						
; PRIOR FILING DATE: 2000-04-03						
; NUMBER OF SEQ ID NOS: 6						
; SOFTWARE: Patent in version 3.0						
; SEQ ID NO 1						
; LENGTH: 3074						
; TYPE: DNA						
; ORGANISM: Homo sapiens						
US-09-813-148-1						
Query Match						
Best Local Similarity 93.0%; Score 2857.4; DB 9; Length 3074;						
Matches 2861; Conservative 1; Mismatches 7; Indels 0; Gaps 0;						
Qy	1	GGCAGCGCATGAAGGATGTGGAGTCGGGCGGGGCGAGGGTGTCTGTAACCTGGCAGCC	60	1081	TGGAAGCCACACTTTGAAGGCTTGCACACCTGCGAGCCTTACCAAGAAAGAACAGGGGAA	1140
Db	206	GGCAGCGCATGAAGGATGTGGAGTCGGGCGGGGCGAGGGTGTCTGTAACCTGGCAGCC	265	1286	TGGAAGCCACACTTTGAAGGCTTGCACACCTGCGAGCCTTACCAAGAAAGAACAGGGGAA	1345
Qy	61	GCCAGGGGCGAGCGCTGTACTGTGGGCAACCGCGCGGCCACGCTTGGTGGCGGGCG	120	1141	GCATCAAGCAGTCAGAGCTTAAGTTTAAAGGCGAGTCGCGCATGGCTAGCCCCCAGGGGC	1200
Db	266	GCCAGGGGCGAGCGCTGTACTGTGGGCAACCGCGCGGCCACGCTTGGTGGCGGGCG	325	1346	GCATCAAGCAGTCAGAGCTTAAGTTTAAAGGCGAGTCGCGCATGGCTAGCCCCCAGGGGC	1405
Qy	121	GCTGGCTGAGGAGAGCCCGGGCAAGCAGGGGGCCCGGATGAGCTTGTCTGGGGAAG	180	1201	CAGATATTAAAGCCGACCAAGCCTCAGTAGTGTCAGAGGAGTCCCCCAAGCAGCATC	1260
Db	326	GCTGGCTGAGGAGAGCCCGGGCAAGCAGGGGGCCCGGATGAGCTTGTCTGGGGAAG	385	1406	CAGATATTAAAGCCGACCAAGCCTCAGTAGTGTCAGAGGAGTCCCCCAAGCAGCATC	1465
Qy	181	CCGCTCTCTTACAGAGTAGCCAGAGTGTCCGGCGCAACGTCAAGTACCGCGGGTCCAG	240	1261	ACAGCCGAGGGCAGTCCCAACCAAGTCAGAGAGCTGGAGCTTCAACGACCGAACCCGC	1320
Db	386	CCGCTCTCTTACAGAGTAGCCAGAGTGTCCGGCGCAACGTCAAGTACCGCGGGTCCAG	445	1466	ACAGCCGAGGGCAGTCCCAACCAAGTCAGAGAGCTGGAGCTTCAACGACCGAACCCGC	1525
				1321	TTCCGGCCCTCGCTCGGCTCAAAAGTTCTCAGGCCAAAACCAAGTATAGATGCTGACACA	1380







1261	GGCAGTCCCAAGTGCAGAGAGCTGGAGCTTCAACGACCGAAACCCGCTTCCGGCCC	1320
1330	TCGCTGGCCCTCAAAAGTTCTCAGCCAAAACCCAGTATAGATGCTGACACAGCCCTTGGC	1389
1321	TCGCTGGCCCTCAAAAGTTCTCAGCCAAAACCCAGTATAGATGCTGACACAGCCCTTGGC	1380
1390	ACTGATGATGATATGATGAAAAAGGATGCCAGTGTGATGATCAGTGGAGAGCTCACC	1449
1381	ACTGATGATGATATGATGAAAAAGGATGCCAGTGTGATGATCAGTGGAGAGCTCACC	1440
1450	CCACCACCTAAACCTGTCATTCGAGCTATCAGATTTAAGATTTGATGTCGAAAAACGG	1509
1441	CCACCACCTAAACCTGTCATTCGAGCTATCAGATTTAAGATTTGATGTCGAAAAACGG	1500
1510	AAGTTTAAAGAAACRRTTACGTCCTATGATGATAAAGATGTCATTTGATGTCGTC	1569
1501	AAGTTTAAAGAAACGTTACGTTCCATATGATGATAAAGATGTCATTTGATGTCGTC	1560
1570	GGTCATCTGGACATGTTGTGTAGAAATTAAAGGCTTCAACACGTTGTGATCAAAATCTT	1629
1561	GGTCATCTGGACATGTTGTGTAGAAATTAAAGGCTTCAACACGTTGTGATCAAAATCTT	1620
1630	GGAAAGGGCAAAATCACATCAGATTAAGAGAGCGGAGAGAAAAATAACAGAGAAACATGAG	1689
1621	GGAAAGGGCAAAATCACATCAGATTAAGAGAGCGGAGAGAAAAATAACAGAGAAACATGAG	1680
1690	ACCACAGACGATCTCAGTATGCTCGGTGCGGTGCTCAAGGTTGAAAAACAGGTACAGTCC	1749
1681	ACCACAGACGATCTCAGTATGCTCGGTGCGGTGCTCAAGGTTGAAAAACAGGTACAGTCC	1740
1750	ATAGAAATCCAGCTGGACCTGCTTACGATCAGTATCAACAGGCTCTTCCGAAAGGCTCT	1809
1741	ATAGAGTCCAGCTGGACCTGCTTACGATCAGTATCAACAGGCTCTTCCGAAAGGCTCT	1800
1810	GCCTCAGCCCTCGCTTGGCTTCAATTCAGTTCCTCCACCTTTTGAATGTGAACAGACATCT	1869
1801	GCCTCAGCCCTCGCTTGGCTTCAATTCAGTTCCTCCACCTTTTGAATGTGAACAGACATCT	1860
1870	GACTATCAAGAGCCCTGGATAGCAAAAGATCTTTGGGTTCCGCAAAAACAGTGGCTGC	1929
1861	GACTATCAAGAGCCCTGGATAGCAAAAGATCTTTGGGTTCCGCAAAAACAGTGGCTGC	1920
1930	TTATCCAGATCAACTAGTGCACATCTCGAGAGGCTCGAGTTCACTTCTGAGCCAAAT	1989
1921	TTATCCAGATCAACTAGTGCACATCTCGAGAGGCTCGAGTTCACTTCTGAGCCAAAT	1980
1990	GAGTTCAAGTCCAGACCTTCTACGCGCTTACGCTTACTATGACAGCTCAAGCAACAGAG	2049
1981	GAGTTCAAGTCCAGACCTTCTACGCGCTTACGCTTACTATGACAGCTCAAGCAACAGAG	2040
2050	GTGCAATTTAGTCAAGAGGATGCTCAGAGTGGCGGACCAACCAACCACTTGCACCAAA	2109
2041	GTGCAATTTAGTCAAGAGGATGCTCAGAGTGGCGGACCAACCAACCACTTGCACCAAA	2100
2110	ATAAATACGGCACCCAGCCAGAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA	2169
2101	ATAAATACGGCACCCAGCCAGAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA	2160
2170	GCCATTAAGCACTTGGCCAGCCAGAAACTCTGCAACCTTAAACCTGACGGCTTACAGGAA	2229
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2221	AGCATTTCTGACGCTCACCACTGCTTGTGTCCTCCAAAGGAAATGTTGAGTTGACAG	2280
2290	TCAAATCTCAACAAAGAGCCGTTCTATGAGGAAAGCTTTGACATGGAGGAGAACTCTG	2349
2281	TCAAATCTCAACAAAGAGCCGTTCTATGAGGAAAGCTTTGACATGGAGGAGAACTCTG	2340
2350	TTGTCGTCTGTCCTCCATGCTGCGAGGACCTTGGGCAAAATCTTTGTCTGTGCAAAAACCTG	2409
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QY 2410 ATCAGGTCGACCGAGGAACCTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2469  
DB 2401 ATCAGGTCGACCGAGGAACCTGAATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460  
QY 2470 GGCAGCCAAAGATTTTACCCCAATGGAGGGAATCCAAATTTGTATTAACCTGATCAAGAG 2529  
DB 2461 GGCAGCCAAAGATTTTACCCCAATGGAGGGAATCCAAATTTGTATTAACCTGATCAAGAG 2520  
QY 2530 GTGGGTCCCGAAGAGACAGACAGACACTTTTGTATGCCGACCGCAGCCTGCCAGGGAA 2589  
DB 2521 GTGGGTCCCGAAGAGACAGACAGACACTTTTGTATGCCGACCGCAGCCTGCCAGGGAA 2580  
QY 2590 GCTGCTTTGATCAGACTCTCTAAGGACTGGAAGGTCAAGATCATCTCAGAGCAATTTGT 2649  
DB 2581 GCTGCTTTGATCAGACTCTCTAAGGACTGGAAGGTCAAGATCATCTCAGAGCAATTTGT 2640  
QY 2650 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAATAA 2703  
DB 2641 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAATAA 2694

## RESULT 7

US-09-810-796-2  
; Sequence 2, Application US/09810796  
; Patent No. US20020102677A1  
; GENERAL INFORMATION:  
; APPLICANT: Jeglia, Timothy James  
; APPLICANT: ICAGEN, Inc.  
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel  
; FILE REFERENCE: 018512-005010US  
; CURRENT APPLICATION NUMBER: US/09/810,796  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 60/190,954  
; PRIOR FILING DATE: 2000-03-21  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 2694  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human outwardly-rectifying, voltage-gated  
; OTHER INFORMATION: potassium channel KCNQ5-1 coding sequence  
; NAME/KEY: CDS  
; LOCATION: (1)..(2694)  
; OTHER INFORMATION: KCNQ5-1  
US-09-810-796-2

Query Match 87.6%; Score 2690.4; DB 9; Length 2694;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2691; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 10 ATGAGGATGTGGAGTCGGCGCGGCGAGGCTGCTGTAACCTCGGACGCCGAGGGGC 69  
DB 1 ATGAGGATGTGGAGTCGGCGCGGCGAGGCTGCTGTAACCTCGGACGCCGAGGGGC 60  
QY 70 GACGCGCTGTACTGCTGGGCACCGCGCGGCCACGCTTGTGTGGCGCGCGGTGGCCTG 129  
DB 61 GACGCGCTGTACTGCTGGGCACCGCGCGGCCACGCTTGTGTGGCGCGCGGTGGCCTG 120  
QY 130 AGGAGAGCCCGGGGCAAGCAGGGGCGCCGGATGAGCCTGTGCTGGGGAAGCCCGCTCT 189  
DB 121 AGGAGAGCCCGGGGCAAGCAGGGGCGCCGGATGAGCCTGTGCTGGGGAAGCCCGCTCT 180  
QY 190 TACACGAGTACGAGCTGCGGCGCAACGCTCAAGTACCGCGCGGTGCAGACTACCTG 249  
DB 181 TACACGAGTACGAGCTGCGGCGCAACGCTCAAGTACCGCGCGGTGCAGACTACCTG 240  
QY 250 TACACGCTGTGGAGAGACCCCGCGCTGGGCGTTTCATCTACCAAGCTTTGTTTTTCTC 309  
DB 241 TACACGCTGTGGAGAGACCCCGCGCTGGGCGTTTCATCTACCAAGCTTTGTTTTTCTC 300

QY 310 CTGTCTTTGGTTCCTTGAATTTTGTCAAGTGTCTTACCATCCCTGACGACACAAATTTG 369  
DB 301 CTGTCTTTGGTTCCTTGAATTTTGTCAAGTGTCTTACCATCCCTGACGACACAAATTTG 360  
QY 370 GCCTCAAGTTGCCCTTCTGATCCTCGAGTTCTGATGATTTGTCGTTCTTTGGTTTGAGTTTC 429  
DB 361 GCCTCAAGTTGCCCTTCTGATCCTCGAGTTCTGATGATTTGTCGTTCTTTGGTTTGAGTTTC 420  
QY 430 ATCAATTCGAATCTGGTCTGCGGGTTGCTGTTTGTTCGATATAGAGGATGCAAGGAACTG 489  
DB 421 ATCAATTCGAATCTGGTCTGCGGGTTGCTGTTTGTTCGATATAGAGGATGCAAGGAACTG 480  
QY 490 AGGTTTGTCTGAAAGCCCTTCTGTTTATAGATACCATTTCTTATCGCTTCAATAGCA 549  
DB 481 AGGTTTGTCTGAAAGCCCTTCTGTTTATAGATACCATTTCTTATCGCTTCAATAGCA 540  
QY 550 GTTGTCTCTGCAAAAACCTCAGGGTAATATTTTTCACGCTCTGCACTCAGAACTCTCCGT 609  
DB 541 GTTGTCTCTGCAAAAACCTCAGGGTAATATTTTTCGACGCTCTGCACTCAGAACTCTCCGT 600  
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DB 661 GGTTCAGTGTGTTATGCTCAGCAAGAAATTAATACAGCTTGGTACATAGGATTTTGT 720  
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DB 841 GACAAAACCTCCCTAACTTGGCTGGGAAGATGCTTCTGCAAGGCTTTCGACTCTCTGGC 900  
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Db 421 ATCAATTCGAACTCTGGTCTGCGGGTGGCTGTTGTCGATATAGAGATGCAAGGAACTG 480  
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Db 481 AGGTTTGTCTGAAAGCCCTCTCTGTGTTATAGATACCAATTTGTTTATCGCTTCAATAGCA 540  
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Db 1501 AAGTTTAAAGGAACGTTTACGTCCATATGATGTAATAAGATGTCATTGAAACAATATTCGTCT 1560  
Qy 1570 GGTCACTCGACATGTTGTGTAGAAATTAATAAGCCCTTCAAAACACGCTGTTGTATCAAAATTC 1629  
Db 1561 GGTCACTCGACATGTTGTGTAGAAATTAATAAGCCCTTCAAAACACGCTGTTGTATCAAAATTC 1620  
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Qy 1750 ATAGAATCCAAGCTGGAATGCTTACTAGACATCTATCAACAGGTCCTTTCGAAAAGGCTCT 1809  
Db 1741 ATAGAGTCCAAGCTGGAATGCTTACTAGACATCTATCAACAGGTCCTTTCGAAAAGGCTCT 1800  
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Qy 1930 TTATCCAGATCAACTAGTGCACCAATCTCGAGAGCCCTGCAAGTTCATTTCTCAACGCAAT 1989  
Db 1921 TTATCCAGATCAACTAGTGCACCAATCTCGAGAGCCCTGCAAGTTCATTTCTCAACGCAAT 1980  
Qy 1990 GAGTTCAGTCCGACATTTCTACGCGTTAGCCCTACTATGCAAGTCAAGCAACACAG 2049  
Db 1981 GAGTTCAGTCCGACATTTCTACGCGTTAGCCCTACTATGCAAGTCAAGCAACACAG 2040  
Qy 2050 GTGCAATTAAGTCAAGCGATGGCTCAGCAGTGCAGCCACCAACACCATTTGCAAAACCA 2109  
Db 2041 GTGCCAATTAAGTCAAGCGATGGCTCAGCAGTGCAGCCACCAACACCATTTGCAAAACCA 2100  
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Db 2281 TCAAAATCTCAACCAAGGACCGTTCTATGAGGAAAAGCTTTTGAATGGGAGGAGAACTCTG 2340  
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Qy 2410 ATCAGGTCGACCGAGGAACTGAATATACAACTTTTCAAGGAGTGAAGTGGCTTCCAGA 2469  
Db 2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTTCAAGGAGTGAAGTGGCTTCCAGA 2460  
Qy 2470 GGCAGCAAGATTTTATCCCAATGGAGGAAATCCAAATGTTTATTAATCTGATGAAGAG 2529  
Db 2461 GGCAGCAAGATTTTATCCCAATGGAGGAAATCCAAATGTTTATTAATCTGATGAAGAG 2520  
Qy 2530 GTGGGTCGCAAGAGACAGAGACAGACTTTTTCATGTCGCGACCCGAGCCCTGCCAGGAA 2589  
Db 2521 GTGGGTCGCAAGAGACAGAGACAGACTTTTTCATGTCGCGACCCGAGCCCTGCCAGGAA 2580  
Qy 2590 GCTCCCTTTGATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2649  
Db 2581 GCTCCCTTTGATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640

Qy 2650 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAATAA 2703  
Db 2641 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAATAA 2694

RESULT 9  
US-09-825-147-1  
; Sequence 1, Application US/09825147  
; Patent No. US2002042505A1  
; GENERAL INFORMATION:  
; APPLICANT: Hu, Yi  
; APPLICANT: Kieke, James Alvin  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Nehls, Michael C.  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. US2002042505A1el Human Ion Channel Protein and  
; FILE REFERENCE: Polynucleotides Encoding the Same  
; CURRENT APPLICATION NUMBER: US/09/825,147  
; CURRENT FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: US 60/194,255  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2772  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-825-147-1

Query Match 85.8%; Score 2635.4; DB 9; Length 2772;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 2673; Conservative 1; Mismatches 2; Indels 27; Gaps 1;

Qy 1 GGCAGCGGATCAAGGATGTGAGTGGGCGGGGCGGGGAGGCTGCTGAACTCGGAGCC 60  
Db 97 GGCAGCGGATCAAGGATGTGAGTGGGCGGGGCGGGGAGGCTGCTGAACTCGGAGCC 156

Qy 61 GCCAGGGGCGAGCGGCTGCTACTGTGGGACCCCGCGGGGCGGCGGCGGCGGCG 120  
Db 157 GCCAGGGGCGAGCGGCTGCTACTGTGGGACCCCGCGGGGCGGCGGCGGCGGCG 216

Qy 121 GGTGGCTGAGGAGAGCGCGCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180  
Db 217 GGTGGCTGAGGAGAGCGCGCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 276

Qy 181 CCGCTCTCTTACACAGTAGTACGAGCTGCGCGGGGCGGCGGCGGCGGCGGCGGCG 240  
Db 277 CCGCTCTCTTACACAGTAGTACGAGCTGCGCGGGGCGGCGGCGGCGGCGGCGG 336

Qy 241 AACTACCTGTACAACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
Db 337 AACTACCTGTACAACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 396

Qy 301 GTTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
Db 397 GTTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 456

Qy 361 ACAAAATGGCCCTCAAGTTGCCCTTTGATCCTGGAGTTCGATGATGATGATGATGAT 420  
Db 457 ACAAAATGGCCCTCAAGTTGCCCTTTGATCCTGGAGTTCGATGATGATGATGATGAT 516

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Db 517 TTGAGTTTCATCATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 576

Qy 481 GGAAGACTCAGGTTTGTCTGAAAGCCCTTCTGTGTTATAGATACCAATGCTTCTTAT 540  
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Db 637 TCAATAGCAGTTGTTTCTGCAAAAACCTCAGGGTAATATATTTTTCGCCACGCTGCACCTCAGA 696

Qy 601 AGTCTCCGTTTCTTACAGATCCTCCGATGCTGCGCATGCGATGCGATGCGATGCGATGCG 660  
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Qy 721 GGATTTTGGTTCCTTATTTTTCGTTCTTCTGTTGCTTATCTGTTGGAAGGATGCGCAAT 780  
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Qy 781 AAAGAGTTTCTACATATGAGATGCTCTGTTGGGCGACAAATTAATTAATTAATTAATTAAT 840  
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Qy 841 GGCTATGGAGACAAAACCTCCCTTAACTTGGCTGGGAGGATGCTTCTGAGGCTTTGCA 900  
Db 937 GGCTATGGAGACAAAACCTCCCTTAACTTGGCTGGGAGGATGCTTCTGAGGCTTTGCA 996

Qy 901 CTCCTTGGCAATTTCTTTTTCGTTTTCGCTGCGGCAATCTTGGCTCAGGTTTTCGATTA 960  
Db 997 CTCCTTGGCAATTTCTTTTTCGTTTTCGCTGCGGCAATCTTGGCTCAGGTTTTCGATTA 1056

Qy 961 AAAGTACAGAAACAAACACCCGAGAAACACTTTGAGAAAGAGGAAACCCAGCTGCGAAC 1020  
Db 1057 AAAGTACAGAAACAAACACCCGAGAAACACTTTGAGAAAGAGGAAACCCAGCTGCGAAC 1116

Qy 1021 CTCATTGAGTGTGTTTGGGCTAGTTACGCAAGTGTAGAGAAATCTGTTTTCATTTGCAACC 1080  
Db 1117 CTCATTGAGTGTGTTTGGGCTAGTTACGCAAGTGTAGAGAAATCTGTTTTCATTTGCAACC 1176

Qy 1081 TGAAGCCACACTTGAAGGCTTGCACCTGCGAGCCCTACCAAGAAAGAAACCAAGGGAA 1140  
Db 1177 TGAAGCCACACTTGAAGGCTTGCACCTGCGAGCCCTACCAAGAAAGAAACCAAGGGAA 1220

Qy 1141 GCATCAGCAGTCAAGAGCTAAAGTTTAAAGAGCGAGTGCATGCTAGCCCCAGGGC 1200  
Db 1221 -----TCAGAACTAAGTTTAAAGAGCGAGTGCATGCTAGCCCCAGGGC 1269

Qy 1201 CAGAGTATTAAGAGCCGACAAAGCCTCAGTATGAGTGAAGAGGTTCCCAAGCAGCGACATC 1260  
Db 1270 CAGAGTATTAAGAGCCGACAAAGCCTCAGTATGAGTGAAGAGGTTCCCAAGCAGCGACATC 1329

Qy 1261 ACAGCCGAGGCGAGTCCCAAGTGCAGAGAGCTGGAGCTTCAACGACCGAACCCGC 1320  
Db 1330 ACAGCCGAGGCGAGTCCCAAGTGCAGAGAGCTGGAGCTTCAACGACCGAACCCGC 1389

Qy 1321 TTCCGGCCCTCGCTGCGCTCAAAAGTTCTCAGCAAAAACAGTGATAGTGTGACACA 1380  
Db 1390 TTCCGGCCCTCGCTGCGCTCAAAAGTTCTCAGCAAAAACAGTGATAGTGTGACACA 1449

Qy 1381 GCCCTGGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440  
Db 1450 GCCCTGGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1509

Qy 1441 GACCTCACCCCAACCACTTAAACCTGTCTATTCGAGCTATCAGAAATTTATGAAATTTTCATG 1500  
Db 1510 GACCTCACCCCAACCACTTAAACCTGTCTATTCGAGCTATCAGAAATTTATGAAATTTTCATG 1569

Qy 1501 GCAAAACGGAAGTTTAAAGAAACCTTACGTCATATGATGATGATGATGATGATGATGATGATG 1560  
Db 1570 GCAAAACGGAAGTTTAAAGAAACCTTACGTCATATGATGATGATGATGATGATGATGATGATG 1629

Qy 1561 TATTCTGCTGCTCATCTGGACATGTTGTGATAGAAATTAAGCCCTTCAAAACGCTGTTGAT 1620  
Db 1630 TATTCTGCTGCTCATCTGGACATGTTGTGATAGAAATTAAGCCCTTCAAAACGCTGTTGAT 1689

Qy 1621 CAAATTTCTTGGAAAGGGGCAAAATCACATCAGATAGAGAGCCGAGGAAATTAACAGCA 1680

Db 1690 CAAATCTTGGAAAGGGCAAAATACATCAGATAGAAAGCCGAGAGAAATAACAGCA 1749  
Qy 1681 GAACATGAGACACAGACGATCTCAGTATGCTCGGTGGGTGGTCAAGGTTGAAAAACAG 1740  
Db 1750 GAACATGAGACACAGACGATCTCAGTATGCTCGGTGGGTGGTCAAGGTTGAAAAACAG 1809  
Qy 1741 GTACAGTCCATAGAAATCCAAAGTGGACTGCGCTACTAGACATCTATCAACAGGTCCTTCGG 1800  
Db 1810 GTACAGTCCATAGAAATCCAAAGTGGACTGCGCTACTAGACATCTATCAACAGGTCCTTCGG 1869  
Qy 1801 AAAGGCTCTGCTCAGCCCTCGCTTGGCTTCATTCAGATGCCACCTTTTGAATGCAA 1860  
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Qy 1861 CAGACATCTGACTATCAAGCCCTGTGATAGCAAAAGATCTTCGGGTTCGCGCAAAAC 1920  
Db 1930 CAGACATCTGACTATCAAGCCCTGTGATAGCAAAAGATCTTCGGGTTCGCGCAAAAC 1989  
Qy 1921 AGTGGCTGCTTATCCAGATCAACTAGTGGCAACATCTCGAGAGGCTGCAATTCATTCG 1980  
Db 1990 AGTGGCTGCTTATCCAGATCAACTAGTGGCAACATCTCGAGAGGCTGCAATTCATTCG 2049  
Qy 1981 ACGCCAATGATGTCAGTCCGACACTTCTACGGCTTAGCCCTACTATGCACAGTCAA 2040  
Db 2050 ACGCCAATGATGTCAGTCCGACACTTCTACGGCTTAGCCCTACTATGCACAGTCAA 2109  
Qy 2041 GCAACACAGGTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGGCCACCAACACCAATT 2100  
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Qy 2101 GCAACCAAAATAATACGGCACCCAAAGCCAGCAGCCCCCAACAACTTTACAGATCCCACT 2160  
Db 2170 GCAACCAAAATAATACGGCACCCAAAGCCAGCAGCCCCCAACAACTTTACAGATCCCACT 2229  
Qy 2161 CCTCTCCAGCCATCAAGCATCTGCCAGGCGCAGAACTCTGCCACCTTAAACCTTGCAGGC 2220  
Db 2230 CCTCTCCAGCCATCAAGCATCTGCCAGGCGCAGAACTCTGCCACCTTAAACCTTGCAGGC 2289  
Qy 2221 TTACAGGAAAGCATTTCTGAGCTCACCACTGCTTGTGTGCTTCAAGGAAATGTTTCAG 2280  
Db 2290 TTACAGGAAAGCATTTCTGAGCTCACCACTGCTTGTGTGCTTCAAGGAAATGTTTCAG 2349  
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Qy 2341 GAAACTCTGTTGCTGTCTGTCCTGTCGCGAGGACTTGGGCAATCTTTGCTCTGTG 2400  
Db 2410 GAAACTCTGTTGCTGTCTGTCCTGTCGCGAGGACTTGGGCAATCTTTGCTCTGTG 2469  
Qy 2401 CAAACCTGATCAGGTCCAGCGAGGAACTGAATATACAACTTTCAGGGAGTGAAGTCAAGT 2460  
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Qy 2461 GGCTCCAGAGCAGCAAGATTTTTCACCAATGGAGGAAATCCAAATGTTTATAACT 2520  
Db 2530 GGCTCCAGAGCAGCAAGATTTTTCACCAATGGAGGAAATCCAAATGTTTATAACT 2589  
Qy 2521 GATGAGAGGTGGTCCGAGAGACAGACAGACACTTTTGTATGCGCGACCCGAGCCT 2580  
Db 2590 GATGAGAGGTGGTCCGAGAGACAGACAGACACTTTTGTATGCGCGACCCGAGCCT 2649  
Qy 2581 GCCAGGGAAGTGCCTTTGCAATCAGACTCTCTAAGGACTGGAAGGTACAGATCATCTCAG 2640  
Db 2650 GCCAGGGAAGTGCCTTTGCAATCAGACTCTCTAAGGACTGGAAGGTACAGATCATCTCAG 2709  
Qy 2641 AGCATTTGTAAGGCAAGGAAAGTACAGATGCGCTCAGCTTGCCTCATGTCAAACTGAAA 2700  
Db 2710 AGCATTTGTAAGGCAAGGAAAGTACAGATGCGCTCAGCTTGCCTCATGTCAAACTGAAA 2769  
Qy 2701 TAA 2703  
|||

Db 2770 TAA 2772  
RESULT 10  
US-10-803-268-1  
; Sequence 1, Application US/10803268  
; Publication No. US20040157259A1  
; GENERAL INFORMATION:  
; APPLICANT: Hu, Yi  
; APPLICANT: Kieke, James Alvin  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Nehls, Michael C.  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: Novel Human Ion Channel Protein and  
; FILE REFERENCE: LEX-0160-USA  
; CURRENT APPLICATION NUMBER: US/10/803,268  
; CURRENT FILING DATE: 2004-03-18  
; PRIOR APPLICATION NUMBER: US/09/825,147  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: US 60/194,255  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2772  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-803-268-1  
Query Match 85.8%; Score 2635.4; DB 18; Length 2772;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 2673; Conservative 1; Mismatches 2; Indels 27; Gaps 1;  
Qy 1 GGCAGCGCATGAAGGATGGAGTCGGCGCGGGCAGGGTGCTGCTGAATCGGCAGCC 60  
Db 97 GGCAGCGCATGAAGGATGGAGTCGGCGCGGGCAGGGTGCTGCTGAATCGGCAGCC 156  
Qy 61 GCCAGGGCGCAGCGCTTACTCTGGGACCCCGCGGGCAGCGTGGTGGGGGGCGC 120  
Db 157 GCCAGGGCGCAGCGCTTACTCTGGGACCCCGCGGGCAGCGTGGTGGGGGGCGC 216  
Qy 121 GGTGGCTGAGGGAGAGCCCGGGGCAAGCAGGGGGCCCGGATGAGCTCTCGGGGAAG 180  
Db 217 GGTGGCTGAGGGAGAGCCCGGGGCAAGCAGGGGGCCCGGATGAGCTCTCGGGGAAG 276  
Qy 181 CCGCTCTTTACAGAGTAGCCAGAGCTGCCGGCGCAACGTCAGTACCGGGGGTGCAG 240  
Db 277 CCGCTCTTTACAGAGTAGCCAGAGCTGCCGGCGCAACGTCAGTACCGGGGGTGCAG 336  
Qy 241 AACTACCTGTACACAGTGTGGAGAGACCCCGCGGCTGGGGGTTTCATCTACACGCTTTC 300  
Db 337 AACTACCTGTACACAGTGTGGAGAGACCCCGCGGCTGGGGGTTTCATCTACACGCTTTC 396  
Qy 301 GTTTTCTCTCTGTCTTGTGTTGCTTGAATTTGTCAAGTGTCTTGTCAATCCCTGAGCAC 360  
Db 397 GTTTTCTCTCTGTCTTGTGTTGCTTGAATTTGTCAAGTGTCTTGTCAATCCCTGAGCAC 456  
Qy 361 ACAAAATTTGGCTCAAGTGTGCTTGTATCTGATCTGAGTTCGTGATGATGTGCTTTGGT 420  
Db 457 ACAAAATTTGGCTCAAGTGTGCTTGTATCTGATCTGAGTTCGTGATGATGTGCTTTGGT 516  
Qy 421 TTGAGTTCATCATTCGAATCTGGTCTGCGGGTGTGTTGTCGATATAGAGGATGGCAA 480  
Db 517 TTGAGTTCATCATTCGAATCTGGTCTGCGGGTGTGTTGTCGATATAGAGGATGGCAA 576  
Qy 481 GGAAAGCTGAGGTTTGTTCGAAAGCCCTTCTGTGTTATAGATACCATTTGTTCTTATCGCT 540  
Db 577 GGAAAGCTGAGGTTTGTTCGAAAGCCCTTCTGTGTTATAGATACCATTTGTTCTTATCGCT 636  
Qy 541 TCAATAGCAGTTGTTTCTGCAAAACTCAGGGTAAATATTTTGGCAGCTGCGACTCAGA 600



1690	CAAAATCTTTGGAAAAGGGCAAAATCAATCAGATAGAAAGACCCGAGAGAAAATTAACAGCA	1749
1681	GAACATGACACACACAGACGATCTCAGTATGCTCGGTCCGGTGGTCAAGGTTGAAAACACAG	1740
1750	GAACATGACACACACAGACGATCTCAGTATGCTCGGTCCGGTGGTCAAGGTTGAAAACACAG	1809
1741	GTACAGTCCATAGAAATCCAAAGCTGGACGCTCTAGACATCTATCAACAGGTCCTTCGG	1800
1810	GTACAGTCCATAGAAATCCAAAGCTGGACGCTCTAGACATCTATCAACAGGTCCTTCGG	1869
1801	AAAGGCTCTGCTTCAGCCCTCGCTTGGCTTCATTCAGTTCGCCAGTTCCTTTGAATGTGAA	1860
1870	AAAGGCTCTGCTTCAGCCCTCGCTTGGCTTCATTCAGTTCGCCAGTTCCTTTGAATGTGAA	1929
1861	CAGACATCTGACTATCAAAAGCCCTGTGGATACAAAGATCTTTTCGGGTTCCGCAACAAAC	1920
1930	CAGACATCTGACTATCAAAAGCCCTGTGGATACAAAGATCTTTTCGGGTTCCGCAACAAAC	1989
1921	AGTGGCTGCTTATCCAGATCAACTAGTGCACACATCTCGAGAGGCTGCGAGTTCATCTCTG	1980
1990	AGTGGCTGCTTATCCAGATCAACTAGTGCACACATCTCGAGAGGCTGCGAGTTCATCTCTG	2049
1981	ACGCCAAATCAGTTCAGTGCACACATCTTACGCGCTTTAGCGCTTATGACAGTCAAA	2040
2050	ACGCCAAATCAGTTCAGTGCACACATCTTACGCGCTTTAGCGCTTATGACAGTCAAA	2109
2041	GCACACAGGTGCGCAATTAGTCAAGCGATGGCTCAGCAGTGCAGCCACCAACACCAAT	2100
2110	GCACACAGGTGCGCAATTAGTCAAGCGATGGCTCAGCAGTGCAGCCACCAACACCAAT	2169
2101	GCACACAAATTAATACGGCACCCAAAGCCAGCAGCCCAACCAACTTTACAGATCCCACT	2160
2170	GCACACAAATTAATACGGCACCCAAAGCCAGCAGCCCAACCAACTTTACAGATCCCACT	2229
2161	CCTCTCCAGCCATCAAGCATCTGCGCAGGCGAGAACTCTGACACCTCAACCTCGCAGC	2220
2230	CCTCTCCAGCCATCAAGCATCTGCGCAGGCGAGAACTCTGACACCTCAACCTCGCAGC	2289
2221	TTACAGGAAAGCATTTCTGAGCTCACCACTGCTTGTTCCTTCCAGGAAATTTGTTTCA	2280
2280	TTACAGGAAAGCATTTCTGAGCTCACCACTGCTTGTTCCTTCCAGGAAATTTGTTTCA	2349
2281	GTTCACAGTCAAAATCTCAACAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGA	2340
2350	GTTCACAGTCAAAATCTCAACAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGA	2409
2341	GAACCTGTTGTTCTGCTGCTCCATGCTGCGGAGGACCTTTGGGCAAAATCTTTGCTGTG	2400
2410	GAACCTGTTGTTCTGCTGCTCCATGCTGCGGAGGACCTTTGGGCAAAATCTTTGCTGTG	2469
2401	CAAAACCTGATCAGTTCGACCCGAGAACTGAAATATACACTTTTTCAGGAGTGCAGT	2460
2470	CAAAACCTGATCAGTTCGACCCGAGAACTGAAATATACACTTTTTCAGGAGTGCAGT	2529
2461	GGCTCAGAGGAGCAAGATTTTACCCCAATTTGAGGGAATCCAAATTTGTTTATACT	2520
2530	GGCTCAGAGGAGCAAGATTTTACCCCAATTTGAGGGAATCCAAATTTGTTTATACT	2589
2521	GATGAAGAGGTGGGTCCGGAAGAGACAGACACTTTTGTATGCGCAGCCGAGCCT	2580
2590	GATGAAGAGGTGGGTCCGGAAGAGACAGACACTTTTGTATGCGCAGCCGAGCCT	2649
2581	GCCAGGAAAGCTGGCTTTGTCATCAGACTCTTAGGACTGGAAGTCAAGATCATCTCAG	2640
2650	GCCAGGAAAGCTGGCTTTGTCATCAGACTCTTAGGACTGGAAGTCAAGATCATCTCAG	2709
2641	AGCATTTGTAAGCGCAGGAAAGTACAGATGCCCTTCAGCTTGCCTCATGTCAAACTGAAA	2700
2710	AGCATTTGTAAGCGCAGGAAAGTACAGATGCCCTTCAGCTTGCCTCATGTCAAACTGAAA	2769
2701	TAA	2703
2770	TAA	2772



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RESULT 11
US-09-810-796-3
; Sequence 3, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1e1 Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2667
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCNQ5-2 coding sequence
; NAME/KEY: CDS
; LOCATION: (1)..(2667)
; OTHER INFORMATION: KCNQ5-2
US-09-810-796-3

Query Match      85.5%; Score 2626.4; DB 9; Length 2667;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2664; Conservative 1; Mismatches 2; Indels 27; Gaps 1;

Qy 10 ATGAAGATGGAGTCCGGCGGGCAGGGTGTGCTGAACTCGGCGAGCCGCCAGGGGC 69
Db 1 ATGAAGATGGAGTCCGGCGGGCAGGGTGTGCTGAACTCGGCGAGCCGCCAGGGGC 60

Qy 70 GACGCCCTGTACTGCTGGGACCCCGCGGCGCACGCTTGTGGCGGGCGGGTGGCCCTG 129
Db 61 GACGCCCTGTACTGCTGGGACCCCGCGGCGCACGCTTGTGGCGGGCGGGTGGCCCTG 120

Qy 130 AGGGAGACCCCGGGGCAAGCAGGGGCGCGGATGAGCTGCTGGGGAAGCCGCTCTCT 189
Db 121 AGGGAGACCCCGGGGCAAGCAGGGGCGCGGATGAGCTGCTGGGGAAGCCGCTCTCT 180

Qy 190 TACAGAGTAGCAGAGCTGCCGGCGCAACGTCAGAGTACCGCGCGGTGCAGAACTACCTG 249
Db 181 TACAGAGTAGCAGAGCTGCCGGCGCAACGTCAGAGTACCGCGCGGTGCAGAACTACCTG 240

Qy 250 TACAACGTGCTGGAGAGACCCCGGGCTGGGGCTTCATCAGCGCTTTCGTTTCTC 309
Db 241 TACAACGTGCTGGAGAGACCCCGGGCTGGGGCTTCATCAGCGCTTTCGTTTCTC 300

Qy 310 CTGTGCTTGTGTGCTGATTTGTGAGTGTGCTTACCATCCCTGAGCAGCAAAATG 369
Db 301 CTGTGCTTGTGTGCTGATTTGTGAGTGTGCTTACCATCCCTGAGCAGCAAAATG 360

Qy 370 GCCTCAAGTGCCTCTGATCCTGGAGTTCGTGATGATGTGCTTGTGGTGGAGTTC 429
Db 361 GCCTCAAGTGCCTCTGATCCTGGAGTTCGTGATGATGTGCTTGTGGTGGAGTTC 420

Qy 430 ATCATTCAATCTGTGCTGGGGTGTGCTGATATAGAGATGAGAGATGCAAGAGACTG 489
Db 421 ATCATTCAATCTGTGCTGGGGTGTGCTGATATAGAGATGAGAGATGCAAGAGACTG 480

Qy 490 AGGTTTGTCCGAAGCCCTTCTGTGATATAGATACCATTTCTTATCGCTTCAATAGCA 549
Db 481 AGGTTTGTCCGAAGCCCTTCTGTGATATAGATACCATTTCTTATCGCTTCAATAGCA 540

Qy 550 GTTGTCTCTGCAAAACTCAGGTAATATTTTTCACGCTGTGCACTCAGAACTCCGT 609
Db 541 GTTGTCTCTGCAAAACTCAGGTAATATTTTTCACGCTGTGCACTCAGAACTCCGT 600
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Qy 610 TTCCTACAGATCTCCCGCATGGTGGCATGAGCCGAGGGAGGACCTTTGGAATTAATCTG 669
Db 601 TTCCTACAGATCTCCCGCATGGTGGCATGAGCCGAGGGAGGACCTTTGGAATTAATCTG 660

Qy 670 GGTTCAGTGGTTTATGCTCACAGCAAGAAATTAATCACAGCTTGTGATCATAGGATTTTG 729
Db 661 GGTTCAGTGGTTTATGCTCACAGCAAGAAATTAATCACAGCTTGTGATCATAGGATTTTG 720

Qy 730 GTTCTTAATTTTTCGTCTTTCTCTGCTATCTGCTGGTGGAAAGGATGCCAATAAAGAGTTT 789
Db 721 GTTCTTAATTTTTCGTCTTTCTCTGCTATCTGCTGGTGGAAAGGATGCCAATAAAGAGTTT 780

Qy 790 TCTACATATGAGATGCTCTCTGCTGGGGCAAAATTAATTAATTAATTAATTAATTAATTA 849
Db 781 TCTACATATGAGATGCTCTCTGCTGGGGCAAAATTAATTAATTAATTAATTAATTAATTA 840

Qy 850 GACAAACTCCCTAACTTTGGCTGGGAAGATTGCTTTCTGCAAGCTTTGCACTCTCTGGC 909
Db 841 GACAAACTCCCTAACTTTGGCTGGGAAGATTGCTTTCTGCAAGCTTTGCACTCTCTGGC 900

Qy 910 ATTTCTTTTTCGCACTTCTCCCGGCATTTCTGGCTCAGGTTTGTCAATTAAGATACAA 969
Db 901 ATTTCTTTTTCGCACTTCTCCCGGCATTTCTGGCTCAGGTTTGTCAATTAAGATACAA 960

Qy 970 GAACAACACCCCGCAGAAACACTTTTGAGAAAGAGAAACCCAGCTGCCAACTCAATCAG 1029
Db 961 GAACAACACCCCGCAGAAACACTTTTGAGAAAGAGAAACCCAGCTGCCAACTCAATCAG 1020

Qy 1030 TGTGTTTGGCGTAGTTACGCACTGATGAGAAATCTGTTTCCATTTGCAACCTGGAAGCCA 1089
Db 1021 TGTGTTTGGCGTAGTTACGCACTGATGAGAAATCTGTTTCCATTTGCAACCTGGAAGCCA 1080

Qy 1090 CACTTGAAGGCTTTGCACTGCACTGCAAGCCCTTCAAGAAAGAAACCAAGGGAAGCATCAAGC 1149
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Db 1116 --TCAGAAAGCTTAAGTTTAAAGAGCGAGTGCGCATGGCTAGCCCGAGGGGCGCAGATATT 1173

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Qy 1270 GGCAGTCCCAACCAAGTGCAGAAAGCTGAGCTTCAACGACCGAACCCGCTTCGGGCC 1329
Db 1234 GGCAGTCCCAACCAAGTGCAGAAAGCTGAGCTTCAACGACCGAACCCGCTTCGGGCC 1293

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Qy 1390 ACTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1449
Db 1354 ACTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1413

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Qy 1510 AAGTTTAAGGAACCTTACGCTCCATATGATGATGATGATGATGATGATGATGATGATGATGAT 1569
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Qy 1570 GGTCACTCGGACATGTTGTGTAGAAATTAAGAGCCCTTCAAAACCGTGTGATGATGATGATGAT 1629
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Qy 1630 GGAAGAGGCGCAATCAGATCAGATAAGAGAGCGGAGAGAAATAAAGAGAGAGAGAGAGAG 1689
Db 1594 GGAAGAGGCGCAATCAGATCAGATAAGAGAGCGGAGAGAAATAAAGAGAGAGAGAGAGAG 1653

Qy 1690 ACCAGAGAGATCTCAGTATGCTCGGTGGGTGGTCAAGGTTGAAAGGATGAGAGAGAGAGAG 1749
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1520	CAAAAGAGCTGGAGCTTCAATGACCCGACACCGCTTCCGGGCAATCTCTGAGACTC-----	1573
1348	TCTCAGCCAAAACCCAGTGATAGATGCTGACACAGCCCTTTGGCACTGATGATATATGAT	1407
1574	-----AAACCCCGCACCCTCTGTGAGGATGCC-----CCTCAGAGGAAGTAGCAGAG	1621
1408	GAATAAGGATGCCAGTGATGATGATCAGTGGAAAGACCTCACCCACCCTTAAACTCTC	1467
1622	GAGAAGAGCTACCAAGTGTGAGCTCACGGTGGACGACATCATCGCTGCTGTGAAGACAGTC	1681
1468	ATTGAGCTATCAGAAATTTAAATTTCTATGTTGCAAAACCGAAGTTTAAAGGAAACRTTA	1527
1682	ATCCGCTCCATCAGGATTTCTCAAGTTCCTGCTGGCCCAAAGGAAATTTCAAGGAGACATG	1741
1528	CGTCCATATGATGTAAAGATGTCAATGAAATAATTTCTGCTGGTCTCATCTGACATGTTG	1587
1742	CGACCGTACGACGTGAAGGACGTCATTTGACGAGTACTCAGCAGGCCACCTGGACATGCTG	1801
1588	TGTAGAAATTAAGCCCTTCAACACGCTGTTGATCAAAATTTCTTGGAAAAGGGC---AAATC	1644
1802	GGCCGGATCAAGAGCCTGCAAACTCGGGGTGACCAAAATTTGTGGTGGGGGCCCGGGGAC	1861
1645	ACATCAGATAAAGAGCGGAGAGAAATAACAGCAGAAACATGAGACCAACAGAGATCTC	1704
1862	AGGAAGGCCCGGAGAGAGGGCGACAAGGGGCCCTCCGACGCGAGGTGGTGGATGAAATC	1921
1705	AGATGCTCGGTGCGGTGCTCAAGTTGAAACACAGGTACAGTCCATAGAAATCCAAAGCTG	1764
1922	AGCATGATGGGACGCGTGGTCAAGGTGGAGAGCAGGTGCGATCCATCGAGCACAAGCTG	1981
1765	GACTGCTACTAGACATCTATCAACAGGTCTCTCGGAAGGCTCTGCTCAGCCCTCGCT	1824
1982	GACCTGCTGTTGGGCTTCTATTCGGCTGCCTGC-----GCTTGGCACCTCGGCCAGC	2035
1825	TTGGCTTCAATCCAGTTCCTCCACCTTTTGAATGTGAAACAGACATCTGACTATCAAGCCCT	1884
2036	CTGGGCGCGTGCAAAGTGCCTGTGTGACCCCGACATCATCTCCGACTACACAGCCCT	2095
1885	GTGGATAGCAAAAGATCTTTTCGGGTTTCGACACAAA	1918
2096	GTGGACCAAGGACATCTCCGCTCCGACAGA	2129
<p>RESULT 14</p> <p>US-10-096-578-88</p> <p>Sequence 88, Application US/10096578</p> <p>Publication No. US20030165874A1</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Leppert, Mark F.</p> <p>APPLICANT: Singh, Nanda</p> <p>APPLICANT: Charlier, Carole</p> <p>TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)</p> <p>TITLE OF INVENTION: AND OTHER EPILEPSIES</p> <p>FILE REFERENCE: 2323-160</p> <p>CURRENT APPLICATION NUMBER: US/10/096,578</p> <p>CURRENT FILING DATE: 2002-03-14</p> <p>PRIOR APPLICATION NUMBER: US 09/177,650</p> <p>PRIOR FILING DATE: 1998-10-23</p> <p>PRIOR APPLICATION NUMBER: US 60/063,147</p> <p>PRIOR FILING DATE: 1997-10-24</p> <p>NUMBER OF SEQ ID NOS: 129</p> <p>SOFTWARE: PatentIn Ver. 2.0</p> <p>SEQ ID NO 88</p> <p>LENGTH: 2273</p> <p>TYPE: DNA</p> <p>ORGANISM: Mus musculus</p> <p>FEATURE:</p> <p>NAME/KEY: CDS</p> <p>LOCATION: (1)..(2271)</p> <p>NAME/KEY: misc_feature</p> <p>LOCATION: (1)..(2273)</p> <p>OTHER INFORMATION: n may be any nucleotide except at position</p>		



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; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
;
; FILE REFERENCE: DC58aDIV
;
; CURRENT APPLICATION NUMBER: US/10/128,870
;
; CURRENT FILING DATE: 2002-04-24
;
; PRIOR APPLICATION NUMBER: 09/105,058
;
; PRIOR FILING DATE: June 26, 1998
;
; PRIOR APPLICATION NUMBER: 60/055,599
;
; PRIOR FILING DATE: August 12, 1997
;
; NUMBER OF SEQ ID NOS: 28
;
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 22
;
; LENGTH: 2169
;
; TYPE: DNA
;
; ORGANISM: MOUSE
;
; US-10-128-870-22

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Query Match	16.7%	Score 511.6	DB 13	Length 2169
Best Local Similarity	58.2%	Pred. No. 1.5e-137		
Matches 1044	Conservative 0	Mismatches 669	Indels 81	Gaps 5
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Db	187	GGAGCGGGGAACCCCGCAAGCAAGCCCTTACCGCAAGCTGCAGAAATTTCTCTAC	246	
Qy	253	AACGTGCTGGAGAGACCCCGGCTGGGCGTTCATCTACACGCTTTCGTTTTCTCTT	312	
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Job time : 1683 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 2, 2005, 21:32:07 ; Search time 9451 Seconds  
(without alignments)  
12368.572 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gsei:\*  
9: gb\_gse2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2115.4	68.9	2729	9 AY407015	AY407015 Mus muscu
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AY407013 genomic survey sequence.  
ACCESSION AY407013  
VERSION AY407013.1 GI:39762984  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2733)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 2733)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
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DEFINITION genomic survey sequence.
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VERSION AY407015.1 GI:39762986
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2729)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2729)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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 ORGANISM Pan troglodytes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 REFERENCE 1 (bases 1 to 2014)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Gargill,M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 2014)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,

Adams, M.D. and Cargill, M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
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HTC; CAP trapper.  
Mus musculus (house mouse)  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
99279253  
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Genome Res. 10 (10), 1617-1630 (2000)  
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Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,  
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20530913  
11076861

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FANTOM Consortium  
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The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
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of 60,770 full-length cDNAs  
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Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, Y.,  
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,  
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,

Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Oheato, N.,  
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
Muramatsu, M. and Hayashizaki, Y.  
Direct Submission  
Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp,  
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/  
Location/Qualifiers  
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## RESULT 5

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DEFINITION CD629762  
ACCESSION CD629762  
VERSION CD629762.1 GI:40278028  
KEYWORDS EST.

## SOURCE

Organism Homo sapiens (human)  
Tissue  
Cell  
Strain

## REFERENCE

1 (bases 1 to 797)  
Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.  
Circular rapid amplification of cDNA ends for high-throughput  
extension cloning of partial genes  
Genomics 84 (1), 205-210 (2004)  
Contact: Fu GK  
Incyte Genomics, Inc.  
3160 Porter Dr., Palo Alto, CA 94304, USA

BG532543
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 EST.
 Homo sapiens (human)
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: CLONETECH Laboratories, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
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 /clone="IMAGE:4699776"
 /tissue\_type="embryonal carcinoma"
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 /notes="Organ: testis; Vector: pDNR-LIB (Clontech); Site\_1: SfII (ggcgctcgcc); Site 2: SfII (ggcgctcgcc); Site 3: SfII (ggcgctcgcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCG-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 clones contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."
 Query Match 22.6%; Score 694; DB 4; Length 734;
 Best Local Similarity 98.4%; Pred. No. 4.3e-180;
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 DB 1 TACAGATCCACCTCTCTCCAGCCATCAAGCATCTGCCAGCCAGGAACTCTGCACC 60
 QY 2207 CTAACCTCTGACAGGCTTACAGGAAAGCATTTCTGACGTCAACCTGCTGCTTGTTCCTCCA 2266
 DB 61 CTAACCTCTGACAGGCTTACAGGAAAGCATTTCTGACGTCAACCTGCTGCTTGTTCCTCCA 120
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 QY 2327 TTGACATGGGAGGAGAACTCTGTTGCTGTCTGCTCCCATGCTGCGGAGGACTTGGGCA 2386
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 DB 241 AATCTTTGCTGTGCAAACTCTGATTCAGTTCGACGAGAACTGAATATCAACTTTCAG 300
 QY 2447 GGAGTGAGTCAAGTGGCTCCAGAGCGACCCAGATTTTACCCAAATGGAGGAAATCCA 2506
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 BG532543.1 GI:13524082
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 Homo sapiens (human)
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: CLONETECH Laboratories, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
 http://image.llnl.gov
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 /clone\_lib="NIH\_MGC\_61"
 /notes="Organ: testis; Vector: pDNR-LIB (Clontech); Site\_1: SfII (ggcgctcgcc); Site 2: SfII (ggcgctcgcc); Site 3: SfII (ggcgctcgcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCG-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 clones contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."
 Query Match 22.6%; Score 694; DB 4; Length 734;
 Best Local Similarity 98.4%; Pred. No. 4.3e-180;
 Matches 722; Conservative 0; Mismatches 10; Indels 2; Gaps 2;
 QY 2147 TACAGATCCACCTCTCTCCAGCCATCAAGCATCTGCCAGCCAGGAACTCTGCACC 2206
 DB 1 TACAGATCCACCTCTCTCCAGCCATCAAGCATCTGCCAGCCAGGAACTCTGCACC 60
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 DB 181 TTGACATGGGAGGAGAACTCTGTTGCTGTCTGCTCCCATGCTGCGGAGGACTTGGGCA 240
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 DB 241 AATCTTTGCTGTGCAAACTCTGATTCAGTTCGACGAGAACTGAATATCAACTTTCAG 300
 QY 2447 GGAGTGAGTCAAGTGGCTCCAGAGCGACCCAGATTTTACCCAAATGGAGGAAATCCA 2506
 DB 301 GGAGTGAGTCAAGTGGCTCCAGAGCGACCCAGATTTTACCCAAATGGAGGAAATCCA 360
 Tue Apr 5 08:26:16 2005
 Tel: 6508454102
 Email: gfu@incyte.com.
 Location/Qualifiers
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 DB 704 AGAATCTGTTTCCATTCGAACTGGAGCCACACTTGAAGGCTTCGACACCTGCGAGCC 645
 QY 1117 CTTACCAAGAAAGCAAGGGAAGCAATCAAGCAGTCAAGAGCTAAGTTTAAAGGAGCGA 1176
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 DB 224 GATGTAAGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 165
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 DB 44 CGGGTGTCAAGGTTGAAAGAGGTACAGTCCATAGATCCA 2
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Db 421 CCGACCCGAGCTGCGCAGGGAAGCTGCTTTGATCAGACTCTCTAAGGACTGGAAGTT 480
QY 2627 CACGATCATCTCAGAGCATTTGTAAAGGAGGAGAAAGTACAGATGCCCTCAGCTTGCCTC 2686
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QY 2687 ATGTCAACTGAAATAGCTTCTCAATTTCTTCCAGGCATAGCAGTTCTTTAGCCATAC 2746
Db 541 ATGTCAACTGAAATAGCTTCTCAATTTCTTCCAGGCATAGCAGTTCTTTAGCCATAC 600
QY 2747 ATATCATTCGATGAATTTTCGAAAGCCCTTTCAAAAAGTTGAAATTCGAAGATCGG 2806
Db 601 ATATCATTCGATGAATTTTCGAAAGCCCTTTCAAAAAGTTGAAATTCGAAGATCGG 660
QY 2807 -AAGAACATGAAGGACGTTTATAGCCGTTACCTTTTAAATTCGATGA -AAATGCAATG 2864
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LOCUS 55049343J1 PFLP Homo sapiens cDNA, mRNA sequence.
DEFINITION CD629756
ACCESSION CD629756
VERSION CD629756.1 GI:40278022
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
JOURNAL Circular rapid amplification of cDNA ends for high-throughput
COMMENT Genomics 84 (1), 205-210 (2004)
CONTACT: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
FEATURES
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Best Local Similarity 99.2%; Pred. No. 4.8e-177;
Matches 727; Conservative 1; Mismatches 1; Indels 4; Gaps 4;
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QY 1082 GGAAGCCACACTTGAAGCCCTTGACACCTGCAGCCCTA-CAAAGAAAGACAA-GGGGA 1139
Db 672 GGAAGCCACACTTGAAGCCCTTGACACCTGCAGCCCTACCAAGAAAGACAAAGGGGA 613
QY 1140 AGCATCAGCAGTCAGAGCTTAAGTTTAAAGGAGGAGTGGCATGGCTAGCCCCAGGG 1199
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QY 1560 ATATTCTGCTGCTCATCTGGACATGTTGTGATGATGATGATGATGATGATGATGATGATG 1619
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Db 132 TCAAAATTTTGGAAAAGGCGCAATCAGATCAGATAAGAGAGCCGAGAGAAAATAACAGC 73
QY 1680 AGAACATGAGACACACAGCATCTCAGTATGCTCGGTGCTGCTGCTGCTGCTGCTGCTGCTG 1739
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LOCUS 55049327J1 PFLP Homo sapiens cDNA, mRNA sequence.
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ACCESSION CD629754
VERSION CD629754.1 GI:40278020
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
JOURNAL Circular rapid amplification of cDNA ends for high-throughput
COMMENT Genomics 84 (1), 205-210 (2004)
CONTACT: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
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KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 678)
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J., and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
JOURNAL extension cloning of partial genes
COMMENT Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.

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QY 1265 CGAGGGCAGTCCCAACCAAGTGCAGAGAGCTGGAGCTTCAACCAACCGAACCCGCTTCC 1324
DB 498 CGAGGGCAGTCCCAACCAAGTGCAGAGAGCTGGAGCTTCAACCAACCGAACCCGCTTCC 439
QY 1325 GGCCTCTGCTGCGCTCAAAAAGTCTCAGCCAAAACCAAGTATGATGCTGACACAGCCC 1384
DB 438 GGCCTCTGCTGCGCTCAAAAAGTCTCAGCCAAAACCAAGTATGATGCTGACACAGCCC 379
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DB 378 TTGGCACTGATGATGATATGATGATAAAGGATGCCAGTGTGATGATGATGATGATGATGATGAT 319
QY 1445 TCACCCCAACCACTTAAACCTGTCATTCGAGCTATCAGAAATATGAAATTTTCATGTTGCAA 1504
DB 318 TCACCCCAACCACTTAAACCTGTCATTCGAGCTATCAGAAATATGAAATTTTCATGTTGCAA 259
QY 1505 AACGGAAGTTTAAAGAAACRTTACGTCATATGATGATAAAGATGCTATGAAACAATATT 1564
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QY 1565 CTGCTGTGATCTGACATGTTGTGTAGATTTAAAGCCTTCAACACGTTGTGTATCAAA 1624
DB 198 CTGCTGTGATCTGACATGTTGTGTAGATTTAAAGCCTTCAACACGTTGTGTATCAAA 139
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DB 138 TTCTTGGAAAAGGGCAATTCATCAGATACAGAGCGGAGAGAAAATAACAGCAGAAC 79
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LOCUS CD629755
DEFINITION 55049343H1 FLP Homo sapiens cDNA, mRNA sequence. EST 12-JAN-2004
ACCESSION CD629755
VERSION CD629755.1 GI:40278021
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 691)
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J., and Stuve, L.L.
TITLE Circular rapid amplification of cDNA ends for high-throughput
JOURNAL extension cloning of partial genes
COMMENT Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
    location/Qualifiers
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QY 865 ACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACCTCTTGGCATTTCTTCTTGA 924
DB 61 ACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACCTCTTGGCATTTCTTCTTGA 120
QY 925 CTCTCTGCGGCATTTCTTGGCTCAGGTTTTCGATTAAAGTACAAGAACACACCGCCAG 984
DB 121 CTCTCTGCGGCATTTCTTGGCTCAGGTTTTCGATTAAAGTACAAGAACACACCGCCAG 180
QY 985 AAACACTTTGAGAAAAGGAAGAACCCAGCTGCCAACCTCATTTAGTGTGTTGGCGTAGT 1044
DB 181 AAACACTTTGAGAAAAGGAAGAACCCAGCTGCCAACCTCATTTAGTGTGTTGGCGTAGT 240
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DB 361 TTTAAGGAGCGAGTGCGCATGCGTCTAGCCCCA-GGGCCAGAGTATTAAAGACCGCAAGCC 419
QY 1225 TCAGTAGTGCAGGAGTCCCAAGCAAGCACCATCACAGCCGA-GGCGAGTCCCAACCA 1283
DB 420 TCAGTAGTGCAGGAGTCCCAAGCAAGCACCATCACAGCCGAAGTCCCAACCA 479
QY 1284 AGTCAGAGAGCTGGAGCTTCAACGACCGCAACCGCTTCCGGCCCTCGCTGCGCTCAA 1343
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QY	1404	TGATGAAAGGATGCGAGTGTGATGATCATGTTGGAAGACTCACCCACCACTTAAAC	1463
Db	600	TGATGAAAGGATGCGAGTGTGATGATCATGTTGGAAGACTCACCCCACTT-AAAC	658
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DEFINITION	55049303J1 FLP Homo sapiens cDNA, mRNA sequence.		
ACCESSION	CD629752		
VERSION	CD629752.1	GI:40278018	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.		
TITLE	Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes		
JOURNAL	Genomics 84 (1), 205-210 (2004)		
COMMENT	Contact: Fu GK Incyte Genomics, Inc. 3160 Porter Dr., Palo Alto, CA 94304, USA Tel: 6508454102 Email: gfu@incyte.com.		
FEATURES			
source	1. .724 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone_lib="FLP" /note="Vector: pDrive Cloning Vector"		
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QY	1105	CACACC-TGAGGCCCTA-CCAGAAAGACAGGGGAAGCATCAGCACTCAGAGCTAA	1162
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QY	1163	GTTTTAAAGGAGCGAGTGCAGTGGCTAGCCCAAGGGGGCCAGAGTATTAAAGCCGACAAG	1222
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QY	1223	CCTCAGTAGTGACAGAGGTGCCCAAGACCCACCATCACAGCCGAGGGCAGTCCCAACCA	1282
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QY	1283	AAGTGACAGAGCTGGAGCTTCAACGACCGAACCCCGCTTCCGGCCCTCGCTCGGCCTCA	1342
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QY	1343	AAAGTTCTCAGCCAAACACGATGATAGTGTGACACAGCCCTTGGCACTGATGATGAT	1402
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QY	1403	ATGATGAAAGGATGCCAGTGTGATGATATCATGTTGGAAGACCTCACCCCACTTAAAA	1462
Db	364	ATGATGAAAGGATGCCAGTGTGATGATATCATGTTGGAAGACCTCACCCCACTTAAAA	305
QY	1463	CTGTCAATTCGAGCTATCAGAAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAAGGAA	1522
Db	304	CTGTCAATTCGAGCTATCAGAAATTATGAAATTTCATGTTGCAAAACGGAAGTTTAAAGTAA	245
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Db	5	AG 4	
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LOCUS	BE158938	658 bp	mRNA linear EST 21-JUN-2000
DEFINITION	MR0-HT0404-210200-001-c04 HT0404 Homo sapiens cDNA, mRNA sequence.		
ACCESSION	BE158938		
VERSION	BE158938.1	GI:8621659	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 658) Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.		
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)		
MEDLINE	20202663		
PUBMED	10737800		
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2=MR0-HT0404-210200-001-c04&t3=2000-02-21&t4=1) 200-001-c04&t3=2000-02-21&t4=1) Seq primer: puc 18 forward High quality sequence stop: 657. Location/Qualifiers 1. .658 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /dev_stage="Adult" /clone_lib="HT0404" /note="Organ: head_neck; Vector: puc18; Site_1: Sma1;		



Search completed: April 3, 2005, 02:34:22  
Job time : 9458 secs

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
1 (bases 1 to 714)  
Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.  
Circular amplification of cDNA ends for high-throughput  
extension cloning of partial genes  
Genomics 84 (1), 205-210 (2004)  
Contact: Fu GK  
Incyte Genomics, Inc.  
3160 Porter Dr., Palo Alto, CA 94304, USA  
Tel: 6508454102  
Email: gfu@incyte.com.  
Location/Qualifiers  
1..714  
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ORIGIN

Query Match 19.1%; Score 586.8; DB 6; Length 714;  
Best Local Similarity 96.3%; Pred. No. 2e-150;  
Matches 643; Conservative 1; Mismatches 17; Indels 7; Gaps 4;  
QY 1077 AACCTGGAGGCACA-CCTGAGGCGCTTGCA-CACCTGCAGCCCTACC---AAGAAAGA 1130  
DB 688 ACCCTGGAGGCACACACCTTGAAGGCTTGACACCTGCAGCCCTACCCAGAAAGAAC 629  
QY 1131 ACAAGGGGAAGCATCAAGCAGTCAGAAGCTTAAGTTTAAAGGAGAGTGCATGGCTAG 1190  
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QY 1191 CCCAGGGGCCAGAGTATTAAAGCCGACAGCTCAGTAGTGACAGGAGTCCCAAG 1250  
DB 568 CCCAGGGGCCAGAGTATTAAAGCCGACAGCTCAGTAGTGACAGGAGTCCCAAG 509  
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QY 1370 ATGCTGACACAGCCCTTGGCAGCTGATGATGATGATGATGATGATGATGATGATGATG 1429  
DB 388 ATGCTGACACAGCCCTTGGCAGCTGATGATGATGATGATGATGATGATGATGATGATG 329  
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QY 1550 TCATTGAACAATATTCTGCTGCTCATCTGGACATGTTGTAGAAATTAAGCCCTTCAA 1609  
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RESULT 2  
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ID AAC85414 standard; cDNA; 3137 BP.  
XX  
AC AAC85414;  
XX  
DT 20-APR-2001 (first entry)  
XX Human KCNQ5 potassium channel subunit coding sequence.  
DE Human; KCNQ5; heteromeric channel; chromosome 6; Parkinson's disease;  
KW central nervous system; CNS; Alzheimer's disease; anxiety; ataxia;  
KW CNS damage; trauma; stroke; neurodegenerative illness; schizophrenia;  
KW compulsive behaviour; dementia; depression; Huntington's disease; mania;  
KW memory impairment; memory dysfunction; spinal cord damage; phobia;  
KW pick's disease; psychosis; stroke; tremor; seizure; convulsion; epilepsy;  
ds.  
XX Homo sapiens.  
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FT CDS 1..2694  
FT /\*tag= a  
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XX WO200077035-A2.  
PD 21-DEC-2000.  
XX  
PF 29-MAY-2000; 2000WO-DK000289.  
XX  
PR 11-JUN-1999; 99DK-00000828.  
XX (NEUR-) NEUROSEARCH AS.  
XX Jentsch TJ;  
XX WPI; 2001-080678/09.  
DR P-PSDB; AAB47046.  
XX  
PT Novel genes encoding KCNQ5 potassium channel subunits, useful for  
FT treating Alzheimer's disease, anxiety, ataxia, stroke, dementia,  
PT depression, Huntington's disease, schizophrenia and Parkinson's disease.  
XX  
PS Claim 2; Page 44-48; 50pp; English.  
XX  
CC This sequence encodes the human KCNQ5 protein. The KCNQ5 protein forms  
CC heteromeric channels with other KCNQ channel subunits, in particular  
CC KCNQ3 and KCNQ4. The KCNQ5 gene has been localised to the long arm of  
CC chromosome 6 (6q14). Chemicals which have the ability to bind to KCNQ5  
CC are useful for diagnosis, treatment, prevention or alleviation of  
CC diseases related to diseases or adverse conditions of the central nervous  
CC system (CNS), including affective disorders, Alzheimer's disease,  
CC anxiety, ataxia, CNS damage caused by trauma, stroke or neurodegenerative  
CC illness, cognitive deficits, compulsive behavior, dementia, depression,  
CC Huntington's disease, mania, memory impairment, memory disorders, memory  
CC dysfunction, motion disorders, motor disorders, neurodegenerative  
CC diseases, Parkinson's disease and Parkinson-like motor disorders,  
CC phobias, pick's disease, psychosis, schizophrenia, spinal cord damage,

CC stroke, tremor, seizures, convulsions and epilepsy

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Best Local Similarity 99.9%; Pred. No. 0;

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22

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Db 121 AGGAGAGCCGCCGGGCAAGCAGGGGCCCGGATGAGCCTGCTGGGAAGCCGCTCTCT 180

QY 190 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAAGTACCGCGGGTGCAGAACTACCTG 249

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209

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360

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490 AGGTTTGCTCGAAAGCCCTTCTGTGTATAGATACCATTTGTTCTTATCGCTTCAATAGCA 549

db 481 AGGTTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTTGTTCTTATCGCTTCAATAGCA 540

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QY 610 TTCTACAGATCCTCCGCATGGTGGCATGGACCGAAGGGAGGCACCTTGAAATTACTG 669

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QY 670 GGTTCAGTGGTTTATGCTCACAGCAAGGAA<sup>TTAATCACAGCTTTGGTACATAGGATTTT</sup>IG 729

D<sub>b</sub> 661 GGTTCAAGTGGTTTATGCTCACAGCAAGGAATTAAATCACAGCTTGGTACATAGGATTTTGTG 720

789

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Db 2041 GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACACACCAATTGCAACCAA 2100  
Qy 2110 ATAAATACGGCAACCAAGCCAGCCGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2169  
Db 2101 ATAAATACGGCAACCAAGCCAGCCGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2160  
Qy 2170 GCCATCAGCATCTGCCAGGCGAGAACTCTGCACTTACCTTACCTGAGGCTTACAGAA 2229  
Db 2161 GCCATCAGCATCTGCCAGGCGAGAACTCTGCACTTACCTTACCTGAGGCTTACAGAA 2220  
Qy 2230 AGCATTTCTGAGCTCACCACCTGCTGCTGCTCCAAAGGAAATGTTTCAGTTGACAG 2289  
Db 2221 AGCATTTCTGAGCTCACCACCTGCTGCTGCTCCAAAGGAAATGTTTCAGTTGACAG 2280  
Qy 2290 TCAATCTCACAAGGACCGTTCTATAGGAAAAGCTTTTGACATGGGAGGAGAACTCTG 2349  
Db 2281 TCAATCTCACAAGGACCGTTCTATAGGAAAAGCTTTTGACATGGGAGGAGAACTCTG 2340  
Qy 2350 TTGTTCTGCTGCTCCATGGTCCGAGGAGCACTTTGGCAAAATCTTTGCTGTCGCAAACTG 2409  
Db 2341 TTGTTCTGCTGCTCCATGGTCCGAGGAGCACTTTGGCAAAATCTTTGCTGTCGCAAACTG 2400  
Qy 2410 ATCAGGTCGACCGAGGAACTGAATATCAACTTTTCAGGAGTGAAGTCAAGTGGCTCCAGA 2469  
Db 2401 ATCAGGTCGACCGAGGAACTGAATATCAACTTTTCAGGAGTGAAGTCAAGTGGCTCCAGA 2460  
Qy 2470 GGCAGCCAAAGATTTTACCCCAATGGAGGAAATCCAAATTTTATTAACATGATGAAG 2529  
Db 2461 GGCAGCCAAAGATTTTACCCCAATGGAGGAAATCCAAATTTTATTAACATGATGAAG 2520  
Qy 2530 GTGGTCCGAGAGACAGACAGACACTTTTGTATGCGGACCGACGCTGCCAGGAA 2589  
Db 2521 GTGGTCCGAGAGACAGACAGACACTTTTGTATGCGGACCGACGCTGCCAGGAA 2580  
Qy 2590 GCTGCTTTGATCAGACTCTCTAAGGACTGGAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 2649  
Db 2581 GCTGCTTTGATCAGACTCTCTAAGGACTGGAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 2640  
Qy 2650 AAGCAGGAGAAAGTACAGATGCGCTCAGCTTGCCTCATGTCAAACTGAAATAAGTTCTT 2709  
Db 2641 AAGCAGGAGAAAGTACAGATGCGCTCAGCTTGCCTCATGTCAAACTGAAATAAGTTCTT 2700  
Qy 2710 CATTTCTTTCCAGCATAGACTTTTATGACATACATATCATGATGATGATGATGATG 2769  
Db 2701 CATTTCTTTCCAGCATAGACTTTTATGACATACATATCATGATGATGATGATGATG 2760  
Qy 2770 AAAGCCCTTTCAAAAGTTGAAATTTGCAAGATCGGAGAACATGAAAGCAGTTTATA 2829  
Db 2761 AAAGCCCTTTCAAAAGTTGAAATTTGCAAGATCGGAGAACATGAAAGCAGTTTATA 2820  
Qy 2830 AGCCCGTTTACCTTTTAAATTCATGAAATGATGTTTATGAGGATGCTTAAATTTCAAGGT 2889  
Db 2821 AGCCCGTTTACCTTTTAAATTCATGAAATGATGTTTATGAGGATGCTTAAATTTCAAGGT 2880  
Qy 2890 GCATCGACATTAACCCACTCATTTAGTAAATGATGATGATGATGATGATGATGATG 2949  
Db 2881 GCATCGACATTAACCCACTCATTTAGTAAATGATGATGATGATGATGATGATGATG 2940  
Qy 2950 AACACAGCTAATGCTATGCGGCTGATGATGATGATGATGATGATGATGATGATG 3009  
Db 2941 AACACAGCTAATGCTATGCGGCTGATGATGATGATGATGATGATGATGATGATG 3000  
Qy 3010 ACATGTATTTTGAATTTATGGAGTAAACACCTTTCAAAATTTCA 3053  
Db 3001 ACATGTATTTTGAATTTATGGAGTAAACACCTTTCAAAATTTCA 3044

RESULT 3  
AAC64371  
ID AAC64371 standard; cDNA; 3718 BP.  
XX  
AC  
AAC64371;

DT 07-FEB-2001 (first entry)  
XX Human KCNQ5 (KCN6q) cDNA sequence SEQ ID NO:2.  
XX Human; KCNQ5; KCN6q; chromosome 6; voltage-gated potassium channel;  
KW Stargardt-like macular dystrophy; cone-rod macular dystrophy;  
KW Salla disease; ophthalmological; auditory; central nervous system;  
KW cardiocactive; anticonvulsant; gastrointestinal; muscular active;  
KW age-related macular degeneration; macular degeneration; deafness;  
KW epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;  
KW gastrointestinal disorder; ss.  
XX Homo sapiens.  
XX WO200061606-A1.  
XX 19-OCT-2000.  
XX 10-APR-2000; 2000WO-US009587.  
XX 14-APR-1999; 99US-0129274P.  
XX (MERI ) MERCK & CO INC.  
XX Petrukhin K, Caskey CT, Li W, Metzker ML;  
XX WPI; 2000-647417/62.  
XX P-PSDB; AAB24241.  
XX Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying  
XX inhibitors and activators which can treat e.g. Stargardt-like macular  
XX dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy.  
XX Claim 3; Fig 2; 99pp; English.  
XX The present sequence encodes the human KCNQ5 (also called KCN6q) protein,  
XX which is a voltage-gated potassium channel protein. Human KCNQ5 has  
XX ophthalmological, auditory, central nervous system (CNS), cardioactive,  
XX anticonvulsant, gastrointestinal and muscular active activities.  
XX Sequences and methods from the present invention are useful for  
XX identifying activators or inhibitors of KCNQ5 protein. These activators  
XX and inhibitors are useful for treating Stargardt-like macular dystrophy,  
XX cone-rod dystrophy, Salla disease, age-related macular degeneration,  
XX other forms of macular degeneration, deafness, epilepsy, and different  
XX forms of neuropsychiatric, heart, gastrointestinal, and muscle disorders.  
XX Stargardt-like macular dystrophy and cone-rod dystrophies are located at  
XX chromosome 6q  
XX Sequence 3718 BP; 1054 A; 845 C; 866 G; 953 T; 0 U; 0 Other;

Query Match 95.6%; Score 2936.2; DB 3; Length 3718;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2941; Conservative 1; Mismatches 9; Indels 0; Gaps 0;  
Qy 103 ACGTTGGTGGCGCGGCTGGCTGAGGAGAGCCGCGGGGCAAGCAGGCGGCCGG 162  
Db 78 ACTGCTGAGGACTCGCGGCTGGCTGAGGAGAGCCGCGGGGCAAGCAGGCGGCCGG 137  
Qy 163 ATGAGCTGCTGGGAGAGCCGCTCTTACACGAGTAGCCAGAGCTGCCGCGCAACGTC 222  
Db 138 ATGAGCTGCTGGGAGAGCCGCTCTTACACGAGTAGCCAGAGCTGCCGCGCAACGTC 197  
Qy 223 AAGTACCGGGGTGCGAGAACTACCTGTACAACTGCTGGAGAGACCCCGGCTGGCG 282  
Db 198 AAGTACCGGGGTGCGAGAACTACCTGTACAACTGCTGGAGAGACCCCGGCTGGCG 257  
Qy 283 TTGATCTACACGCTTTGCTTTTCTGTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTT 342  
Db 258 TTGATCTACACGCTTTGCTTTTCTGTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTT 317  
Qy 343 TCTACCATCCCTGAGCAGACAAATTCGCTCAAGTTGCTTGAATCCTCGAGTTCGTG 402  
Db 318 TCTACCATCCCTGAGCAGACAAATTCGCTCAAGTTGCTTGAATCCTCGAGTTCGTG 377



Db 2538 GATGCGCACCCAGCCTGCCAGGAAGTGCCTTTGTCATCAGACTCTCTAAGGACTGGA 2597  
QY 2623 AGGTCAACGATCTCAGAGCATTTTGAAGCGAGGAGAAAGTACAGATGCCCTCAGCTTG 2682  
Db 2598 AGGTCAACGATCTCAGAGCATTTTGAAGCGAGGAGAAAGTACAGATGCCCTCAGCTTG 2657  
QY 2683 CCTCATGTCMAACTGAATTAAGTCTTCTCATTTTCTTCCAGGCATAGCAGTCTTTAGCC 2742  
Db 2658 CCTCATGTCMAACTGAATTAAGTCTTCTCATTTTCTTCCAGGCATAGCAGTCTTTAGCC 2717  
QY 2743 ATACATATCATTCATGAATTAATTCGAAAGCCCTTCTTAAAGTTGAAATTCGAAGAT 2802  
Db 2718 ATACATATCATTCATGAATTAATTCGAAAGCCCTTCTTAAAGTTGAAATTCGAAGAT 2777  
QY 2803 CGGGAAGAACATGAAGGAGGTTTATAAGCCGTTTACCTTTTAAATTGCATGAAATGCAT 2862  
Db 2778 CGGGAAGAACATGAAGGAGGTTTATAAGCCGTTTACCTTTTAAATTGCATGAAATGCAT 2837  
QY 2863 GTTTAGGATGCTTAAATTCGAAGTGCATGACATTAACCCACTCATTTAGTAAATGTA 2922  
Db 2838 GTTTAGGATGCTTAAATTCGAAGTGCATGACATTAACCCACTCATTTAGTAAATGTA 2897  
QY 2923 CTTGAGTTAAAGCCCTGAGAAACCAACACAGCTTAATGCTATGGGTGTATGAATATG 2982  
Db 2898 CTTGAGTTAAAGCCCTGAGAAACCAACACAGCTTAATGCTATGGGTGTATGAATATG 2957  
QY 2983 TCAAGTTAGGTCATTTAGAAGATTGACACTGTATTTTGAATTTATGGAGTAAACACC 3042  
Db 2958 TCAAGTTAGGTCATTTAGAAGATTGACACTGTATTTTGAATTTATGGAGTAAACACC 3017  
QY 3043 TTCAAAATTCA 3053  
Db 3018 TTCAAAATTCA 3028

## RESULT 4

AAH43634  
ID AAH43634 standard; cDNA; 3111 BP.  
XX AC AAH43634;  
DT 21-JAN-2002 (first entry)  
XX Human ion-channel forming protein coding sequence.  
DE Ion-channel forming protein; voltage-gated potassium channel; fetal;  
KW brain; thymus; prostate; heart; skeletal muscle; probe; ss.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH CDS 59..2831  
FT /\*tag= a  
FT /product= "Human ion-channel forming protein"  
XX  
XX WO200175108-A1.  
XX 11-OCT-2001.  
XX 03-APR-2001; 2001WO-US010875.  
XX 03-APR-2000; 2000US-0194255P.  
XX (LEXI-) LEXICON GENETICS INC.  
XX Hu Y, Kieke JA, Turner AC, Nehls MC, Friedrich G, Zambrowicz B;  
PI Sands AT;  
XX WPI; 2001-656987/75.  
XX P-PSDB; AAB47678.  
XX New human ion channel protein and polynucleotides encoding the protein,

PT useful in diagnosing or treating diseases, in drug screening, and in  
XX clinical trial monitoring.

XX Disclosure; Page 37-38; 41pp; English.

CC The sequences in AAH43633-34 encode a novel ion-channel forming protein.  
CC The protein shares structural similarity with mammalian ion channel  
CC proteins, particularly voltage-gated potassium channel proteins. The  
CC protein is expressed in many human cell lines including fetal brain,  
CC brain, thymus, prostate, heart and skeletal muscle. The novel protein can  
CC be used in the diagnosis or treatment of diseases, in drug screening, and  
CC in clinical trial monitoring. The oligonucleotides may be used as  
CC hybridization probes for screening libraries, and assessing gene  
CC expression patterns (particularly using a micro array or high throughput  
CC chip format). The nucleic acids and novel protein can also be used in the  
CC identification, selection and validation of novel molecular targets for  
CC drug discovery, to screen collections of genetic material from patients  
CC who have a particular medical condition, to identify mutations associated  
CC with a particular disease, as a diagnostic or prognostic assay, and to  
CC screen for drugs which can be used to treat symptomatic or phenotypic  
CC manifestations of perturbing the normal function of novel human protein.  
CC The polypeptides are further used in generating antibodies

XX SQ Sequence 3111 BP; 814 A; 771 C; 789 G; 737 T; 0 U; 0 Other;

Query Match 94.1%; Score 2890.8; DB 5; Length 3111;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 2951; Conservative 1; Mismatches 3; Indels 29; Gaps 3;

QY 1 GGCAGCGCATGAAGGATGTGGAGTCGGCGCGGCGGCGAGGTCGCTGAACCTCGGCAGCC 60  
Db 156 GGCAGCGCATGAAGGATGTGGAGTCGGCGCGGCGGCGAGGTCGCTGAACCTCGGCAGCC 215  
QY 61 GCCAGGGCGCAGCGGCTGCTACTCTGGGCACCCGCGCGGCGGCGAGGTCGCTGGCGGCGC 120  
Db 216 GCCAGGGCGCAGCGGCTGCTACTCTGGGCACCCGCGCGGCGGCGAGGTCGCTGGCGGCGC 275  
QY 121 GGTGGCTGAGGGAGAGCGCGCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAG 180  
Db 276 GGTGGCTGAGGGAGAGCGCGCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAG 335  
QY 181 CCGCTCTCTTACACGAGTAGCAGAGCTGCCGCGCGCAACGTCAGTACCGGGGTGCGAG 240  
Db 336 CCGCTCTCTTACACGAGTAGCAGAGCTGCCGCGCGCAACGTCAGTACCGGGGTGCGAG 395  
QY 241 AACTACCTGTACAACTGCTGGAGAGACCCCGCGGCTGGGGGTTTCATCTACACGCTTTC 300  
Db 396 AACTACCTGTACAACTGCTGGAGAGACCCCGCGGCTGGGGGTTTCATCTACACGCTTTC 455  
QY 301 GTTTTCTCCTTGTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 360  
Db 456 GTTTTCTCCTTGTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 515  
QY 361 ACAAAATGGCTCAAGTTCCTTCTGATCTGAGTTCGTTGATGATGTTGTTGTTGTTGTTGTTGTT 420  
Db 516 ACAAAATGGCTCAAGTTCCTTCTGATCTGAGTTCGTTGATGATGTTGTTGTTGTTGTTGTTGTT 575  
QY 421 TTGGAGTTTCATTCGAAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGATGGCAA 480  
Db 576 TTGGAGTTTCATTCGAAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGATGGCAA 635  
QY 481 GGAAGACTGAGGTTTGTCTCGAAAGCCCTTCTGTTTATAGATACATTTGTTTCTTATCGCT 540  
Db 636 GGAAGACTGAGGTTTGTCTCGAAAGCCCTTCTGTTTATAGATACATTTGTTTCTTATCGCT 695  
QY 541 TCAATACAGTTGTTCTGCAAAACCTCAGGGTAATATTTTGGCAGCTGCTGCACTCAGA 600  
Db 696 TCAATACAGTTGTTCTGCAAAACCTCAGGGTAATATTTTGGCAGCTGCTGCACTCAGA 755  
QY 601 AGTCTCGGTTTCTTACAGATCCTCCGATGGTGGCATGGACCGAAGGGGAGGACCTTGG 660  
Db 756 AGTCTCGGTTTCTTACAGATCCTCCGATGGTGGCATGGACCGAAGGGGAGGACCTTGG 815



Qy	661	AAATTA	CTGGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATA	720
Db	816	AAATTA	CTGGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATA	875
Qy	721	GGATTTT	TGGTTCCTTATTTTTCGTTCTTCTGTTCTATCTGGTGGAAAGGATGCCAAT	780
Db	876	GGATTTT	TGGTTCCTTATTTTTCGTTCTTCTGTTCTATCTGGTGGAAAGGATGCCAAT	935
Qy	781	AAAGAGT	TTTCTACATATGAGATGCTCTCTGGTGGGGGCAAAATACATTTGACAACTATT	840
Db	936	AAAGAGT	TTTCTACATATGAGATGCTCTCTGGTGGGGGCAAAATACATTTGACAACTATT	995
Qy	841	GGCTATG	GAGACAAAACCTCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAAGCTTTGCA	900
Db	996	GGCTATG	GAGACAAAACCTCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAAGCTTTGCA	1055
Qy	901	CTCCTTG	GCATTCTTTTGGCATCTTCTCGCGGCATTCTTGGCTCAGTTTTCGATT	960
Db	1056	CTCCTTG	GCATTCTTTTGGCATCTTCTCGCGGCATTCTTGGCTCAGTTTTCGATT	1115
Qy	961	AAAGTAC	AAAGAACACCGCCAGAAACACTTTTGAGAAAAGAGAAACCCAGCTGCCAAC	1020
Db	1116	AAAGTAC	AAAGAACACACCGCCAGAAACACTTTTGAGAAAAGAGAAACCCAGCTGCCAAC	1175
Qy	1021	CTCATTT	CAGTGTGTTTGGCGTAGTTACGCACTGATGAGAAATCTGTTTCCATTGCAACC	1080
Db	1176	CTCATTT	CAGTGTGTTTGGCGTAGTTACGCACTGATGAGAAATCTGTTTCCATTGCAACC	1235
Qy	1081	TGGAAGC	CACTTTGAAGGCCTTGCAACCTTGAGCCCTTACCAAGAAAGAACAGGGGAA	1140
Db	1236	TGGAAGC	CACTTTGAAGGCCTTGCAACCTTGAGCCCTTACCAAGAAAGAACAGGGGAA	1279
Qy	1141	GCATCA	AGCAGTCAGAACTAAGTTTAAAGAGCGAGTGCCATGGCTAGGCCCCAGGGGC	1200
Db	1280	-----	-----TCAGAGCTAAGTTTAAAGAGCGAGTGCCATGGCTAGGCCCCAGGGGC	1328
Qy	1201	CAGAGTA	TTAAGAGCCGCAAGCCCTCAGTAGGTGACAGGAGTCCCCAAGCACCGACATC	1260
Db	1329	CAGAGTA	TTAAGAGCCGCAAGCCCTCAGTAGGTGACAGGAGTCCCCAAGCACCGACATC	1388
Qy	1261	ACAGCGA	GGGCGAGTCCCAACCAAGTGCAGAGAGCTGGAGCTTCAACGACCGAACCCGC	1320
Db	1389	ACAGCGA	GGGCGAGTCCCAACCAAGTGCAGAGAGCTGGAGCTTCAACGACCGAACCCGC	1448
Qy	1321	TTCCGGC	CTCGCTCGGCTCAAAAGTTCTCAGCCAAAACCAAGTATGATGCTGACACA	1380
Db	1449	TTCCGGC	CTCGCTCGGCTCAAAAGTTCTCAGCCAAAACCAAGTATGATGCTGACACA	1508
Qy	1381	GCCCTTG	GCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1440
Db	1509	GCCCTTG	GCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1568
Qy	1441	GACCTCA	CCCCCACCCTTAAACTGTCTATCGAGCTATCAGAAATATGAAATTTCACTGT	1500
Db	1569	GACCTCA	CCCCCACCCTTAAACTGTCTATCGAGCTATCAGAAATATGAAATTTCACTGT	1628
Qy	1501	GCAAAA	CGGAAGTTTAAAGAAACRTTACGTCCATATGATGATGATGATGATGATGATGATG	1560
Db	1629	GCAAAA	CGGAAGTTTAAAGAAACRTTACGTCCATATGATGATGATGATGATGATGATGATG	1688
Qy	1561	TATCTGT	GTGTCATCTGGACATGTTGTGATGATGATGATGATGATGATGATGATGATGATG	1620
Db	1689	TATCTGT	GTGTCATCTGGACATGTTGTGATGATGATGATGATGATGATGATGATGATGATG	1748
Qy	1621	CAAAAT	CTTGGAAAGGCAATACATCAGATAGAGAGCCGAGAGAAATTAACAGCA	1680
Db	1749	CAAAAT	CTTGGAAAGGCAATACATCAGATAGAGAGCCGAGAGAAATTAACAGCA	1808
Qy	1681	GAACAT	TGAGACCAAGAGCATCTCAGTATGCTCGGTGGGTGAGAGGTTGAAAAACAG	1740
Db	1809	GAACAT	TGAGACCAAGAGCATCTCAGTATGCTCGGTGGGTGAGAGGTTGAAAAACAG	1868
Qy	1741	GTACAGT	CCATAGAAATCCAGCTGCACTGCTTACTAGACATCTATCAACAGGTCCTTCGG	1800

Db	1869	GTACAGT	CCATAGAAATCCAGCTGGACTGCTACTAGACATCTATCAACAGGTCCTTCGG	1928
Qy	1801	AAAGGCT	CTCGCTCAGCCCTCGCTTGGCTTCAATCCAGTTCACACCTTTTGAATGAA	1860
Db	1929	AAAGGCT	CTCGCTCAGCCCTCGCTTGGCTTCAATCCAGTTCACACCTTTTGAATGAA	1988
Qy	1861	CAGACAT	CTGACTATCAAAAGCCCTTGAGTAGCAAAAGATCTTTCCGGTTCGCGACAAAAC	1920
Db	1989	CAGACAT	CTGACTATCAAAAGCCCTTGAGTAGCAAAAGATCTTTCCGGTTCGCGACAAAAC	2048
Qy	1921	AGTGGCT	GTCTTATCCAGATCAATAGTGCCAAATCTCGAGAGCCCTGCAATCTCTG	1980
Db	2049	AGTGGCT	GTCTTATCCAGATCAATAGTGCCAAATCTCGAGAGCCCTGCAATCTCTG	2108
Qy	1981	ACGCCAA	TAGTTCAGTGCCAGACTTTCTACGCGCTTAGCCCTACTATGCAAGTCAA	2040
Db	2109	ACGCCAA	TAGTTCAGTGCCAGACTTTCTACGCGCTTAGCCCTACTATGCAAGTCAA	2168
Qy	2041	GCAACAC	CAGGTGCAATTAGTCAAAAGCGATGGCTCAGCAGTGGCAGCCACCAACCAATT	2100
Db	2169	GCAACAC	CAGGTGCAATTAGTCAAAAGCGATGGCTCAGCAGTGGCAGCCACCAACCAATT	2228
Qy	2101	GCAAAAC	CAAAATAAATACGGCACCCAGCCAGCAGCCCAACAACTTTACAGATCCCACCT	2160
Db	2229	GCAAAAC	CAAAATAAATACGGCACCCAGCCAGCAGCCCAACAACTTTACAGATCCCACCT	2288
Qy	2161	CCTCTCC	AGCCATCAAGCATCTGCCAGCCAGAAACTCTGCACCCCTAACCCCTGCAGGC	2220
Db	2289	CCTCTCC	AGCCATCAAGCATCTGCCAGCCAGCAGAAACTCTGCACCCCTAACCCCTGCAGGC	2348
Qy	2221	TTACAGAA	AGCACTTTCTGACGTCAACCTGCTTGTTCCTTCCAAAGGAAAATGTTTCAG	2280
Db	2349	TTACAGAA	AGCACTTTCTGACGTCAACCTGCTTGTTCCTTCCAAAGGAAAATGTTTCAG	2408
Qy	2281	GTTGCA	CAGTCAAACTCTCAACAGGACCTTCTATGAGGAAAAGCTTTGACATGGGAGGA	2340
Db	2409	GTTGCA	CAGTCAAACTCTCAACAGGACCTTCTATGAGGAAAAGCTTTGACATGGGAGGA	2468
Qy	2341	GAAACT	CTGTTGCTGTCTGCTCCATGCTGCCAGGAGCTTTGGGCAAAATCTTTGCTCTGTG	2400
Db	2469	GAAACT	CTGTTGCTGTCTGCTCCATGCTGCCAGGAGCTTTGGGCAAAATCTTTGCTCTGTG	2528
Qy	2401	CAAAAC	CTGATCAGGTGCGACCGAGGAACTGAAATATACAACTTTTCAGGAGTGAGTCAAGT	2460
Db	2529	CAAAAC	CTGATCAGGTGCGACCGAGGAACTGAAATATACAACTTTTCAGGAGTGAGTCAAGT	2588
Qy	2461	GGCTCC	AGAGGCGCCCAAGATTTTACCCCAAAATGGAGGGAATCCAAATTTGTTTATAACT	2520
Db	2589	GGCTCC	AGAGGCGCCCAAGATTTTACCCCAAAATGGAGGGAATCCAAATTTGTTTATAACT	2648
Qy	2521	GATGAAG	AGGTGGGTCCCGAAGACAGACAGACACTTTTGTATGCGCGCACCCAGCCCT	2580
Db	2649	GATGAAG	AGGTGGGTCCCGAAGACAGACAGACACTTTTGTATGCGCGCACCCAGCCCT	2708
Qy	2581	GCCAGGA	AGGTGCTTTGATCAGACTCTCTAAGCTGGAAGGTCAAGATCATCTCTCAG	2640
Db	2709	GCCAGGA	AGGTGCTTTGATCAGACTCTCTAAGCTGGAAGGTCAAGATCATCTCTCAG	2768
Qy	2641	AGCAAT	TTGTAAGGCGAGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAA	2700
Db	2769	AGCAAT	TTGTAAGGCGAGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAA	2828
Qy	2701	TAAAGT	CTTCTTCCAGGCGATAGCAGTTCTTTTAGCCATATACATCATTTGCAATGA	2760
Db	2829	TAAAGT	CTTCTTCCAGGCGATAGCAGTTCTTTTAGCCATATACATCATTTGCAATGA	2888
Qy	2761	ACTATTT	CGAAAAGCCCTTCTAAAAGTTGAAAATGCGGAGAAATCGGGAAGACATGAAGG	2820
Db	2889	ACTATTT	CGAAAAGCCCTTCTAAAAGTTGAAAATGCGGAGAAATCGGGAAGACATGAAGG	2948
Qy	2821	CAGTTTA	TATAGCCGTTTACCTTTTAAATTTGCATGAAAATGATGTTTAAAGGATGCTTAAAA	2880



Db 2949 CAGTTTATAAGCCGTTACCTTTTAATTCATGAAATGCATGTTTAGGGATGGCTAATA 3008  
AAH49499  
QY 2881 TTCCAAGTGATGACATTAACCCACATCTATTAGTAATGACCTTGAATTAATAAGCCT 2940  
Db 3009 TTCCAAGTGATGACATTAACCCACCTCA-TTAGTAATGACCTTGAATTAATAAGCCT 3067  
QY 2941 GAGAAACCAACACAGC-TAATGCTATGGGTGATGAATGT 2983  
Db 3068 GAGAAACCAACACAGCTTAATGCTATGGGGGTATGAATGT 3111

## RESULT 5

AAH49499

ID AAH49499 standard; DNA; 3074 BP.

XX AC

AAH49499;

XX DT 11-DEC-2001 (first entry)

XX DE Human KCNQ5 DNA.

XX KCNQ5; potassium channel protein; human; neurological; cardiovascular;  
KW anticonvulsant; excitability modulator; membrane potential; neuron;  
KW voltage-dependent KCNQ5 potassium channel; cardiomyocyte; epilepsy;  
KW screening; central nervous system disease; cardiovascular disease; ds.  
XX OS Homo sapiens.

XX FH

Key Location/Qualifiers

XX CDS 110..2908

FT /\*tag= a

FT /product= "KCNQ5"

XX DE1013732-A1.

XX PN

27-SEP-2001.

XX PF

21-MAR-2000; 2000DE-01013732.

XX PR

21-MAR-2000; 2000DE-01013732.

XX PA (AVET ) AVENTIS PHARMA DEUT GMBH.

XX PI Steinmeyer K, Lerche C, Scherer C, Seeborn G, Busch AE;

XX DR WPI; 2001-571700/65.

XX DR P-PSDB; AAB86979.

XX PT New DNA sequence encoding potassium channel KCNQ5, useful in screening

XX PT for specific modulators, potential agents for treating central nervous

XX PS system and cardiovascular diseases.

XX PS Claim 2a; Page 9-10; 20pp; German.

XX CC This invention describes a novel DNA sequence (I) encoding: (i) a

XX CC polypeptide (ii) with potassium channel KCNQ5 activity; (iii) a

XX CC polypeptide with the amino acid (aa) sequence of KCNQ5. The products of

XX CC the invention have neurological, cardiovascular and anticonvulsant

XX CC activity and act as modulators of the voltage-dependent KCNQ5 potassium

XX CC channel, a key regulator of membrane potential and modulator of

XX CC excitability of electrically activated cells such as neurons and

XX CC cardiomyocytes. KCNQ5 may be implicated in some forms of epilepsy. (ii)

XX CC are used to screen for compounds that modulate the activity of KCNQ5,

XX CC potentially useful for treating central nervous system (e.g. epilepsy)

XX CC and cardiovascular diseases. This sequence encodes the human potassium

XX CC channel KCNQ5 protein described in the invention

XX SQ Sequence 3074 BP; 788 A; 784 C; 789 G; 713 T; 0 U; 0 Other;

Query Match 93.0%; Score 2857.4; DB 4; Length 3074;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 2861; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGCAGCGCGCATGAAGGATGTGAGTCGGGCGGGGCGAGGTCGCTGCTGAACCTCGGCAGCC 60  
Db 206 GGCAGCGCGCATGAAGGATGTGAGTCGGGCGGGGCGAGGTCGCTGCTGAACCTCGGCAGCC 265  
QY 61 GCCAGGGGCGACGCGCTGCTACTGCTGGGCAACCGCGCGGCGACGCTTGGTGGCGGCGGC 120  
Db 266 GCCAGGGGCGACGCGCTGCTACTGCTGGGCAACCGCGCGGCGACGCTTGGTGGCGGCGGC 325  
QY 121 GGTGGCCTGAGGGAGAGCGCGCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAG 180  
Db 326 GGTGGCCTGAGGGAGAGCGCGCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGC 385  
QY 181 CCGCTCTCTTACACGAGTACGAGCTGCGCGGGCGCAACGTCAGTACCGGGGGTGCAG 240  
Db 386 GCGCTCTCTTACACGAGTACGAGCTGCGCGGGCGCAACGTCAGTACCGGGGGTGCAG 445  
QY 241 AACTACCTGTACAACTGCTGGAGAGAGCCCGCGGCTGGGGGCTTCATCTACACGCTTTC 300  
Db 446 AACTACCTGTACAACTGCTGGAGAGAGCCCGCGGCTGGGGGCTTCATCTACACGCTTTC 505  
QY 301 GTTTTCTCTCTGTCTTTGGTGTGATTTGTGATTTGTGATTTGTGATTTGTGATTTGTGATTT 360  
Db 506 GTTTTCTCTCTGTCTTTGGTGTGATTTGTGATTTGTGATTTGTGATTTGTGATTTGTGATTT 565  
QY 361 ACAAAATGGCCTCAAGTTGCTTGTATCTGATCTGAGTTCGATGATGATGATGATGATGAT 420  
Db 566 ACAAAATGGCCTCAAGTTGCTTGTATCTGATCTGAGTTCGATGATGATGATGATGATGAT 625  
QY 421 TTGCAGTTCATCATTCGAACTCTGCTGCGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
Db 626 TTGCAGTTCATCATTCGAACTCTGCTGCGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 685  
QY 481 GGAAGACTGAGGTTTGTCTCGAAAGCCCTTCTGCTTATAGATACCATTTGTTCTTATCGCT 540  
Db 686 GGAAGACTGAGGTTTGTCTCGAAAGCCCTTCTGCTTATAGATACCATTTGTTCTTATCGCT 745  
QY 541 TCAATAGCAGTTGTTCTGCAAAACTCAGGGTAATATTTTGGCACTGCTGCACTCAGA 600  
Db 746 TCAATAGCAGTTGTTCTGCAAAACTCAGGGTAATATTTTGGCACTGCTGCACTCAGA 805  
QY 601 AGTCTCGGTTTCTACAGATCTCCGATGTCGCGATGGACCGAAGGGGAGGACATTGG 660  
Db 806 AGTCTCGGTTTCTACAGATCTCCGATGTCGCGATGGACCGAAGGGGAGGACATTGG 865  
QY 661 AAATTACTGGGTTTCAAGTGGTTTATGCTCACAAGCAAGAAATTAATCAGAGCTTGGTACATA 720  
Db 866 AAATTACTGGGTTTCAAGTGGTTTATGCTCACAAGCAAGAAATTAATCAGAGCTTGGTACATA 925  
QY 721 GGATTTTGGTTCATATTTTTCGCTTCTGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
Db 926 GGATTTTGGTTCATATTTTTCGCTTCTGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 985  
QY 781 AAAGAGTTTCTACATATGAGATGCTCTCTGCTGGGGGCAATTAATCAGATTCACAACTATT 840  
Db 986 AAAGAGTTTCTACATATGAGATGCTCTCTGCTGGGGGCAATTAATCAGATTCACAACTATT 1045  
QY 841 GGCTATGAGACAAAACCTCCCTAACTTGGCTGGGAAGATGCTTCTGCAAGGCTTTGCA 900  
Db 1046 GGCTATGAGACAAAACCTCCCTAACTTGGCTGGGAAGATGCTTCTGCAAGGCTTTGCA 1105  
QY 901 CTCCTTGGCATTTCTTTTGTGCACTTCCTGCGGCAATCTTTGGCTCAGGTTTGGCATTA 960  
Db 1106 CTCCTTGGCATTTCTTTTGTGCACTTCCTGCGGCAATCTTTGGCTCAGGTTTGGCATTA 1165  
QY 961 AAAGTACAGAACCAACCCGAGAACTTTTTCAGAAAGAAAGCAAGCAAGCAAGCAAGCAAGCA 1020  
Db 1166 AAAGTACAGAACCAACCCGAGAACTTTTTCAGAAAGAAAGCAAGCAAGCAAGCAAGCAAGCA 1225  
QY 1021 CTCAATTCAGTGTGTTTGGCGTAGTTAGCGAGCTGATGAGAAATCTGTTTTCATTTGCAACC 1080  
Db 1226 CTCAATTCAGTGTGTTTGGCGTAGTTAGCGAGCTGATGAGAAATCTGTTTTCATTTGCAACC 1285  
QY 1081 TGGAAAGCCACACTTGAAGGCGCTTGCAACCTGCGAGCCCTTACCAAGAAAGAAAGGGGAA 1140

Db TGGAGGCACACTTGAAGGCTTGCACACCTGCGAGCCTACCAAGAAAGAACAGGGGAA 1345  
Qy GCATCAAGCAGTCAAGAGCTAAGTTTAAAGAGCGAGTGGCGATGGCTAGCCCCAGGGG 1200  
Db GCATCAAGCAGTCAAGAGCTAAGTTTAAAGAGCGAGTGGCGATGGCTAGCCCCAGGGG 1405  
Qy CAGAGTATTAAAGAGCGAGAGCTCAGTATGTCAGAGAGGTCGCCAAGCAGCGACATC 1260  
Db CAGAGTATTAAAGAGCGAGAGCTCAGTATGTCAGAGAGGTCGCCAAGCAGCGACATC 1465  
Qy ACAGCGAGGCGAGTCCACCAAGTGCAGAGAGCTGGAGCTTCAACGAGCCGAGCCGC 1320  
Db ACAGCGAGGCGAGTCCACCAAGTGCAGAGAGCTGGAGCTTCAACGAGCCGAGCCGC 1525  
Qy TTCCGGCCCTCGCTGCGCCTCAAAAGTTCAGAGCCCAAAAGCTGATAGATGCTGACACA 1380  
Db TTCCGGCCCTCGCTGCGCCTCAAAAGTTCAGAGCCCAAAAGCTGATAGATGCTGACACA 1585  
Qy GCCCTTGGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440  
Db GCCCTTGGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1645  
Qy GACCTCACCCCACTTAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500  
Db GACCTCACCCCACTTAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1705  
Qy GCAAAAGCGAGTTTAAAGAGCTTAAAGAGCTTAAAGAGCTTAAAGAGCTTAAAGAGCTTAA 1560  
Db GCAAAAGCGAGTTTAAAGAGCTTAAAGAGCTTAAAGAGCTTAAAGAGCTTAAAGAGCTTAA 1765  
Qy TATTCTGCTGCTCATCTGCAATGTTGTTAGAAATTTAAAGCTTCAAAAGCTTCAAAAGCTT 1620  
Db TATTCTGCTGCTCATCTGCAATGTTGTTAGAAATTTAAAGCTTCAAAAGCTTCAAAAGCTT 1825  
Qy CAATTTCTTGGAAAGGGCAATCATCATGATGATGATGATGATGATGATGATGATGATGATGAT 1680  
Db CAATTTCTTGGAAAGGGCAATCATCATGATGATGATGATGATGATGATGATGATGATGATGAT 1885  
Qy GAAATGAGACACAGAGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740  
Db GAAATGAGACACAGAGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1945  
Qy GTACAGTCCATAGAAATCCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 2005  
Db GTACAGTCCATAGAAATCCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1860  
Qy AAAGCTCTGCTGAGCCCTGCTTGGCTTCAATTCAGTTCCAGCTTCCAGCTTCCAGCTTCCAG 2065  
Db AAAGCTCTGCTGAGCCCTGCTTGGCTTCAATTCAGTTCCAGCTTCCAGCTTCCAGCTTCCAG 1920  
Qy CAGACATCTGACTATCAAGAGCCCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2125  
Db CAGACATCTGACTATCAAGAGCCCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980  
Qy AGTGCTCTTATCCAGATCAACTAGTGCACATCTCGAGAGGCTGAGTTCATTTCTG 2185  
Db AGTGCTCTTATCCAGATCAACTAGTGCACATCTCGAGAGGCTGAGTTCATTTCTG 2040  
Qy AGCCCAATGAGTTGAGTGGCCAGCTTCTACGGCTTACGGCTTACGGCTTACGGCTTACGGCT 2245  
Db AGCCCAATGAGTTGAGTGGCCAGCTTCTACGGCTTACGGCTTACGGCTTACGGCTTACGGCT 2100  
Qy GCAACACAGGTGCCAATTAAGTCAAGAGCTGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 2305  
Db GCAACACAGGTGCCAATTAAGTCAAGAGCTGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 2160  
Qy GCAACACCAATTAATTAAGTGGCAAGTGGCAAGTGGCAAGTGGCAAGTGGCAAGTGGCAAGT 2365  
Db GCAACACCAATTAATTAAGTGGCAAGTGGCAAGTGGCAAGTGGCAAGTGGCAAGTGGCAAGT 2220  
Qy CCTCTCCAGCCATCAGCATCTGCGAGGCGAGAACTCTGCACTTAAACCTTCCAGGCTGAGG 1345

Db CCTCTCCAGCCATCAGCATCTGCCAGGCCAGAAACTCTGCACCCCTAACCCCTGCAGGC 2425  
Qy TTACAGGAAAGCAATTTCTGACGTCACCACTGCTGCTTGGCTCCCAAGGAAATGTTTCTG 2280  
Db TTACAGGAAAGCAATTTCTGACGTCACCACTGCTGCTTGGCTCCCAAGGAAATGTTTCTG 2485  
Qy GTTGCACAGTCAATCTCACCAGGACCGTTCTATAGGAAAGCTTGTGATGGGAGGA 2340  
Db GTTGCACAGTCAATCTCACCAGGACCGTTCTATAGGAAAGCTTGTGATGGGAGGA 2545  
Qy GAAACTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400  
Db GAAACTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2605  
Qy CAAACCTGATCAGTCCAGGAGCACTGAAATATACAACTTTCAGGAGTGGAGTCAAGT 2460  
Db CAAACCTGATCAGTCCAGGAGCACTGAAATATACAACTTTCAGGAGTGGAGTCAAGT 2665  
Qy GGCTCCAGAGGCGAGCAAGATTTTACCCAAATGGAGGAAATCCAAATTTGTTTATAACT 2520  
Db GGCTCCAGAGGCGAGCAAGATTTTACCCAAATGGAGGAAATCCAAATTTGTTTATAACT 2725  
Qy GATCAAGAGTGGTCCGAGGAGACAGACAGACACTTTTGTATGCCGACCGCAGCCT 2580  
Db GATCAAGAGTGGTCCGAGGAGACAGACAGACACTTTTGTATGCCGACCGCAGCCT 2785  
Qy GCCAGGGAAGCTGCTTGGCATCAGACTCTTAAGGACTGGAAGTCCAGTATCATCTCAG 2640  
Db GCCAGGGAAGCTGCTTGGCATCAGACTCTTAAGGACTGGAAGTCCAGTATCATCTCAG 2845  
Qy AGCAATTTGTAAGGAGGAGAAAGTACAGATGCCCTCAGTTGCCCTCATGTCAAACTGAAA 2700  
Db AGCAATTTGTAAGGAGGAGAAAGTACAGATGCCCTCAGTTGCCCTCATGTCAAACTGAAA 2905  
Qy TAAAGTCTTCTTCTTCCAGCATGACAGTCTTGTAGCCATACATATCATTCATTCATG 2760  
Db TAAAGTCTTCTTCTTCCAGCATGACAGTCTTGTAGCCATACATATCATTCATTCATG 2965  
Qy ACTATTTTCGAAAGCCCTTCTTAAAGGTTGAAATTCGAGAAATCGGGAAGCAATGAAAG 2820  
Db ACTATTTTCGAAAGCCCTTCTTAAAGGTTGAAATTCGAGAAATCGGGAAGCAATGAAAG 3025  
Qy CAGTTTAAAGCCGTTTACCTTTTAAATGATGAAATGATGTTTGG 2869  
Db CAGTTTAAAGCCGTTTACCTTTTAAATGATGAAATGATGTTTGG 3074

RESULT 6

ADB78684  
ID ADB78684 standard; cDNA; 3074 BP.

XX ADB78684;

XX AC

XX AC

DT 04-DEC-2003 (first entry)

XX Human potassium channel subunit mutant cDNA SEQ ID NO:55.

ss; gene; mutant; ion channel; ion channel subunit; ICS; nootropic;  
neuroprotective; inotropic; antipyrretic; antiarrhythmic; antimigraine;  
antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;  
nephrotropic; antidiabetic; ophthalmological; epilepsy;  
ion channel dysfunction; human.

XX Synthetic.

OS Homo sapiens.

XX WO2003008574-A1.

FN 30-JAN-2003.

XX 08-JUL-2002; 2002WO-AU000910.

XX 18-JUL-2001; 2001AU-00006452.

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PR 05-MAR-2002; 2002AU-00000910.
XX 13-MAY-2002; 2002AU-00002292.
PA (BION-) BIONOMICS LTD.
PA (WALL/) WALLACE R W.
XX
XX Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
PI Berkovic SF, Scheffer IE;
XX WPI; 2003-239332/23.
XX
XX Identifying predisposition to an ion channel dysfunction, such as
XX periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
XX schizophrenia, anxiety and depression, by detecting encoding-gene
XX mutation events.
PS Claim 6; SEQ ID NO 55; 106pp; English.
XX
XX The invention relates to a novel method for identifying a subject
XX predisposed to a disorder associated with ion channel dysfunction. The
XX method comprises ascertaining if at least one of the genes encoding ion
XX channel subunits (ICS) has undergone a mutation event so that a cDNA
XX derived from the subject has any of 134 nucleotide sequences. The method
XX of the invention has nootropic, neuroprotective, inotropic, antipyretic,
XX antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
XX neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
XX ophthalmological activity. A polynucleotide of the invention acts as an
XX ion channel agonist, or ion channel antagonist. The methods, isolated
XX nucleic acids, polypeptides, antibody, selective agonist, antagonist or
XX modulator of an ion channel, cells and genetically modified non-human
XX animal, are useful for the diagnosis and treatment of epilepsy and/or a
XX disorder associated with ion channel dysfunction, such as hyper- or hypo-
XX kalemic periodic paralysis, myotonias, malignant hyperthermia,
XX myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
XX disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
XX depression, phobic obsessive symptoms, neuropathic pain, inflammatory
XX pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
XX Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
XX fibrosis, congenital stationary night blindness and total colour
XX blindness. The present sequence represents a mutant cDNA of the
XX invention. The sequence data for this patent is not represented in the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
XX Sequence 3074 BP; 787 A; 784 C; 789 G; 714 T; 0 U; 0 Other;
Query Match 93.0%; Score 2855.8; DB 10; Length 3074;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2860; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
QY 1 GGCAGCGCATGAAGGATGTGGAGTCTGGGCGGGGCGAGGGTGTCTGAACTGGCGAGCC 60
DB 206 GGCAGCGCATGAAGGATGTGGAGTCTGGGCGGGGCGAGGGTGTCTGAACTGGCGAGCC 265
QY 61 GCCAGGGCGAGCGGCTCTACTCTGGGACCCCGCGGCGGCGGCTGGTGGCGGGCG 120
DB 266 GCCAGGGCGAGCGGCTCTACTCTGGGACCCCGCGGCGGCGGCTGGTGGCGGGCG 325
QY 121 GGTGGCTCTGAGGAGAGCGCGCGGGCAAGCAGGGGGGCGCGGATGAGCTGTGGGGAG 180
DB 326 GGTGGCTCTGAGGAGAGCGCGCGGGCAAGCAGGGGGGCGCGGATGAGCTGTGGGAGC 385
QY 181 CGCTCTCTTACAGAGTAGCAGAGCTGCGCGGCGCAACGTCAGTACCGCGGGTGCAG 240
DB 386 CGCTCTCTTACAGAGTAGCAGAGCTGCGCGGCGCAACGTCAGTACCGCGGGTGCAG 445
QY 241 AACTACCTGTACACGTCGTGGAGAGACCCCGCGGCTGGGCTTCATCTACACGCTTTC 300
DB 446 AACTACCTGTACACGTCGTGGAGAGACCCCGCGGCTGGGCTTCATCTACACGCTTTC 505
QY 301 GTTTTCTCTTGTCTTTGGTGTGTTGTTGTCAGTGTGTTTCTTACCATCCCTGAGCAC 360
DB 506 GTTTTCTCTTGTCTTTGGTGTGTTGTTGTCAGTGTGTTTCTTACCATCCCTGAGCAC 565
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1441 GACCTCCACCCACCACTTAAACCTGTCTATTCGAGCTATCAGAAATTAACAAATTCATGTT 1500  
1446 GACCTCCACCCACCACTTAAACCTGTCTATTCGAGCTATCAGAAATTAACAAATTCATGTT 1705  
1501 GCAAAACGGAAGTTTAAAGGAACCTTACGTCATATGATGTAAGATGTCATTGAAACAA 1560  
1706 GCAAAACGGAAGTTTAAAGGAACCTTACGTCATATGATGTAAGATGTCATTGAAACAA 1765  
1561 TATTCTGCTGTCATCTGGACATCTGTGTAGAAATTAAGAGCCTTCAAAACAGGTGTTGAT 1620  
1766 TATTCTGCTGTCATCTGGACATCTGTGTAGAAATTAAGAGCCTTCAAAACAGGTGTTGAT 1825  
1621 CAATTTCTTGAAGAGGCAATCACATCAATGAAGAGCCGAGAGAAATTAACAGCA 1680  
1826 CAATTTCTTGAAGAGGCAATCACATCAATGAAGAGCCGAGAGAAATTAACAGCA 1885  
1681 GAAATGAGACCAAGAGGATCTCAGTATGCTCGGTGGGTGTCAGAGTTGAAAGAACAG 1740  
1886 GAAATGAGACCAAGAGGATCTCAGTATGCTCGGTGGGTGTCAGAGTTGAAAGAACAG 1945  
1741 GTACAGTCCATAGAAATCAAGCTGCACTGCTTACATGATCTATCAACAGGTCTCTCGG 1800  
1946 GTACAGTCCATAGAAATCAAGCTGCACTGCTTACATGATCTATCAACAGGTCTCTCGG 2005  
1801 AAAGGCTCTGCTCAGCCCTCGCTTTGGCTTCAATTCAGATTCCTCCACCTTTTGAATGAA 1860  
2006 AAAGGCTCTGCTCAGCCCTCGCTTTGGCTTCAATTCAGATTCCTCCACCTTTTGAATGAA 2065  
1861 CAGACATCTGACTATCAAGGCTGTGTAGTAAAGATCTTTCGGGTTCGGCAACAAAC 1920  
2066 CAGACATCTGACTATCAAGGCTGTGTAGTAAAGATCTTTCGGGTTCGGCAACAAAC 2125  
1921 AGTGGCTCTTATCCAGATCAACTAGTGCACCACTCTCGAGAGGCTCGAGTTCATCTG 1980  
2126 AGTGGCTCTTATCCAGATCAACTAGTGCACCACTCTCGAGAGGCTCGAGTTCATCTG 2185  
1981 AGCCCAATGAGTTCAGTCCCGCAGACTTCTACGGCTTACGCTTACATGATCAAGTCAA 2040  
2186 AGCCCAATGAGTTCAGTCCCGCAGACTTCTACGGCTTACGCTTACATGATCAAGTCAA 2245  
2041 GCAACACAGGTGCGAATTAAGTCAAGCGATGGCTCAGCAGTGGCGAGCCACCAACACCAAT 2100  
2246 GCAACACAGGTGCGAATTAAGTCAAGCGATGGCTCAGCAGTGGCGAGCCACCAACACCAAT 2305  
2101 GCAACACCAATTAATACGGCACCACCAAGCAGCAGCCCAACCACTTTACAGATCCCACT 2160  
2306 GCAACACCAATTAATACGGCACCACCAAGCAGCAGCCCAACCACTTTACAGATCCCACT 2365  
2161 CCTCTCCAGCCATCAAGCATCTGCCAGGCGAGAACTCTGCACCCCTAACCCCTGCAGGC 2220  
2366 CCTCTCCAGCCATCAAGCATCTGCCAGGCGAGAACTCTGCACCCCTAACCCCTGCAGGC 2425  
2221 TTACAGGAAGCAATTTCTGAGCTCAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280  
2426 TTACAGGAAGCAATTTCTGAGCTCAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2485  
2281 GTTGACACAGTCAAACTCTCACCAGGACCGTCTATGAGGAAAGCTTTGACATGGGAGGA 2340  
2486 GTTGACACAGTCAAACTCTCACCAGGACCGTCTATGAGGAAAGCTTTGACATGGGAGGA 2545  
2341 GAACTCTGTTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400  
2546 GAACTCTGTTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2605  
2401 CAAACCTGATCAGTCCAGCAGGAACTGAATATACAACTTTACAGGAGTGAAGTCAAGT 2460  
2606 CAAACCTGATCAGTCCAGCAGGAACTGAATATACAACTTTACAGGAGTGAAGTCAAGT 2665  
2461 GGCTCCAGAGGACCAAGATTTTACCCCAATGAGGGAATCCAAATTTGTTTAACT 2520  
2666 GGCTCCAGAGGACCAAGATTTTACCCCAATGAGGGAATCCAAATTTGTTTAACT 2725  
2521 GATGAAGAGGTGGTCCCGAAGAGACAGACAGACAGACACTTTTGTATGCGCCGACCGAGCT 2580

2726 GATGAAGAGGTGGTCCCGAAGAGACAGACACTTTTGTATCCGACCGAGCCT 2785  
2581 GCCAGGGAAGCTGCTTTTGCATCAGACTCTTAAGGACTGGAAGGTCAAGATCATCTCAG 2640  
2786 GCCAGGGAAGCTGCTTTTGCATCAGACTCTTAAGGACTGGAAGGTCAAGATCATCTCAG 2845  
2641 AGCATTTTGAAGGACGAGGAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACGTGAAA 2700  
2846 AGCATTTTGAAGGACGAGGAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACGTGAAA 2905  
2701 TAAGTTCCTCATTTTCTTCCAGGATAGCAGTCTTTAGCCATACATATCATGTCATGA 2760  
2906 TAAGTTCCTCATTTTCTTCCAGGATAGCAGTCTTTAGCCATACATATCATGTCATGA 2965  
2761 ACTATTTCGAAGCCCTTCTTAAAGAGTTGAAATTCGAAGATCGGAAGAACATGAAAGG 2820  
2966 ACTATTTCGAAGCCCTTCTTAAAGAGTTGAAATTCGAAGATCGGAAGAACATGAAAGG 3025  
2821 CAGTTTATAGCCCGTTACCTTTTAAATTGCATGCAAAATGCATGTTAGG 2869  
3026 CAGTTTATAGCCCGTTACCTTTTAAATTGCATGCAAAATGCATGTTAGG 3074

## RESULT 7

AAS14652

ID AAS14652 standard; cdna; 2694 BP.

XX AAS14652;

XX DT 18-DEC-2001 (first entry)

XX DE Human cDNA encoding a voltage gated potassium channel hKCNQ5-1.

XX KW Human; ss; voltage-gated potassium channel; hKCNQ5-1; nootropic;  
cerebroprotective; neurotropic; analgesic; vision disorder;  
central nervous system disorder; epilepsy; migraine; hearing disorder;  
psychotic disorder; seizure; learning disorder; memory disorder; stroke;  
pain; gene therapy; splice variant.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
FT CDS 1..2994

FT FT /\*tag= a

FT FT /product= "hKCNQ5-1"

XX PN WO200170759-A1.

XX PD 27-SEP-2001.

XX PF 20-MAR-2001; 2001WO-US009328.

XX PR 21-MAR-2000; 2000US-0190954P.

XX PA (ICAG-) ICAGEN INC.

XX PI Jegla TJ;

XX DR WPI; 2001-611467/70.

XX DR P-PSDB; AAU03020.

XX PT Polypeptides and polynucleotides of potassium channel KCNQ5 for  
identifying a compound modulating ion flux in eukaryotic cell or cell  
membrane expressing the protein, comprises KCNQ approximately alpha-subunits.  
XX PS Claim 5; Page 62-63; 78pp; English.

XX CC The invention relates to an isolated polypeptide comprising an alpha-  
subunit of a KCNQ potassium channel, with a subsequence having 65%  
sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence  
and forms a KCNQ potassium channel having the characteristic of voltage-  
gating with at least an additional KCNQ alpha-subunit. Also included in

the scope of the invention are the nucleic acids encoding hKNQ5 (including splice variants encoding hKNQ5-1 and hKNQ5-2), expression vectors encoding them, antibodies against them, the use of 3-dimensional computer modelling to identify molecules that bind to a hKNQ5 containing potassium channel and modulate ion flux through the channel. The hKNQ5 polypeptide is useful for identifying a compound that increases or decreases ion flux through a potassium channel expressed in an eukaryotic host cell or cell membrane. The compound (and the hKNQ5 nucleic acid when used in gene therapy) is useful as a pharmaceutical agent for treating diseases involving abnormal ion flux, such as disorders of the central nervous system, such as epilepsy, migraines, hearing and vision problems, psychotic disorders, seizures, learning and memory disorders, stroke and pain. The antibodies are useful for detecting a hKNQ5 polypeptide in a human tissue and the use of a nucleotide sequence of hKNQ5 to search computer databases to find variants of the sequence which are associated with disease states, is useful for screening mutations of hKNQ5. The present sequence is a splice variant of hKNQ5 encoding hKNQ5-1.

SQ Sequence 2694 BP; 714 A; 671 C; 669 G; 640 T; 0 U; 0 Other;

Query Match 87.6%; Score 2690.4; DB 4; Length 2694;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2691; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

10 ATGAGGATGTTGGAGTCGGCGCGGGGAGGCTGCTGTAACCTGGGAGCGCCAGGGGC 69  
1 ATGAGGATGTTGGAGTCGGCGCGGGGAGGCTGCTGTAACCTGGGAGCGCCAGGGGC 60  
70 GACGGCTGCTACTGCTGGGACCGCGCGGCCAGCTTGTGTGGCGGGGGTGGCTG 129  
61 GACGGCTGCTACTGCTGGGACCGCGCGGCCAGCTTGTGTGGCGGGGGTGGCTG 120  
130 AGGAGAGCCCGCGGGGCAAGCAGGGGCGCCGGATGAGCTGCTGGGAAAGCCGCTCT 189  
121 AGGAGAGCCCGCGGGGCAAGCAGGGGCGCCGGATGAGCTGCTGGGAAAGCCGCTCT 180  
190 TACAGGATACAGAGTCGGCGGCCAAGCTCAAGTACCGGGGGTGGCAAGTACCTG 249  
181 TACAGGATACAGAGTCGGCGGCCAAGCTCAAGTACCGGGGGTGGCAAGTACCTG 240  
250 TACAGGATACAGAGTCGGCGGCCAAGCTCAAGTACCGGGGGTGGCAAGTACCTG 309  
241 TACAGGATACAGAGTCGGCGGCCAAGCTCAAGTACCGGGGGTGGCAAGTACCTG 300  
310 CTGCTGTTGGTGTGATTTGTCAGTGTGTTTCTACCATCCCTGGAGCACACAAATG 369  
301 CTGCTGTTGGTGTGATTTGTCAGTGTGTTTCTACCATCCCTGGAGCACACAAATG 360  
370 GCCTCAAGTGTGCTTGGATCTGGAGTTCGTGATGATGTCGTTTGGTGGAGTTC 429  
361 GCCTCAAGTGTGCTTGGATCTGGAGTTCGTGATGATGTCGTTTGGTGGAGTTC 420  
430 ATCATTCGAATCTGCTGCGGGTGTGTTGTCGATATAGAGTGGCAAGGAGACTG 489  
421 ATCATTCGAATCTGCTGCGGGTGTGTTGTCGATATAGAGTGGCAAGGAGACTG 480  
490 AGGTTTGTCTGAAAGCCCTTCTGTGTTATAGATACCAATGTTCTATCGCTTCAATAGCA 549  
481 AGGTTTGTCTGAAAGCCCTTCTGTGTTATAGATACCAATGTTCTATCGCTTCAATAGCA 540  
550 GTTGTTCCTGCAAAACTCAGGGTAATATTTTGGCAGCTGTGCACTCAGAAAGTCTCGT 609  
541 GTTGTTCCTGCAAAACTCAGGGTAATATTTTGGCAGCTGTGCACTCAGAAAGTCTCGT 600  
610 TTCTTACAGATCTCCGATGGTGGCATGGACCGAGGGGAGGACCTTGGAAATTAATG 669  
601 TTCTTACAGATCTCCGATGGTGGCATGGACCGAGGGGAGGACCTTGGAAATTAATG 660  
670 GGTTCAGTGGTTTATGCTCACAGCAAGGAAATTAATCACAGCTTGGTATAGGATTTT 729  
661 GGTTCAGTGGTTTATGCTCACAGCAAGGAAATTAATCACAGCTTGGTATAGGATTTT 720  
730 GTTCTTATTTTTCGCTTTTCTGCTATCTGTTGGGAAAGGATGCGCAATAAGAGTTT 789

721 GTTCTTATTTTTCGCTTTTCTCTGTCTATCTGTTGGAAAGGATGCGCAATAAGAGTTT 780  
790 TCTACATATGCAGATGCTCTCTGTTGGGGCAATATACATTGACAACCTATTGGCTATGGA 849  
781 TCTACATATGCAGATGCTCTCTGTTGGGGCAATATACATTGACAACCTATTGGCTATGGA 840  
850 GACAAAACCTCCCTAACTTGGCTGGGAAGATTGCTTCTGCGAGCTTTGCACTCTCTGGC 909  
841 GACAAAACCTCCCTAACTTGGCTGGGAAGATTGCTTCTGCGAGCTTTGCACTCTCTGGC 900  
910 ATTTCTTTTCTTGGCACCTTCTGCGGCATCTCTGCTCAGTCTTGGCTTTGCAATAAAGTACA 969  
901 ATTTCTTTTCTTGGCACCTTCTGCGGCATCTCTGCTCAGTCTTGGCTTTGCAATAAAGTACA 960  
970 GAACAACACCGCCAGAAACACTTTTGAGAAAAGAGAAACCCAGCTGCGCAACCTCATTCAG 1029  
961 GAACAACACCGCCAGAAACACTTTTGAGAAAAGAGAAACCCAGCTGCGCAACCTCATTCAG 1020  
1030 TGTGTTTGGGCTAGTTACGACAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1089  
1021 TGTGTTTGGGCTAGTTACGACAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080  
1090 CACTTTGAAGGCTTTGACACCTGACGCTTACCAAGAAAGAAACAAAGGGAAGCATCAAGC 1149  
1081 CACTTTGAAGGCTTTGACACCTGACGCTTACCAAGAAAGAAACAAAGGGAAGCATCAAGC 1140  
1150 AGTCAGAAGCTTAAGTTTAAAGGAGCGAGTGGCATGCTAGCCCCAGGGGCGCAGATATT 1209  
1141 AGTCAGAAGCTTAAGTTTAAAGGAGCGAGTGGCATGCTAGCCCCAGGGGCGCAGATATT 1200  
1210 AAGAGCGCAGCAAGCCTCAGTAGTGACAGAGTTCCTCCAGCAGCAGCATCACAGCCGAG 1269  
1201 AAGAGCGCAGCAAGCCTCAGTAGTGACAGAGTTCCTCCAGCAGCAGCATCACAGCCGAG 1260  
1270 GGCACTCCCAAGGTCAGAGCTGGAGCTTCAACGACCGAACCCGCTTCGCGGCC 1329  
1261 GGCACTCCCAAGGTCAGAGCTGGAGCTTCAACGACCGAACCCGCTTCGCGGCC 1320  
1330 TCGCTGCGCTTCAAAAGTTTCTCAGCCAAACCAAGTATGCTGATGCTGACACAGCCCTTGGC 1389  
1321 TCGCTGCGCTTCAAAAGTTTCTCAGCCAAACCAAGTATGCTGATGCTGACACAGCCCTTGGC 1380  
1390 ACTGATGATATATGATGAAAAAGGATGCGAGTGTGATGATGATGATGATGATGATGATGAT 1449  
1381 ACTGATGATATATGATGAAAAAGGATGCGAGTGTGATGATGATGATGATGATGATGATGAT 1440  
1450 CCACCACTTAAAGCTGCTTCAAGCTATCAGATTTATGAAATTTCAATTTGTCGCAAAAGCG 1509  
1441 CCACCACTTAAAGCTGCTTCAAGCTATCAGATTTATGAAATTTCAATTTGTCGCAAAAGCG 1500  
1510 AAGTTTAAAGGAAACCTTACGCTCCATATGATGAAAAAGTGTCAATTTGAACCAATATTTGCT 1569  
1501 AAGTTTAAAGGAAACCTTACGCTCCATATGATGAAAAAGTGTCAATTTGAACCAATATTTGCT 1560  
1570 GGTCACTGGAATGTTGTGATGATTTAAAGCCTTCAACACAGCTGTTGATCAAAATCTT 1629  
1561 GGTCACTGGAATGTTGTGATGATTTAAAGCCTTCAACACAGCTGTTGATCAAAATCTT 1620  
1630 GGAAGAGGCAATATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1689  
1621 GGAAGAGGCAATATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680  
1690 ACCACAGACGATCTCAGTATGCTCGGTGGGTGCTCAAGGTTGAAAAACAGGTACAGTCC 1749  
1681 ACCACAGACGATCTCAGTATGCTCGGTGGGTGCTCAAGGTTGAAAAACAGGTACAGTCC 1740  
1750 ATAGAATCCAAGCTGGAATGCTTACTAGACATCTATCAACAGGCTTCTCGGAAAGGCTCT 1809  
1741 ATAGAATCCAAGCTGGAATGCTTACTAGACATCTATCAACAGGCTTCTCGGAAAGGCTCT 1800  
1810 GCCTCAGCCCTCGCTTTGGCTTCAATTCAGTTCCTCCAGTTCCTTTGATTTGATGAGACATCT 1869

D	b	1801	GCCTCAGCCCTCGCTTTGGCTTCAATTCAGATCCACCTTTTGAATGGAACAGACATCT	1860	K	W
Q	y	1870	GACTATCAAGCCCTGTGATAGCAAGATCTTTCCGGTTCCGCACAAAAACAGTGGCTGC	1929	K	W
D	b	1861	GACTATCAAGCCCTGTGATAGCAAGATCTTTCCGGTTCCGCACAAAAACAGTGGCTGC	1920	K	W
Q	y	1930	TTATCCAGATCAACTAGTGCACCAATCTCGAGAGCCCTGACGTTTCATTCTCAGCCCAAT	1989	K	W
D	b	1921	TTATCCAGATCAACTAGTGCACCAATCTCGAGAGCCCTGACGTTTCATTCTCAGCCCAAT	1980	K	W
Q	y	1990	GAGTTAGTCCGACGATTTTACGGCTTAGCCCTACTATGCAAGTCAAGCAACACAG	2049	K	W
D	b	1981	GAGTTAGTCCGACGATTTTACGGCTTAGCCCTACTATGCAAGTCAAGCAACACAG	2040	K	W
Q	y	2050	GTGCGAATTAGTCAAGCGATGGCTCAGCAGTGCAGCCACCAACATTTGCAACCAA	2109	K	W
D	b	2041	GTGCGAATTAGTCAAGCGATGGCTCAGCAGTGCAGCCACCAACATTTGCAACCAA	2100	K	W
Q	y	2110	ATAAATACGGCACCAAGCCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA	2169	K	W
D	b	2101	ATAAATACGGCACCAAGCCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA	2160	K	W
Q	y	2170	GCCATCAAGCATCTGCCAGCCGCAAACTCTGCAACCTAACCCCTGCAGGCTTACAGAA	2229	K	W
D	b	2161	GCCATCAAGCATCTGCCAGCCGCAAACTCTGCAACCTAACCCCTGCAGGCTTACAGAA	2220	K	W
Q	y	2230	AGCATTTCTGACGTCACCACTGCTTGTGCTCCCAAGGAAATGTTTCAGGTTGCACAG	2289	K	W
D	b	2221	AGCATTTCTGACGTCACCACTGCTTGTGCTCCCAAGGAAATGTTTCAGGTTGCACAG	2280	K	W
Q	y	2290	TCAAATCTCACAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAACTCTG	2349	K	W
D	b	2281	TCAAATCTCACAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAACTCTG	2340	K	W
Q	y	2350	TTGTCTGTCTGCCATGTCGCAAGACATTTGGGCAAAATCTTTGTCTGTGCAAAACCTG	2409	K	W
D	b	2341	TTGTCTGTCTGCCATGTCGCAAGACATTTGGGCAAAATCTTTGTCTGTGCAAAACCTG	2400	K	W
Q	y	2410	ATCAGTTCGCGAGGAACTCAATATACAACTTTTCAGGAGTGAATCAAGTGGCTCCAGA	2469	K	W
D	b	2401	ATCAGTTCGCGAGGAACTCAATATACAACTTTTCAGGAGTGAATCAAGTGGCTCCAGA	2460	K	W
Q	y	2470	GGCAGCCAAAGATTTTACCCCAATGGAGGAAATCCAAATTTTATAACTGTATGAAGAG	2529	K	W
D	b	2461	GGCAGCCAAAGATTTTACCCCAATGGAGGAAATCCAAATTTTATAACTGTATGAAGAG	2520	K	W
Q	y	2530	GTGGTCCGGAAGACAGACAGACACTTTTATGTCGCGACCGACCTGCAGGGAA	2589	K	W
D	b	2521	GTGGTCCGGAAGACAGACAGACACTTTTATGTCGCGACCGACCTGCAGGGAA	2580	K	W
Q	y	2590	GCTGCTTTGATCAGACTCTTAAGGACTGGAAGTCAACATCATCTCAGACATTTGT	2649	K	W
D	b	2581	GCTGCTTTGATCAGACTCTTAAGGACTGGAAGTCAACATCATCTCAGACATTTGT	2640	K	W
Q	y	2650	AAGCAGGAGAAAGTACAGATGCGCTCAGTTGCTCATGTCAAACCTGAATAA	2703	K	W
D	b	2641	AAGCAGGAGAAAGTACAGATGCGCTCAGTTGCTCATGTCAAACCTGAATAA	2694	K	W
RESULT 8						
AAD27192						
ID		AAD27192 standard; cDNA; 2694 BP.				
AC		AAD27192;				
XX						
DT		09-APR-2002 (first entry)				
DE		Human potassium channel polypeptide, KCNQ5 cDNA.				
XX						
KW		Human; potassium channel polypeptide; KCNQ5; pain; migraine; stroke;				
KW		dementia; trauma; epilepsy; seizure; amyotrophic lateral sclerosis; ALS;				
KW		multiple sclerosis; MS; Parkinson's disease; ataxia; depression;				
KW		anxiety disorder; bipolar disorder; sleep disorder; eating disorder;				

addiction; myokymia; Alzheimer's disease; age-associated memory loss; learning deficiency; cognitive disorder; motor disease; neuron disease; neurophysiological disorder; neuropsychological disorder; asthma; neuron cell death; brain tumour; gene therapy; antisense therapy; synaptic transmission; electrical excitability; ss.

Homo sapiens.

Key	Location/Qualifiers
CDS	1..2694
	/*tag= a
	/product= "Human KCNQ5 protein"

WO200192526-A1.

06-DEC-2001.

24-MAY-2001; 2001WO-US017314.

26-MAY-2000; 2000US-0207389P.

(BRIM ) BRISTOL-MYERS SQUIBB CO.

Dworetzky SI, Ramanathan CS, Trojnakci JT, Boissard CG; Gribkoff VK;

WPI: 2002-122069/16.

P-PSDB; AAE16599.

Novel potassium channel polypeptide, KCNQ5 and polynucleotide encoding it, for diagnosing, treating and identifying modulators useful in treating neurological, neurophysiological and neuropsychological diseases.

Claim 3; Fig 1; 128pp; English.

The invention relates to potassium channel polypeptides referred to as KCNQ5 and nucleic acid molecules encoding such polypeptides. KCNQ5 polypeptides are useful for identifying compounds that modulate their biological activity. The compounds identified and KCNQ5 polynucleotides are useful for treating acute and chronic pain, migraine, acute stroke, dementia, trauma, epilepsy, seizure, amyotrophic lateral sclerosis (ALS), multiple sclerosis (MS), Parkinson's disease, ataxia, anxiety disorders, depression, bipolar disorder, sleep disorders, eating disorders, addiction, myokymia, Alzheimer's disease, age-associated memory loss, learning deficiencies, cognitive disorders and motor neuron diseases. The nucleic acid molecules of the invention are further useful for treating neurophysiological, neuropsychological disorders, asthma, neuron cell death and brain tumours. They are also used in gene therapy and antisense therapy. KCNQ5 polypeptides modulate synaptic transmission and electrical excitability in the brain and are useful for generating antibodies. They are also useful to affinity purify biological effectors from biological materials e.g. disease tissues or cells. The present sequence is human KCNQ5 cDNA

Sequence 2694 BP; 714 A; 671 C; 669 G; 640 T; 0 U; 0 Other;

Query Match 87.6%; Score 2690.4; DB 6; Length 2694;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2691; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	10	ATGAAGGATGTGGAGTCGGGCCGAGGAGTGTCTGTAACTCGGCAGCGCCAGGGGC	69
D	b	1	ATGAAGGATGTGGAGTCGGGCCGAGGAGTGTCTGTAACTCGGCAGCGCCAGGGGC
Qy	70	GACGGCTGTACTGTCTGGGACACCGCGCGGCCACGCTTGTGTGGCGGGCGGTG	129
D	b	61	GACGGCTGTACTGTCTGGGACACCGCGCGGCCACGCTTGTGTGGCGGGCGGTG
Qy	130	AGGAGAGCCCGCGGCAAGCAGGGGGCCCGGATGAGCTGCTGGGAGACCGCTCT	189
D	b	121	AGGAGAGCCCGCGGCAAGCAGGGGGCCCGGATGAGCTGCTGGGAGACCGCTCT

Qy	190	TACACGAGTAGCAGAGCTGCCGGCGCAACGTCAAGTACCCGGCGGTGCAGAACTACTCTG	249
Db	181	TACACGAGTAGCAGAGCTGCCGGCGCAACGTCAAGTACCCGGCGGTGCAGAACTACTCTG	240
Qy	250	TACAACTGCTGGAGAGACCCCGCGTTCATCTACCAACGCTTCCTGTTTTCTC	309
Db	241	TACAACTGCTGGAGAGACCCCGCGTTCATCTACCAACGCTTCCTGTTTTCTC	300
Qy	310	CTTGCTTTGGTTGCTTGAATTTTCTCAGTGTGTTTCTACCATCCCTGAGCACACAAAATTG	369
Db	301	CTTGCTTTGGTTGCTTGAATTTTCTCAGTGTGTTTCTACCATCCCTGAGCACACAAAATTG	360
Qy	370	GCCTCAAGTTGCCCTTTGATCCTGGAGTTCGTGATGATGTCGTCTTTGGTTGAGATTC	429
Db	361	GCCTCAAGTTGCCCTTTGATCCTGGAGTTCGTGATGATGTCGTCTTTGGTTGAGATTC	420
Qy	430	ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATACAGATGCGAAGGAAGACTG	489
Db	421	ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATACAGATGCGAAGGAAGACTG	480
Qy	490	AGGTTTGCTCGAAAAGCCCTTCTGTGTTATAGATACCAATGTTCTTATCGCTTCAATAGCA	549
Db	481	AGGTTTGCTCGAAAAGCCCTTCTGTGTTATAGATACCAATGTTCTTATCGCTTCAATAGCA	540
Qy	550	GTTGTTTCTGCAAAAATCTCAGGGTAATATTTTGGCAGCTCTGCATCAGAACTCTCGGT	609
Db	541	GTTGTTTCTGCAAAAATCTCAGGGTAATATTTTGGCAGCTCTGCATCAGAACTCTCGGT	600
Qy	610	TTCTCAGAGTCCCTCCGATGGTGGCATGGAACCGAAGGGGAGGACCTTGGAAATTAAGT	669
Db	601	TTCTCAGAGTCCCTCCGATGGTGGCATGGAACCGAAGGGGAGGACCTTGGAAATTAAGT	660
Qy	670	GGTTCACTGGTTATGCTTCAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTGTG	729
Db	661	GGTTCACTGGTTATGCTTCAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTGTG	720
Qy	730	GTTCCTATTTTTTTCGCTCTTCTCTGTTCTATCTGCTGGAAAAGGATGCCAATAAAGATTT	789
Db	721	GTTCCTATTTTTTTCGCTCTTCTCTGTTCTATCTGCTGGAAAAGGATGCCAATAAAGATTT	780
Qy	790	TCTACATATGCAGATGCTCTCTGGTGGGCACAATTAATGACAACATATTTGGCTATGGA	849
Db	781	TCTACATATGCAGATGCTCTCTGGTGGGCACAATTAATGACAACATATTTGGCTATGGA	840
Qy	850	GACAAAATCCCTTAACTTGGCTGGGAAGATTGCTTCTGCAAGCTTTGCATCTCTTGGC	909
Db	841	GACAAAATCCCTTAACTTGGCTGGGAAGATTGCTTCTGCAAGCTTTGCATCTCTTGGC	900
Qy	910	ATTTCTTTTCTTGTGCACTTCTCTGCGGCATTTCTGGCTCAGGTTTTTGATTAAGAGTACAA	969
Db	901	ATTTCTTTTCTTGTGCACTTCTCTGCGGCATTTCTGGCTCAGGTTTTTGATTAAGAGTACAA	960
Qy	970	GAACAAACCGCCAGAAACACTTTGAAAAGAGGAACCCAGCTGCCAACCTCATTTGAG	1029
Db	961	GAACAAACCGCCAGAAACACTTTGAAAAGAGGAACCCAGCTGCCAACCTCATTTGAG	1020
Qy	1030	TGTTGTTGGCTAGTTACGCAAGCTGATGAGAAATCTGTTTCCATTGCAACTCTGGAAGCCA	1089
Db	1021	TGTTGTTGGCTAGTTACGCAAGCTGATGAGAAATCTGTTTCCATTGCAACTCTGGAAGCCA	1080
Qy	1090	CACTTGAAGCCTTTCACACCTGACGCCCTACCAAGAAAGAACCAAGGGGAGCATCAAGC	1149
Db	1081	CACTTGAAGCCTTTCACACCTGACGCCCTACCAAGAAAGAACCAAGGGGAGCATCAAGC	1140
Qy	1150	AGTCAGAAGCTTAAGTTTTTAAGGACGAGTGGCGATGCGTAGCCCGCCAGGGGCGAGATTT	1209
Db	1141	AGTCAGAAGCTTAAGTTTTTAAGGACGAGTGGCGATGCGTAGCCCGCCAGGGGCGAGATTT	1200
Qy	1210	AAGAGCCGACAAAGCCTCAGTAGGTGACAGGAGTCCCAAGCACCAGATCACAGCCGAG	1269
Db	1201	AAGAGCCGACAAAGCCTCAGTAGGTGACAGGAGTCCCAAGCACCAGATCACAGCCGAG	1260
Qy	1270	GGCAGTCCCAAGAGTCAGAAAGAGCTGGAGCTTCAACGACCCGAAACCCGCTTCCCGGCC	1329



Db	2341	TTGTCGTCTGTCCATCTGGTGGCCGGAAGCACTTGGGGAAAATCTTTGTCTGTGCGAAACCTG	2400
Qy	2410	ATCAGGTGACCGAGGAACCTGAATATATACAACTTTTCAGGGAGTGAGTCAAGTGGCTCCAGA	2469
Db	2401	ATCAGGTGACCGAGGAACCTGAATATATACAACTTTTCAGGGAGTGAGTCAAGTGGCTCCAGA	2460
Qy	2470	GGCAGCCCAAGATTTTATCCCAATGAGGGGAATCCAAATTTGTTTATACTGATGAAGAG	2529
Db	2461	GGCAGCCCAAGATTTTATCCCAATGAGGGGAATCCAAATTTGTTTATACTGATGAAGAG	2520
Qy	2530	GTGGGTCCCGAAGACAGACAGACACACTTTTGTATCCGACCGCAGCCTGCCAGGGAA	2589
Db	2521	GTGGGTCCCGAAGACAGACAGACACACTTTTGTATCCGACCGCAGCCTGCCAGGGAA	2580
Qy	2590	GCTGCTTTTCATCAGACTCTTAAGACATGGAGGTGACGATCATCTCAGAGCATTTGT	2649
Db	2581	GCTGCTTTTGATCAGACTCTTAAGACATGGAGGTGACGATCATCTCAGAGCATTTGT	2640
Qy	2650	AAGCAGAGAAAGTACAGATGCCTTCAGCTTGCTTCATGTCAACTGAATAA	2703
Db	2641	AAGCAGAGAAAGTACAGATGCCTTCAGCTTGCTTCATGTCAACTGAATAA	2694

## RESULT 9

RESOLUT 3  
AAH43633  
ID AAH43633 standard: cDNA: 2772 bp.

AA  
AC  
AAH43633;

21-JAN-2002 (first entry)

Human ion-channel forming protein ORF.

Ion-channel forming protein; voltage-gated potassium channel; fetal; brain; thymus; prostate; heart; skeletal muscle; probe; ss.

OS Homo sapiens.

PN WO200175108-A1.

PD 11-OCT-2001.

03-APR-2001; 2001WO-US010875.

PR 03-APR-2000; 2000US-0194255P.

PA (LEXI-) LEXICON GENETICS INC.

PI Hu Y, Kieke JA, Turner AC, Nehls MC, Friedrich G, Zambrowicz B;  
PI Sands AT;

DR WPI; 2001-656987/75.

DR P-PSDB; AAB47678.

PT New human ion channel protein and polynucleotides encoding the protein,  
PT useful in diagnosing or treating diseases, in drug screening, and in  
PT clinical trial monitoring.

PS Claim 1; Page 34-35; 41pp; English.

The sequences in AH43633-34 encode a novel ion-channel forming protein. The protein shares structural similarity with mammalian ion channel proteins, particularly voltage-gated potassium channel proteins. The protein is expressed in many human cell lines including fetal brain, brain, thymus, prostate, heart and skeletal muscle. The novel protein can be used in the diagnosis or treatment of diseases, in drug screening, and in clinical trial monitoring. The oligonucleotides may be used as hybridization probes for screening libraries, and assessing gene expression patterns (particularly using a micro array or high throughput chip format). The nucleic acids and novel protein can also be used in the identification, selection and validation of novel molecular targets for drug discovery, to screen collections of genetic material from patients who have a particular medical condition, to identify mutations associated



PN WO200170759-A1.  
XX 27-SEP-2001.  
XX 20-MAR-2001; 2001WO-US009328.  
XX 21-MAR-2000; 2000US-0190954P.  
XX (ICAG-) ICAGEN INC.  
XX Jegla TJ;  
PI WPI; 2001-611467/70.  
DR P-PSDB; AAU09021.  
XX Polypeptides and polynucleotides of potassium channel KCNQ5 for  
PT identifying a compound modulating ion flux in eukaryotic cell or cell  
PT membrane expressing the protein, comprises KCNQ approximately- subunits.  
XX  
XX Claim 5; Page 63-64; 78pp; English.  
XX  
XX The invention relates to an isolated polypeptide comprising an alpha-  
CC subunit of a KCNQ potassium channel, with a subsequence having 65%  
CC sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence  
CC and forms a KCNQ potassium channel having the characteristic of voltage-  
CC gating with at least an additional KCNQ alpha-subunit. Also included in  
CC the scope of the invention are the nucleic acids encoding hKCNQ5  
CC (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression  
CC vectors encoding them, antibodies against them, the use of 3-dimensional  
CC computer modelling to identify molecules that bind to a KCNQ containing  
CC potassium channel and modulate ion flux through the channel. The KCNQ  
CC polypeptide is useful for identifying a compound that increases or  
CC decreases ion flux through a potassium channel expressed in an eukaryotic  
CC host cell or cell membrane. The compound (and the KCNQ nucleic acid when  
CC used in gene therapy) is useful as a pharmaceutical agent for treating  
CC diseases involving abnormal ion flux, such as disorders of the central  
CC nervous system, such as epilepsy, migraines, hearing and vision problems,  
CC psychotic disorders, seizures, learning and memory disorders, stroke and  
CC pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a  
CC human tissue and the use of a nucleotide sequence of KCNQ5 to search  
CC computer databases to find variants of the sequence which are associated  
CC with disease states, is useful for screening mutations of KCNQ5. The  
CC present sequence is a splice variant of hKCNQ5 encoding hKCNQ5-2  
XX  
SQ Sequence 2667 BP; 701 A; 667 C; 660 G; 639 T; 0 U; 0 Other;  
  
Query Match 85.5%; Score 2626.4; DB 4; Length 2667;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 2664; Conservative 1; Mismatches 2; Indels 27; Gaps 1;  
  
QY 10 ATGAAGGATGTGGAGTCGGCGCGGGCAGGGTGTGCTGAACTCGGACGCCGCGAGGGGC 69  
DB 1 ATGAAGGATGTGGAGTCGGCGCGGGCAGGGTGTGCTGAACTCGGACGCCGCGAGGGGC 60  
  
QY 70 GACGCGCTGTACTGTCTGGGACCCCGCGCCACCGTGTGTGCGCGCGGGTGGCGCTG 129  
DB 61 GACGCGCTGTACTGTCTGGGACCCCGCGCCACCGTGTGTGCGCGCGGGTGGCGCTG 120  
  
QY 130 AGGGAGACCCCGCGGGCAAGCAGGGGGCCCGGATGAGCTGTGGGGAACCCGCTCTCT 189  
DB 121 AGGGAGACCCCGCGGGCAAGCAGGGGGCCCGGATGAGCTGTGGGGAACCCGCTCTCT 180  
  
QY 190 TACACGAGTACGACGAGTGTGGCGGCAACGTCAGTACCGCGGGTGCAGAACTACCTG 249  
DB 181 TACACGAGTACGACGAGTGTGGCGGCAACGTCAGTACCGCGGGTGCAGAACTACCTG 240  
  
QY 250 TACAACTGTGTGGAGAGACCCCGGGCTGGCGGTTTCATCTACCAAGCTTTCGTTTTCTC 309  
DB 241 TACAACTGTGTGGAGAGACCCCGGGCTGGCGGTTTCATCTACCAAGCTTTCGTTTTCTC 300  
  
QY 310 CTGTCTTTGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 369  
DB 301 CTGTCTTTGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 360

370 GCCTCAAGTTGCCTCTTTGATCTCTGGAGTTCTGATGATGTTCTGTTTGGTTTGGATTC 429  
361 GCCTCAAGTTGCCTCTTTGATCTCTGGAGTTCTGATGATGTTCTGTTTGGTTTGGATTC 420  
430 ATCAATCGAATCTGGTCTGGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAGACTG 489  
421 ATCAATCGAATCTGGTCTGGGGTTGCTGTTGTCGATATAGAGGATGGCAAGGAGACTG 480  
490 AGGTTTGTCTGAAAGCCCTTCTGTTATAGATACCATTTCTTATCGCTTCAATAGCA 549  
481 AGGTTTGTCTGAAAGCCCTTCTGTTATAGATACCATTTCTTATCGCTTCAATAGCA 540  
550 GTTGTCTTCTGCAAAAACCTCAGGGTAAATATTTTGGCCACGCTCTGCACCTCAGAAGTCTCCGT 609  
541 GTTGTCTTCTGCAAAAACCTCAGGGTAAATATTTTGGCCACGCTCTGCACCTCAGAAGTCTCCGT 600  
610 TTCTTACAGATCTCTCGCATGGTGGCATGAGCGAAGGGGAGGACCTTGGAAATTAATCTG 669  
601 TTCTTACAGATCTCTCGCATGGTGGCATGAGCGAAGGGGAGGACCTTGGAAATTAATCTG 660  
670 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTGG 729  
661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTGG 720  
730 GTTCTTATTTTTCGTTCTTCTTCTATCTGTTGGAAGGATGCCAATAAAGAGTTT 789  
721 GTTCTTATTTTTCGTTCTTCTTCTATCTGTTGGAAGGATGCCAATAAAGAGTTT 780  
790 TCTACATATGAGATGCTCTCTGGTGGGGCACAATTAATTAATTAATTAATTAATTAATTAATTA 849  
781 TCTACATATGAGATGCTCTCTGGTGGGGCACAATTAATTAATTAATTAATTAATTAATTAATTA 840  
850 GACAAAATCCCTAACTCTGCTGGGGAAGATGCTTCTGAGGCTTTCACCTCTCTTGGC 909  
841 GACAAAATCCCTAACTCTGCTGGGGAAGATGCTTCTGAGGCTTTCACCTCTCTTGGC 900  
910 ATTTCTTTTCTTTCGCTTCTGCTGGGCAATTTTGGCTCAGTTTTCATTTAAAGTACAA 969  
901 ATTTCTTTTCTTTCGCTTCTGCTGGGCAATTTTGGCTCAGTTTTCATTTAAAGTACAA 960  
970 GAACACACGCCGAGAAACACTTTGAGAAAGGAGGACCCAGCTGCAACCTCATTCAG 1029  
961 GAACACACGCCGAGAAACACTTTGAGAAAGGAGGACCCAGCTGCAACCTCATTCAG 1020  
1030 TGTGTTTGGGTAGTTTACGCGAGCTGATGAGAAATCTGTTTCCATTGCAACTGGAAGCCA 1089  
1021 TGTGTTTGGGTAGTTTACGCGAGCTGATGAGAAATCTGTTTCCATTGCAACTGGAAGCCA 1080  
1090 CACTTGAAGGCTTTGCAACACTGCGAGCCCTTACCAAGAAAGAACCAAGGGGAGCATCAAGC 1149  
1081 CACTTGAAGGCTTTGCAACACTGCGAGCCCTTACCAAGGCTTACCAAGGCTTACCAAGGCTT 1115  
1150 AGTCAGAAAGCTTAAAGTTTAAAGGAGCGAGTGGCATGCTAGCCCGGAGGCGAGTATTT 1209  
1116 --TCAGAAAGCTTAAAGTTTAAAGGAGCGAGTGGCATGCTAGCCCGGAGGCGAGTATTT 1173  
1210 AAGAGCGGACAAAGCTCAGTAGGTGACAGGAGTTCCTCAAGCAGCCGACATCACAGCCGAG 1269  
1174 AAGAGCGGACAAAGCTCAGTAGGTGACAGGAGTTCCTCAAGCAGCCGACATCACAGCCGAG 1233  
1270 GGCAGTCCCAACCAAGTGCAGAAAGCTGAGCTTCAACGACCGAAACCCGCTTCCGCGCC 1329  
1234 GGCAGTCCCAACCAAGTGCAGAAAGCTGAGCTTCAACGACCGAAACCCGCTTCCGCGCC 1293  
1330 TCGTGGCGCTCAAAAGTCTCAGCCAAACCAAGTATAGTCTGATGCTGACAGCCCTTGGC 1389  
1294 TCGTGGCGCTCAAAAGTCTCAGCCAAACCAAGTATAGTCTGATGCTGACAGCCCTTGGC 1353  
1390 ACTGATGATGATATGATGAAAGGATGCCAGTGTGATGATGATGATGATGATGATGATGATGATG 1449  
1354 ACTGATGATGATATGATGAAAGGATGCCAGTGTGATGATGATGATGATGATGATGATGATGATG 1413

1450 CCACACCTTAAACCTGCTCATTGCGACTATCAGATTATGAATTTTCATGTTGCAAAACGG 1509  
Db 1414 CCACACCTTAAACCTGCTCATTGCGAGCTATCAGAAATTTATGAATTTTCATGTTGCAAAACGG 1473  
Qy 1510 AAGTTTAAAGGAAACCTTACGTCCTATATGATGTAAAGATGTCAATTGAACAATATTCGTCT 1569  
Db 1474 AAGTTTAAAGGAAACCTTACGTCCTATATGATGTAAAGATGTCAATTGAACAATATTCGTCT 1533  
Qy 1570 GGTCAATCTGGAATGTTGTTGTAGAAATTTAAAGCCCTTCAAAACGCTGTTGATCAAAATCTT 1629  
Db 1534 GGTCAATCTGGAATGTTGTTGTAGAAATTTAAAGCCCTTCAAAACGCTGTTGATCAAAATCTT 1593  
Qy 1630 GGAAGAAGGCAAAATCACATCAGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1689  
Db 1594 GGAAGAAGGCAAAATCACATCAGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1653  
Qy 1690 ACCACAGACGATCTCAGTATGCTCGGTGCGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1749  
Db 1654 ACCACAGACGATCTCAGTATGCTCGGTGCGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1713  
Qy 1750 ATAGAAATCCAAAGCTGGACTGCTACTAGACATCTATCAACAGGTCCTTCGGAAGGCTCT 1809  
Db 1714 ATAGAGTCCAAAGCTGGACTGCTACTAGACATCTATCAACAGGTCCTTCGGAAGGCTCT 1773  
Qy 1810 GCCTCAGCCCTCGCTTGGCTTCATTCAGTTCCTCCACCTTTTGAATGTGAACAGACATCT 1869  
Db 1774 GCCTCAGCCCTCGCTTGGCTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT 1833  
Qy 1870 GACTATCAAAAGCCCTGTGGATAGCAAAAGATCTTTGCGGTTCCGACAAACAGTGGCTGC 1929  
Db 1834 GACTATCAAAAGCCCTGTGGATAGCAAAAGATCTTTGCGGTTCCGACAAACAGTGGCTGC 1893  
Qy 1930 TTATCCAGATCAACTAGTGCCAAACATCTCGAGAGCCCTGCAAGTTCATTTCAACGCCAAAT 1989  
Db 1894 TTATCCAGATCAACTAGTGCCAAACATCTCGAGAGCCCTGCAAGTTCATTTCAACGCCAAAT 1953  
Qy 1990 GAGTTCAGTCCCGAGACTTTCTACGCGTTAGCCCTACTATGCAAGTCAAGTCAAGCAACAG 2049  
Db 1954 GAGTTCAGTCCCGAGACTTTCTACGCGTTAGCCCTACTATGCAAGTCAAGTCAAGCAACAG 2013  
Qy 2050 GTGCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGCAGCACCAACACCATTTGCAAAACCAA 2109  
Db 2014 GTGCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGCAGCACCAACACCATTTGCAAAACCAA 2073  
Qy 2110 ATAAATACGGCAACCAAGCCAGCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA 2169  
Db 2074 ATAAATACGGCAACCAAGCCAGCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA 2133  
Qy 2170 GCCATCAGCATCTGCCAGGCCAGAACTCTGACCCCTAACCCCTGCAAGGCTTACAGGAA 2229  
Db 2134 GCCATCAGCATCTGCCAGGCCAGAACTCTGACCCCTAACCCCTGCAAGGCTTACAGGAA 2193  
Qy 2230 AGCATTTCTGACGTCACCACTGCTCTGCTGCTCCTCAAGGAAATGTTTCAGGTTGCACAG 2289  
Db 2194 AGCATTTCTGACGTCACCACTGCTCTGCTGCTCCTCAAGGAAATGTTTCAGGTTGCACAG 2253  
Qy 2290 TCAATCTCAACAAGACCGTTCTATAGGAAAAAGCTTTTGAATGGAGGAGAACTCTG 2349  
Db 2254 TCAATCTCAACAAGACCGTTCTATAGGAAAAAGCTTTTGAATGGAGGAGAACTCTG 2313  
Qy 2350 TTGCTGCTCTCCCATGTCGCGAGGACATTTGGCAAACTTTTGTCTGTGTCGCAAAACCTG 2409  
Db 2314 TTGCTGCTCTGTCCTCATGTCGCGAGGACATTTGGCAAACTTTTGTCTGTGTCGCAAAACCTG 2373  
Qy 2410 ATCAGGTCCGACCGAGGAACTGAATATCAAACTTTTCAGGAGTGAAGTGGCTCCAGA 2469  
Db 2374 ATCAGGTCCGACCGAGGAACTGAATATCAAACTTTTCAGGAGTGAAGTGGCTCCAGA 2433  
Qy 2470 GGCAGCCAAAGATTTTACCCCAATGGAGGAAATCCAAATTTTATTAATCTGATGAAGAG 2529  
Db 2434 GGCAGCCAAAGATTTTACCCCAATGGAGGAAATCCAAATTTTATTAATCTGATGAAGAG 2493  
Qy 2530 GTGGGTCCCGAAGAGACAGACAGACACTTTTGTGTCGCGCACCGCAGCCTGCCAGGAA 2589

Db 2494 GTGGGTCCCGAAGAGACAGACAGACACTTTTGTGTCGCGCACCGCCTGCCAGGGAA 2553  
Qy 2590 GCTGCCCTTTGCATCAGACTCTCTTAAGGACTGGAAGGTACAGATCATCTCAGAGCATTTGT 2649  
Db 2554 GCTGCCCTTTGCATCAGACTCTCTTAAGGACTGGAAGGTACAGATCATCTCAGAGCATTTGT 2613  
Qy 2650 AAGCAGAGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAATAA 2703  
Db 2614 AAGCAGAGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAATAA 2667

RESULT 11  
AAC64370  
ID AAC64370 standard; DNA; 125910 BP.  
XX AAC64370;  
AC AAC64370;  
XX  
DT 07-FEB-2001 (first entry)  
XX  
XX Human KCNQ5 (KCN6q) gene sequence SEQ ID NO:1.  
XX Human; KCNQ5; KCN6q; chromosome 6; voltage-gated potassium channel;  
KW Stargardt-like macular dystrophy; cone-rod macular dystrophy;  
KW Salla disease; ophthalmological; auditory; central nervous system;  
KW cardioactive; anticonvulsant; gastrointestinal; muscular active;  
KW age-related macular degeneration; macular degeneration; deafness;  
KW epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;  
XX gastrointestinal disorder; ds.  
XX Homo sapiens.  
XX  
XX WO200061606-A1.  
XX  
XX 19-OCT-2000.  
XX  
XX 10-APR-2000; 2000WO-US009587.  
XX  
XX 14-APR-1999; 99US-0129274P.  
XX  
XX (MERI ) MERCK & CO INC.  
XX  
XX Petrukhin K, Caskey CT, Li W, Metzker ML;  
XX  
XX WPI; 2000-647417/62.  
XX  
XX P-PSDB; AAB24241.  
XX  
XX Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying  
XX inhibitors and activators which can treat e.g. Stargardt-like macular  
XX dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy.  
XX  
XX Claim 3; Fig 1; 99pp; English.  
XX  
XX The present sequence represents the human KCNQ5 (also called KCN6q) gene,  
XX which encodes a voltage-gated potassium channel protein. Human KCNQ5 has  
XX ophthalmological, auditory, central nervous system (CNS), cardioactive,  
XX anticonvulsant, gastrointestinal and muscular active activities.  
XX Sequences and methods from the present invention are useful for  
XX identifying activators or inhibitors of KCNQ5 protein. These activators  
XX and inhibitors are useful for treating Stargardt-like macular dystrophy,  
XX cone-rod dystrophy, Salla disease, age-related macular degeneration,  
XX other forms of macular degeneration, deafness, epilepsy, and different  
XX forms of neuropsychiatric, heart, gastrointestinal, and muscle disorders.  
XX Stargardt-like macular dystrophy and cone-rod dystrophies are located at  
XX chromosome 6q  
XX  
XX Sequence 125910 BP; 40132 A; 24180 C; 23166 G; 38360 T; 0 U; 72 Other;

Query Match 42.8%; Score 1313.4; DB 3; Length 125910;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1314; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1739 AGGTACAGTCCATAGATCCAGTGGACTGCTACTAGACATCTATCAACAGGCTCTTC 1798

123624 AGGTACAGTCCATAGAAATCCAAAGCTGGACCTGCTACTAGACATCATCAACAGGTCCTTC 123683  
1799 GGAAGGCTCTGCTCAGCCCTCGTCTGGCTTCATTCAGTCCGACCTTTGAAATGTG 1858  
123684 GGAAGGCTCTGCTCAGCCCTCGTCTGGCTTCATTCAGATCCACCTTTGAAATGTG 123743  
1859 AACGACATCTGACTATCAAGACCCCTGGATAGCAAGATCTTTCCGGTTCCGACAAA 1918  
123744 AACGACATCTGACTATCAAGACCCCTGGATAGCAAGATCTTTCCGGTTCCGACAAA 123803  
1919 ACAGTGGCTGCTTATCCAGATCAACTAGTGCACATCTCGAGAGGCTCGAGTTCATTC 1978  
123804 ACAGTGGCTGCTTATCCAGATCAACTAGTGCACATCTCGAGAGGCTCGAGTTCATTC 123863  
1979 TGAGCCCAATAGTTCAGTGCACGACTTCTTAGCGCTTAGCGCTACTATGACAGTC 2038  
123864 TGAGCCCAATAGTTCAGTGCACGACTTCTTAGCGCTTAGCGCTACTATGACAGTC 123923  
2039 AAGCAACACAGTGCACATTAAGTCAAGCGATGCTCAGCAGTGCAGCCACCAACACCA 2098  
123924 AAGCAACACAGTGCACATTAAGTCAAGCGATGCTCAGCAGTGCAGCCACCAACACCA 123983  
2099 TTGCAACCAATTAATACGACCCCAAGCCAGCAGCCCAACAACTTTACAGATCCAC 2158  
123984 TTGCAACCAATTAATACGACCCCAAGCCAGCAGCCCAACAACTTTACAGATCCAC 124043  
2159 CTCCTCTCCAGCCATCAAGCATCTGCCAGCCGAGAACTCTGACCCCTAACCTCGAG 2218  
124044 CTCCTCTCCAGCCATCAAGCATCTGCCAGCCGAGAACTCTGACCCCTAACCTCGAG 124103  
2219 GCTTACAGGAAGCAATTTCTGACGTCACACTGCTGTTGCTCCCAAGGAAATGTT 2278  
124104 GCTTACAGGAAGCAATTTCTGACGTCACACTGCTGTTGCTCCCAAGGAAATGTT 124163  
2279 AGTTGCAAGTCAATCTCAACAGGACCGTTCTATGAGGAAAGCTTTGACATGGAG 2338  
124164 AGTTGCAAGTCAATCTCAACAGGACCGTTCTATGAGGAAAGCTTTGACATGGAG 124223  
2339 GAGAACTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2398  
124224 GAGAACTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 124283  
2399 TGCAAACTCTGATCAGTGCAGCCGAGGAACTGAATATACAACTTTTCAGGAGTGAATCAA 2458  
124284 TGCAAACTCTGATCAGTGCAGCCGAGGAACTGAATATACAACTTTTCAGGAGTGAATCAA 124343  
2459 GTGGCTCCAGAGGCAAGCAATTTTACCCCAATGAGGGAATCCAAATTTGTTTATAA 2518  
124344 GTGGCTCCAGAGGCAAGCAATTTTACCCCAATGAGGGAATCCAAATTTGTTTATAA 124403  
2519 CTGATGAGAGTGGTCCGAGAGAGACAGACAGACACTTTTGATGCCGACCGCAGC 2578  
124404 CTGATGAGAGTGGTCCGAGAGAGACAGACAGACACTTTTGATGCCGACCGCAGC 124463  
2579 CTGCCAGGAAGCTGCTTTGATCAGACTCTCTAAGGACTGGAAGTCAAGTCAATCTC 2638  
124464 CTGCCAGGAAGCTGCTTTGATCAGACTCTCTAAGGACTGGAAGTCAAGTCAATCTC 124523  
2639 AGAGCAATTTGAGGAGAGGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGA 2698  
124524 AGAGCAATTTGAGGAGAGGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGA 124583  
2699 AATAAGTCTCTCATTTCTTCCAGGCATAGCAGTCTTTAGCCATACATATCATTCAT 2758  
124584 AATAAGTCTCTCATTTCTTCCAGGCATAGCAGTCTTTAGCCATACATATCATTCAT 124643  
2759 GAACTATTTGAAAGCCCTTCTTAAAGAGTTGAAATTCGAAGATCGGAAGAACATGAAA 2818  
124644 GAACTATTTGAAAGCCCTTCTTAAAGAGTTGAAATTCGAAGATCGGAAGAACATGAAA 124703  
2819 GCGAGTTTATAGCCCGTTACCTTTTAATGATGAAATGATGTTAGGATGCTTAA 2878

Db 124704 GCAGGTTTAAAGCCCGTTACCTTTTAATGCAAGAAATGCAATGTTAGGGATGGCTAA 124763  
Qy 2879 AATTCAAGGTGATCGACATTAACCCACTCATTTAGTAAATGATGTTAGTTTAAAGC 2938  
Db 124764 AATTCAAGGTGATCGACATTAACCCACTCATTTAGTAAATGATGTTAGTTTAAAGC 124823  
Qy 2939 CTGAGAAACCAACACAGCTTAATGCTATGGGTGATGAATATGTCAGGTTTAAAGTCATT 2998  
Db 124824 CTGAGAAACCAACACAGCTTAATGCTATGGGTGATGAATATGTCAGGTTTAAAGTCATT 124883  
Qy 2999 TAGAAGATTGACACTGTTATTTGAATATGAGGATTAACACCTTCAAAATTTCA 3053  
Db 124884 TAGAAGATTGACACTGTTATTTGAATATGAGGATTAACACCTTCAAAATTTCA 124938

RESULT 12  
AAA47618  
ID AAA47618 standard; cDNA; 2335 BP.  
XX  
AC AAA47618;  
XX  
08-NOV-2000 (first entry)  
XX  
KCNQ4 Potassium channel gene.  
XX  
DE  
XX  
KW KCNQ4; potassium channel; cardiac arrhythmia; neonatal epilepsy;  
KW deafness; probes; treatment; therapy; transgenic animal; antibody;  
KW agonist; antagonist; tinnitus; hearing loss; neonatal deafness;  
KW presbycusis; affective disorder; Alzheimer's disease; anxiety; ataxia;  
KW cognitive deficits; compulsive behavior; dementia; depression;  
KW Huntington's disease; mania; memory impairment; motor disorders;  
KW neurodegenerative disease; Parkinson's disease; Pick's disease;  
KW psychosis; schizophrenia; spinal cord damage; stroke; tremor; ds.  
XX  
OS Homo sapiens.  
XX  
Key Location/Qualifiers  
CDS 83..2170  
FT /\*tag= a  
FT /product= "KCNQ4 Potassium channel polypeptide"  
XX  
FN WO200044786-A1.  
XX  
PD 03-AUG-2000.  
XX  
PF 19-JAN-2000; 2000WO-DK000024.  
XX  
PR 26-JAN-1999; 99DK-00000076.  
PR 19-MAY-1999; 99DK-00000893.  
XX  
PA (NEUR-) NEUROSEARCH AS.  
XX  
PI Jentsch TJ;  
XX  
XX WPI; 2000-548813/50.  
DR P-PSDB; AAB01476.  
XX  
PT Nucleic acids encoding the novel KCNQ4 potassium channel subunit, useful  
PT e.g. for treating tinnitus, deafness, Alzheimer's and Parkinson's  
XX diseases.  
XX  
PS Claim 1; Page 43-48; 65pp; English.  
XX  
CC Mutations in 3 known genes of the KCNQ branch of the potassium channel  
CC gene family underlie inherited cardiac arrhythmia's, neonatal epilepsy  
CC and in some cases associated with deafness. KCNQ4 has been mapped to the  
CC DFNA2 locus for autosomal dominant hearing loss, and a dominant negative  
CC KCNQ4 mutation that causes deafness in a DFNA2 pedigree has been  
CC identified. KCNQ4 is the first potassium channel gene underlying non-  
CC syndromic deafness. KCNQ4 forms heteromeric channels with other KCNQ  
CC channel subunits, especially KCNQ3. Nucleotides encoding the KCNQ4  
CC protein and the protein itself may be used in the prevention, treatment  
CC and diagnosis of diseases associated with inappropriate KCNQ4 expression.







```
QY 946 TCAGGTTTTCATTAAGTACAGAACACACCGCCAGAAACACTTTGAGAAAGAGG 1005
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1040 TCCGGCTTTGGCTTCAAGGTCAGAGCAGACCGGCGAAGACATCTCGAAGCGGAG 1099
QY 1006 AACCCAGCTGCCAACCCTCATTCAGTGTCTTTGGGGTAGTTACGAGCTGTAGAGAAATCT 1065
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1100 ATGCGGCGAGCAACCTCATTCAGGCTGCCTGGGCGCTGTACTCACCGATATAGCCGG 1159
QY 1066 GTTTCATTGCAACCTGGAAGCCACATTTGAAGGCTTTGCACACCTGCGAGC- 1116
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1160 GCCTACCTGACAGCCACCTGTGTACTATGACAGTATCCTCCCATCTTCAGAGAGCTG 1219
QY 1117 CCTACCAAGAAGACACAGGGGAGCATCAAGCAGTCAAGAGCTA- 1161
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1220 GCCCTCTTTGTTGAGCACGTCAACCGGCGCCGCAATGGGGGCTTACGGCCCTCGAGGTG 1279
QY 1162 ----- 1161
DB
1280 CGGCGGCGCGGTACCCGACGGAGCACCTTCCGTTACCCGCGGTTGCCACCTGCCAC 1339
QY 1162 -----AGTTTAAAGAGCGA 1176
DB
1340 CGGCGGCGCAGCACCTCTCTGCTCCTGGGGAAGCAGCCGGATGGGCATCAAGAGACGC 1399
QY 1177 GTGCGCATGGCTAGCCCGAGGGCCAGA-----GTATTAGAGCGCAGACCTCAGTA 1230
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1400 ATCCGCATGGCAGCATCCCGAGCGGCGAGCGGTCTTCCAAAGCAGCAGCTGGCACCTCCA 1459
QY 1231 GGTGACAGAGGTCCCAAGCAGCAGCATCACAGCCGAGG--GCAGTCCCAACAAAGTG 1287
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1460 AATATGCCACTTCCCAAGCAGCAGCAGGTGGTGAGGCCACAGCCCGCCACCAAGGTG 1519
QY 1288 CAGAAGAGCTGGAGCTTCAACAGCCGAAACCGCTTCCGGCCCTCGCTGCGCTCAAAAGT 1347
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1520 CAAAAGAGCTGGAGCTTCAATGACCGCACCCGCTTCCGGGCTCTCTGAGACTC----- 1573
QY 1348 TCTAGCCAAACACAGTATAGATCTGACACAGCCCTTGGCACTGATGTATATGAT 1407
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1574 -----AAACCCCGCACCTCTGCTGAGGATGCC---CCTCAGAGGAAGTAGCAGAG 1621
QY 1408 GAAAGAGTGCAGTGTGATGATATCAGTGGAGACCTCACCCACCACTTTAAACCTGTC 1467
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1622 GAGAAGACTACAGTGTGAGCTACGCTGAGCAGCATCATGCTGCTGTGAGACAGTGC 1681
QY 1468 ATTGAGCTATCAGAAATATGAATTTTCATGTTGCAAAACGGAAAGTTTAAAGAAACRTTA 1527
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1682 ATCCGCTCCATCAGGATTTCTCAAGTTCCTGTGGCCAAAGGAAATTCAGAGGACACTG 1741
QY 1528 CGTCCATATGATGTAAGAGATGTCAATGAACAATATCTGCTGTGCTATCTGGACATGTTG 1587
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1742 CGACCGTACGACGTGAAGGAGCTATTGAGCAGTACTCAGCAGGCGCCTGGACATGCTG 1801
QY 1588 TGTAGATTAAAGGCTTTCAACACAGTGTGATCAAAATTTCTTGGAAAGGGGC---AAATC 1644
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1802 GGCCGGATCAGAGCTCGCAACTCGGTGGACCAATTTGGTTCGGGGGCCCGGGGAC 1861
QY 1645 ACATCAGATATAGAGCGGAGAGAAATATACAGCAGAACATATGACACACAGCATCTC 1704
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1862 AGGAAGCGCCGGAGAGGGGACAAAGGGGCCCTCCGACGGGAGTGGTGGATGMAATC 1921
QY 1705 AGTATGCTCGGTGGGTGTCAGGTTGAAAGACAGTACAGTCCATAGATCCAGCTG 1764
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1922 AGCATGATGGGACCGGTGTCAGGTGGAGAAGCAGGTGCGATTCATCGACACCAAGCTG 1981
QY 1765 GACTGCTTACTAGACATCTATCAACAGGTCTCTTGGAAAGGCTCTGCTCAGCCCTCGCT 1824
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1982 GACCTGCTGTTGGGTTCTATTCGGCTGCTGCTG-----GCTTGGGACCTCGGCCAGC 2035
QY 1825 TTGGCTTCATTCCAGTTCCTCCACCTTTTGAATGTGAACAGACATCTGACTATCAAGCCCT 1884
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2036 CTGGGCGCGTGCAAGTGCCTGTTTCGACCCCGACATCACTCCGACTACACAGCCCT 2095
QY 1895 GTGGATAGCAAGATCTTTTCGGGTTCCCGCAAAA 1918
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DB 2096 GTGGACCACGAGGACATCTCGTCTCCGCACAGA 2129
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
RESULT 14
AAX57140
ID AAX57140 standard; DNA; 2273 BP.
XX AAX57140;
AC AC
XX 22-JUL-1999 (first entry)
DT XX
DE Mouse KCNQ2 cDNA.
XX KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;
KW benign familial neonatal epilepsy; BFNE; juvenile myotonic epilepsy; JME;
KW rolandic epilepsy; mutant; treatment; screening; epilepsy; detection;
KW gene therapy; drug screening; ss.
XX Mus musculus.
OS
FH Key Location/Qualifiers
FT CDS 1..2273
FT a
FT /product= "KCNQ2"
FT /note= "Partial sequence, no stop codon given"
XX
FN W09921875-A1.
XX
PD 06-MAY-1999.
XX
PF 23-OCT-1998; 98WO-US022375.
XX
PR 24-OCT-1997; 97US-0063147P.
XX
PA (UTAH ) UNIV UTAH RES FOUND.
XX
PI Singh NA, Leppert MF, Charlier C;
DR WPI; 1999-312938/26.
XX P-PSDB; AAY08345.
XX
PT Nucleic acid encoding potassium channels KCNQ2 and 3.
XX
PS Claim 1; Page 153-156; 195pp; English.
XX
CC This invention describes novel human and mouse potassium channel proteins
CC KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or
CC KCNQ3, or the loss of one copy of these genes, is used for diagnosis and
CC prognosis of benign familial neonatal epilepsy (BFNE), juvenile myotonic
CC epilepsy (JME) or rolandic epilepsy (RE). Cells (or transgenic animals)
CC that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves
CC in cell-free form) are used to screen for agents that can be used to
CC treat or prevent these forms of epilepsy. Fragments of the encoding
CC nucleic acids are used as probes or primers, either for detecting
CC mutations or for isolation of related sequences, while the complete
CC sequences may be used in gene therapy to provide wild-type protein.
CC Antibodies specific for mutant or wild-type proteins are used as
CC diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins are
CC useful in rational design of drugs and therapeutically (in replacement
CC therapies). The forms of epilepsy associated with mutations in KCNQ2 and
CC 3 sequences can now be diagnosed early (before symptoms are manifest),
CC and better treatment options will be available
XX
SQ Sequence 2273 BP; 486 A; 670 C; 653 G; 448 T; 0 U; 16 Other;
Query Match 16.9%; Score 517.6; DB 2; Length 2273;
Best Local Similarity 57.7%; Pred. No. 4.7e-134;
Matches 1031; Conservative 2; Mismatches 683; Indels 72; Gaps 4;
QY 73 GGCTGCTACTGCTGGGACACCGCGGCCACGCTTGGTGGCGCGGTGGCTGAGG 132
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 67 GGCTTCGTGGGCTGGGACCCCGCGCGCCGANTCCACACGCGGCGNCTACTCATC 126
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133 GAGAGCGCGGCGCAAGCAGGCGCGCGGATGAGCTGTGGGAAGCGCTCTTAC 192  
127 GCGGGCTCCGAGGCGCCCAAGCGCGGCGGAGGAGCGCGGAGCGCGGCGGCG 186  
193 ACGAGTAGCAGAGCTGCGCGCGCAAGCTCAAGTACCGGGGGGTGAGAACTACCTGTAC 252  
187 GGANCCGGGAAGCCCCNANCGCAAGCGCTTCTACCGCAAGCTGAGAAATTCCTCTAC 246  
253 AACGTGCTGGAGAGACCCCGCGGTGGCGGCTTCACTACCAAGCTTTCGTTTTCTCCTT 312  
247 AACGTGCTAGAGCGCGCGCGGCTGCGGCTTCACTACCAAGCTTTCGTTTTCTCCTT 306  
313 GTCTTTGGTTCGTTGATTTGCTGAGTGTCTTACCATCCTGTAGCAGACAAATTTGGCC 372  
307 GTTTTCTCCTGCTGCTTCTGTTTCTTCCACCATCAAGGAGTACGAGAGAGCTCT 366  
373 TCAAGTTGCCCTTCTGATCCTCGAGTTCGTGATGATGTCGTTCTTTGGTGGATTCATC 432  
367 GAGGGGCGCTCTACATCTTGGAAATCGTGACTATCGTGATTCGTTGAGTACTTT 426  
433 ATTCGAATCTGGTCTGCGGGTGTCTGTTGTCGATATAGAGATGCGAAGAGACTGAGG 492  
427 GTGAGGATCTGGGCTGAGGCTGCTGTTGCGGCTATCGAGGCTGGAGGCGGAGCTCAAG 486  
493 TTTGCTCGAAGCCCTTCTGTTGTTATAGATACCATGTTCTTATCGCTTCAATAGCAGTT 552  
487 TTTGCGAAGAGCGGCTCTGTTGATGATATCAATGTTGCTGATGCTCAATGCTGTG 546  
553 GTTCTGCAAAAACCTCAGGGTAATATTTTTCACAGCTGTGCACTCAGAACTCTCGTTTC 612  
547 CTGGCTGCTGTTCCAGGCAATGTTCTTTGCCACATCTGCGCTTCGAGCTTCGCGTTC 606  
613 CTAAGATCTCCGATGCTGCGATGCAACCGAAGGGGAGGCACTTGGAAATTTACTGGT 672  
607 TTGCAAAATCTTGGGATGATCCGATGACCGAGGGGTGACCTGGAAGCTCTTGGA 666  
673 TCAGTGGTTTATGCTCAGCAAGAAATTAATCAGAGCTTGGTACATAGGATTTTGGTT 732  
667 TCGTAGTCTAGCTCAGCAAGAGGCTGGTACTGCTGCTACATTTGGCTTCTCTGC 726  
733 CTTATTTTTCGTTCTTCTGCTGTATCTGGTGGAAAGAGTGCACATTAAGAGTTTCT 792  
727 CTATCTCTGGCTCATTTCTGGTGTACTTGGCAGAAAAGGGTGAATGACCACCTTGAC 786  
793 ACATATGAGATGCTCTCTGGTGGGCGCAATTAATTGACAACTATTGGCTATGGAGAC 852  
787 ACCTACGAGATGCACTCTGGTGGGCTGTGATCCTTGACCACTTTGGCTACGGGAC 846  
853 AAAAATCCCTTAACCTTGGCTGGGAAGATTGCTTTCTGCAAGGCTTTGCACTCTTGGCAT 912  
847 AAGTACCTCAGACCTGGAAACGGAGGCTGCTGGCAGCGACCTTTACCTCATTTGGTGC 906  
913 TCTTTCTTGGATCTTCTCGCGGATCTTGGCTCAGGTTTGGATTAAGAGTACAGAA 972  
907 TCGTTCTTGGCTTCTCGGCTGGCATTTTGGATCCGCTTTGGCTGAAAGTCAAGAG 966  
973 CAACACCGCGAGAAACATTTTCAGAAAAGAGAAACCGAGTCCCACTCATTCAGTGT 1032  
967 CAGATCGGCAAAACATTTTGAAGAACCGCGGAACCTTGGCGAGTCTGATCCAGTCT 1026  
1033 GTTTGGCGTGTACGAGCTGAT----- 1056  
1027 GCTTGAGATTTCTATGCTACTAATCCTCTCAGCAGCGACCTGCACTCCACGTGGAGTAC 1086  
1057 ----GAGAAATCTGTTTCCATTGCAACCTGGAGCCACACTTGAAGGCTTGGCACCTGC 1113  
1087 TAGAGCGNACAGTCACTGCTCCCCATGTACAGCTCAAACTCAAACTATGGGCGCTCC 1146  
1114 AG-----CCTTACCAAGAAAGAACAGGGGAGAGCATCAAGAGTCAAGAGCTTAAGTTTA 1168  
1147 AGACTCATCCACCTCTGAACAGGCTGGAGCTGCTGAGGAATCTCAAGAGCAAACTGGA 1206

1169 AGGAGCGAGTGGCGCATGTAGTCCCGAGGGGCGCAGAGTATTAGAGCCGCAAGCCTCAG 1228  
1207 CTCACCTTCAGGAGGAGCCACAGCCAGAGCCATCACCAAGCCCGGAGCATGGTGC 1266  
1229 TAGGTGACAGGAGTTCCTCCCAAGCACCGACATCACAGC----- 1265  
1267 AAGGGAAGAGGGGTCTCCCGAGGCCAGACGGTCCGCGGTCCCGAGTCCGAGTCAAGAT 1326  
1266 --CGAGGCGAGTCCCAACCAAGTGCAGAGAGCTGAGCTTCAACGACCGAACCCGCTTC 1323  
1327 CTTGATGACAGCCCGAGCAAGGTGCCAAGAGCTGGAGTTCGGTACCGCAGCCGACAC 1386  
1324 CGGCCCTCGCTGCGCTCAAAAGTCTCAGCCAAACCAAGTATGATGCTGACACAGCC 1383  
1387 CGCAGGCTTTCGCGCATCAAGGGTCTGCATCCCGGCAGAACTCAGAAGAAGCAAGCCTC 1446  
1384 CTTGGCAGCTGATGATGATATGATGAAAAGAGTGCAGTGTGATGATATCAGTGGAGAC 1443  
1447 CTTGGGGAGGACATCGTAGAGGCAACAGAGCTGTAACCTGCGAGTTTGTGACTGAAGAT 1506  
1444 CTCACCCCAACCACTTAAACTGTCTTCGAGCTATCAGAAATATGAAATTTTCATGTTGCA 1503  
1507 CTTACCCCTGGCTCAAGTYAGCATCAGACCGTGTGTGTATGCGTTCTTTGATCT 1566  
1504 AAACGGAAGTTTAAAGAACTTTACGTTCATATGATGATAAAGATGTCATTGAACTAT 1563  
1567 AAGCGAAAGTTTCAAGAGAGTCTGCGCCCATATGATGATGACGTCTATCGAACAGTAC 1626  
1564 TCTGCTGCTCATCTGCACATGTTGTGTAAGATTTAAAGCCTTCAAAACAGCTTGTATCAA 1623  
1627 TCGGCTGGACACTTGGATATGTTGTCGCAATCAGAGCTGCGAGCAGAGTGGACCAG 1686  
1624 ATTCTTGGAAAAGGGCAAAATCAGATCAGATAAGAGCGCGAGAGAAAATAACAGCAGAA 1683  
1687 ATTGTGGGCGGGGCCCAACAATAACGATTAAGGA---TCGCACCAAGGCCCGCGGAA 1743  
1684 CATGAGACACACAGCATCTCAGTATGCTCGGTCCGGTGTGCTGAGGTTGAAACAGGTA 1743  
1744 ACGGAGTGTCCGGAAGACCCAGCATGATGGGAGCGCTTGGGAGGTGGGAAACAGGTC 1803  
1744 CAGTCCATAGAAATCCAGCTGGAGTGCCTACTAGACATCTATCAACAG 1791  
1804 TTGTCATGAAAAGAGCTCGACTTCTTGGTGGCATCTATACAG 1851

RESULT 15  
AA26588  
ID AA26588 standard; DNA; 2169 BP.  
XX  
AC AA26588;  
XX  
DT (first entry)  
XX  
DE Nucleotide sequence of murine KCNQ2 (formerly known as (KvLR1)).  
XX  
KW KCNQ protein; nervous system-specific potassium channel;  
KW neuronal excitability; neurotransmitter release; KCNQ modulator; ataxia;  
KW myokymia; seizure; Alzheimer's disease; Parkinson's disease;  
KW age-associated memory loss; learning deficiency; motor neuron disease;  
KW epilepsy; stroke; ss.  
XX  
OS Mus sp.  
XX  
FH Key  
FT 1. 2169  
FT CDS /\*tag= a  
XX  
FN WO9907832-A1.  
XX  
PD 18-FEB-1999.  
XX  
PF 26-JUN-1998; 98WO-US013276.  
XX

PR 12-AUG-1997; 97US-0055599P.  
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX  
PI Blar MA, Dworetzky S, Yang W, Levesque PC, Gribkoff VK;  
PI Neubauer MG, Little WA;  
XX  
DR WPI, 1999-190047/16.  
XX P-PSDB; AAY01530.  
XX  
PT New potassium channels, KCNQ2 and KCNQ3 - may be involved in  
PT neurotransmission and neuroprotection, used to treat, e.g. ataxia.  
XX  
PS Claim 7; Fig 10A-D; 64pp; English.  
XX  
CC The present sequence encodes murine KCNQ2/KVLR1. KCNQ proteins are  
CC nervous system-specific potassium channels. In neurons, potassium  
CC channels regulate neuronal excitability, action potential shape and  
CC firing pattern, and neurotransmitter release. KCNQ modulators may be used  
CC to treat disorders such as ataxia, myokymia, seizures, Alzheimer's  
CC disease, Parkinson's disease, age-associated memory loss, learning  
CC deficiencies, motor neuron diseases, epilepsy, and stroke  
XX  
SQ Sequence 2169 BP; 466 A; 622 C; 635 G; 446 T; 0 U; 0 Other;  
Query Match 16.7%; Score 511.6; DB 2; Length 2169;  
Best Local Similarity 58.2%; Pred. NO. 2.2e-132;  
Matches 1044; Conservative 0; Mismatches 669; Indels 81; Gaps 5;  
QY 73 GGCTGCTACTGCTGGGACCCGCGGCCACCGCTTGGTGGCGGGGCTGAGG 132  
DB 67 GCCTTCTGCTGGGCTGGACCCGCGGCCGCGCCGACTCCACACGCGCGCGCTACTCATC 126  
QY 133 GAGAGCCCGCGGGCAAGCAGCGGGGCCGCGATGAGCTGTGGGAAAGCCCTCTCTTAC 192  
DB 127 GCGGCTCCGAGGCCGCCAAGCGGGCAGCGTTTGGACAAAGCCGCGGCGGCG 186  
QY 193 ACGAGTACAGAGCTGCGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 252  
DB 187 GGAGCGGGGAAGCCCGAAGCGCAACCGCTTACCGCAAGCTGCAGATTTCTCTAC 246  
QY 253 AAGTGTCTGGAGAGACCCGCGGCTGGCGCTTCTATCCACGCTTCTGTTTCTCTCT 312  
DB 247 AAGTGTCTGGAGAGACCCGCGGCTGGCGCTTCTATCCACGCTGCTGTTTCTCTT 306  
QY 313 GTCTTGTGCTGATTTGTGAGTGTCTTGTGAGTGTCTTGTGAGTGTCTTGTGAGT 372  
DB 307 GTCTTCTCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 366  
QY 373 TCAAGTTCCTCTGATCTGAGTGTCTGATGATGCTGCTTGTGCTTGTGAGTTCATC 432  
DB 367 GAGGGGCGCTCTACATCTTGGAAATCGTACTATCGTGTGATTTGCTGTTGAGTACTT 426  
QY 433 ATTCAATCTGCTGCGGGTGTGCTGCTGATATAGAGTGCAGAGGAGTCTGAGG 492  
DB 427 GTGAGATCTGGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 486  
QY 493 TTTGCTCGAAAGCCCTCTGCTGTTATAGATACCAATGTTTCTTATCGCTTCAATAGCAGTT 552  
DB 487 TTTGCGAAGAGCGCTTCTGCTGATGATGATGATGATGATGATGATGATGATGATG 546  
QY 553 GTTTCTGAAATCTCAGGGAATATTTTGTGCGAGTCTGCACTCAGAGTCTCGGTTTC 612  
DB 547 CTGGCTGTGTTTCCAGGGAATGCTTCTTGTGCAATCTGCGCTTCCGAGCTTCCG 606  
QY 613 CTACAGATCTCCGATGCTGCGATGACCGAAGGGGAGGACCTTGGAAATTAAGTGGT 672  
DB 607 TTGCAATCTTGGGATGATCGTATGACCGGAGGGGTGGACCTGGAAGCTCTTGGGA 666  
QY 673 TCAGTGTGTTTGTCTCACAGCAAGGAATTAATCAAGCTTGTGATCATAGGATTTTGGTT 732  
DB 667 TCGGTAGTCTACGCTCACAGCAAGGAGCTGGTGTGCTGCTGCTGCTGCTGCTGCTG 726

QY 733 CTTATTTTTCCTTCTCTATCTGCTGGAAGGATGCCAATAAAGAGTTTCT 792  
DB 727 CTCATCTGCGCTCAITTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 786  
QY 793 ACATATGCAGATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 852  
DB 787 ACCTACGAGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 846  
QY 853 AAAAATCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 912  
DB 847 AAGTACCTCAGACCTGGAACCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 906  
QY 913 TCTTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 972  
DB 907 TCGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 966  
QY 973 CAACACCGCAGAACTTTGAGAAAAGAGAACCCAGCTGCGCAACCTCATTTCACTGCTGCT 1032  
DB 967 CAGCATCGGCAAAACACTTTGAGAAACCGGCGAACCTTGGCGAGGCTCTGATCCAGTCT 1026  
QY 1033 GTTTGGCTAGTTACGAGCTGATGAGAAAT----- 1063  
DB 1027 GCCTGGAGATCTATGCTACTTAACCTCTCAGCACCGACCTGCTCCTCAGCTGGCAGTAC 1086  
QY 1064 -----CTGTTTCCATTTGCACTTGGAGCCACACTTTGAAGCCCTTGCAC 1107  
DB 1087 TAGAGCGGACAGTCACTGCTGCCCATGTACAGACTCATCCCACTCTGGAACAGCTGAG 1146  
QY 1108 ACCTGCAGCCCTACCAAGA-----AAGAAACAAGGGAA 1140  
DB 1147 CTGCTGAGGATCTCAGAGCAATCTGGACTACCTTCAGGAAGGACCCACAGCCAGAG 1206  
QY 1141 GCATCAAGCAGCTAGAACTAAGTTTAAAGAGCGAG---TGCAGTGGCTAGCCCCAGG 1197  
DB 1207 CCATCAACAAGTCAAGAGGCTGCTTGAAGAGTGTGCTTCTCAGCCCCCGAGGCTG 1266  
QY 1198 GGCAGAGTATTAGAGCCGACAGCCCTCAGTAGGTGACAGAGGTCCTCAGAGCACCCAC 1257  
DB 1267 GCTGCCAAGGAAAGGGGCTCTCCCGCCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 1326  
QY 1258 ATCAGCGCGAGGCGAGTCCCAACAAAGTGCAGAAAGCTGAGCTTCAACGACCGAAC 1317  
DB 1327 CAGAGTCTTATGACAGCCCGAGCAGTGCCTCAGAGCTGAGCTTGTGCTGAGCGCAGC 1386  
QY 1318 CGCTTCCGCGCTCGCTGCGCTCAAAAGTTCTCAGCCAAACCCAGTGATAGTGTGCTGAC 1377  
DB 1387 CGCACAGCGCAGGCTTCCCGCATCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1446  
QY 1378 ACAGCCCTTGCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1437  
DB 1447 C---TCCCTGGGAGGAGATCGTAGAGGACAAAGAGCTGTAACCTGCGAGTTTGTGACT 1503  
QY 1438 GAAGACCTCAACCCACCACTTAAACCTGCTATTGAGCTATCAGAAATTTATGAAATTTTCT 1497  
DB 1504 GAAGATCTTACCTTGGCTTCAAGTTAGCATCAGAGCTGCTGCTGCTGCTGCTGCTGCTG 1563  
QY 1498 GTTGCAAAACGGAAGTTTAAAGAAACRTTACGTCATATGATGATGATGATGATGATGATG 1557  
DB 1564 GTATCTAAGCGAAAGTTTCAAGAGAGTCTGCGCCCATATGATGATGATGATGATGATGATG 1623  
QY 1558 CAATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1617  
DB 1624 CAGTACTCGGCTGAGACCTTGGATATGTTGCTCCGCTATCAAGAGCCTGCGAGCTGCGAG 1683  
QY 1618 GATCAAAATCTTGGAAAGGCGCAATCACTACATCAAGAGAGAGCGGAGAGAAATAACA 1677  
DB 1684 GACCAAGTTTGGGCGGCGGCCCAACAAATACGATTAAGGA---TCGACCAAGGCGCCA 1740  
QY 1678 GCAGAAATGAGACCAAGAGAGATCTCAGTATGCTCGGTGCGGTGCTGAGGTGAGGAA 1737  
DB 1741 GCGGAAACGAGAGTGTCCCGAAGACCCAGCATGATGAGAGCGGCTTGGAGAGGTGAGAAA 1800  
QY 1738 CAGTACAGTCCATAGAAATCCAGCTGAGTCCCTACTAGACATCTATCAACAG 1791

Db 1801 CAGGCTTGTCCATCGAAAGAGCTCGACTTCTTGGTGAGCATCTATACAG 1854

Search completed: April 2, 2005, 23:56:47  
Job time : 1556 secs





Qy 761 SerAenLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780  
Db 2281 TCAATCTCACCAGGACCGTCTTATAGGAGAAAGCTTTGACATGGGAGGAGAACTCTG 2340  
Qy 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800  
Db 2341 TTGCTGTCTGCCCATGGTCCGAGGACCTTGGCAAAATCTTTGTCTGTGCAAAACCTG 2400  
Qy 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 820  
Db 2401 ATCAGGTCGACCGAGGAACTGAATATACAACTTTTCCAGGAGTGAGTCAAGTGGCTCCAGA 2460  
Qy 821 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840  
Db 2461 GCGAGCCCAAGATTTTATCCCCAAATGGAGGAAATCCAAATTTGTATTAACATGATGAAGAG 2520  
Qy 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 860  
Db 2521 GTGGTCCCGAGAGAGACAGACAGACACTTTTGTATGCCGACCCGACGCTGCCAGGGA 2580  
Qy 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 880  
Db 2581 GCTGCTTTGTCATCAGACTCTCTAAGGACTGGAAGGTCAAGATCATCTCAGAGCATTTGT 2640  
Qy 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897  
Db 2641 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCCTCATGTCAAACCTGAAA 2691

## RESULT 2

US-09-813-148-1  
; Sequence 1, Application US/09813148  
; Patent No. 6617131  
; GENERAL INFORMATION:  
; APPLICANT: STEINMEYER, Klaus  
; APPLICANT: LERCHE, Christian  
; APPLICANT: SCHERER, Constanze  
; APPLICANT: SEBOHM, Guiscard  
; APPLICANT: BUSCH, Andreas E.  
; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CEN  
; TITLE OF INVENTION: NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM  
; FILE REFERENCE: 38005-119  
; CURRENT APPLICATION NUMBER: US/09/813,148  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 3074  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-813-148-1

Alignment Scores:  
Pred. No.: 0 Length: 3074  
Score: 4574.00 Matches: 895  
Percent Similarity: 99.78% Conservative: 0  
Best Local Similarity: 99.78% Mismatches: 2  
Query Match: 99.69% Indels: 0  
DB: 4 Gaps: 0

US-09-810-796-4 (1-897) x US-09-813-148-1 (1-3074)

Qy 1 MetLysAspValGluSerGlyArgGlyValLeuLeuAsnSerAlaAlaArgGly 20  
Db 215 ATGAAGGATGTGAGTTCGGGCGGGGAGGGTGTGCTGAACCTGGCAGCGCGGAGG 274  
Qy 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40  
Db 275 GACGCGCTGCTACTGCTGGGACCCCGCGGCGGACGCTTGTGTGGCGGGGCTGGCTG 334

Qy 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60  
Db 335 AGGAGAGACCCCGCGGGCAAGCAGGGGCGCGGATAGCCTGCTGCTGGGAAGCGCCCTCTCT 394  
Qy 61 TyrThrSerSerGlnSerCysArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80  
Db 395 TACACGAGTAGCCAGAGCTGCCGGCGCAACCTCAAGTACCCGGCGGTGCAGAACTACCTG 454  
Qy 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100  
Db 455 TACAACGTGCTGGAGAGACCCCGCGGCTGGGCGTTTCATCTACACGCTTTTCGTTTTCTCT 514  
Qy 101 LeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120  
Db 515 CTTCTCTTTGGTCTTGAATTTTGTCAAGTGTCTTCTACCATCCTCGAGCAGCACAATAATG 574  
Qy 121 AlaSerSerCysLeuLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe 140  
Db 575 GCCTCAAGTTGCCCTCTTGATCCTGGAGTTCTGATGATTGTTCGCTTTTGGTTTGGAGTTC 634  
Qy 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160  
Db 635 ATCATTGCAATCTGCTCTGGGGTTGCTGTTGTGATATAGAGGATGSCAAGGAAGACTG 694  
Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuLeuAlaSerIleAla 180  
Db 695 AGGTTTGTCTCGAAAGCCCTTCTGTGTTATAGATACCATTTGTTCTTATCGCTTCAATAGCA 754  
Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200  
Db 755 GTTGTCTGCAAAACTCAGGGTAATATTTTCCAGCTCTGCACCTCAGAAAGTCTCCGT 814  
Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220  
Db 815 TTCCTACAGATCTCTCCGATGTCGCGATGCGACGAGGAGGAGGACCTTGGAAATTAATCTG 874  
Qy 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaThrTyrIleGlyPheLeu 240  
Db 875 GGTTTCAGTGGTTTATGCTACAGCAAGGAATTAATCAAGCTTGGTATACATAGGATTTTGT 934  
Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260  
Db 935 GTTCTTATTTTTCGTTCTTCTCTGCTGCTGGAAGATTTGCTTTTCGAGGCTTTGCACTCCCTTGGC 1054  
Qy 261 SerThrTyrAlaAspAlaLeuTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280  
Db 995 TCTACATATGAGATGCTCTCTGCTGGGCGCACAAATTACATTGACAACTATTGGCTATGGA 1054  
Qy 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300  
Db 1055 GACAAAACTCCCTTAACCTTGGCTGGGAAGATTTGCTTTTCGAGGCTTTGCACTCCCTTGGC 1114  
Qy 301 IleSerPhePheAlaLeuProAlaGlyLysLeuGlySerGlyPheAlaLeuLysValGln 320  
Db 1115 ATTTCTTTTTCGCTTCTCCCGGCACTTCTGGCTCAGGCTTTTGGCTTTTGAAGTACAA 1174  
Qy 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340  
Db 1175 GAACAACACCGCCAGAAACACTTTTGAGAAAAAGAGAACCCAGCTGCCAACCTCATTTCCAG 1234  
Qy 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360  
Db 1235 TGTGTTTGGCGTAGTTACGAGCTGATGAGAAATCTGTTTTCATTGCAACCTGGAAGCA 1294  
Qy 361 HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyGluAlaSerSer 380  
Db 1295 CACTTGAAGGCTTTCACACTGCGAGCCCTACCAAGAAAGAACAGGGAAGCATCAAGC 1354  
Qy 381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400  
Db 1355 AGTCAGAAGCTAAGTTTTAGGAGCGAGTGGCATGGCTAGCCCCCAGGGGCCAGAGTATT 1414



QY	401	LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu	420	Db	2495	TCAATCTCACCAGGACCGTTCTATGAGGAAAAGCTTGTGACATGGGAGGAGAACTCTG	2554
Db	1415	AAGAGCCGACAGGCTCAGTAGGTGACAGAGGTCCCAAGCACCGACATCACAGCCGAG	1474	QY	781	LeuSerValCysProMetValprolyAspLeuGlyysSerLeuSerValGlnAsnLeu	800
QY	421	GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro	440	Db	2555	TTGTCTGTCTGTCCCATCGTCCGGAAGGACTTGGGCAAAATCTTTGTCTGTGCAAAACCTG	2614
Db	1475	GGCAGTCCCAACCAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCCTTCGCGCCC	1534	QY	801	IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg	820
QY	441	SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly	460	Db	2615	ATCAGGTCCACCGAGAACTGAAATATACAACTTTTCAGGAGTGAGTCAAGTGGCTCCAGA	2674
Db	1535	TCGCTGCCGCCCTCAAAAGTTCTCAGCCAAACACCATGATAGTGTGACACAGCCCTTGGC	1594	QY	821	GlySerGlnAspPheTyPProlySerTrpArgGluSerLysLeuPheIleThrAspGluGlu	840
QY	461	ThrAspAspValTyAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr	480	Db	2675	GGCAGCCAAAGATTTTATCCCAATGAGGAATCCAAATTTGTTTATTAACATGATGAAGAG	2734
Db	1595	ACTGATGATGATATGATGAAGAGGATGCCAGTGTGATGATCATCAGTGGAGAGCCCTCACC	1654	QY	841	ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu	860
QY	481	ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg	500	Db	2735	GTGGGTCCCGAAGACAGACAGACACTTTTGTATGGCGCACCCGACGCTGCCAGGAA	2794
Db	1655	CCACCACCTTAAACACTGTCTATCGAGCTATCAGAAATATGAATTTTCATGTTGCCAAACGG	1714	QY	861	AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys	880
QY	501	LysPheLysGluThrLeuArgProTyAspValLysAspValIleGluGlnTySerAla	520	Db	2795	GCTGCCCTTTCATCAGACTCTCTAAGGACTGGAGAGTCCAGATCATCTCAGAGCATTTGT	2854
Db	1715	AGTTTAAAGGAACATTACGTCATATGATGATAAAGATGTCAATTGAACAAATATCTGCT	1774	QY	881	LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys	897
QY	521	GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu	540	Db	2855	AAGCGAGGAGAAATACAGATGCCCTCAGCTTGCCTTCATGTCAAACTGAA	2905
Db	1775	GGTCATCTGGACATGTGTGTAGAATTAAAGCCCTTCAACACACGTTGTGATCAAAATCTT	1834	RESULT 3			
QY	541	GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu	560	US-09-825-147-1			
Db	1835	GGAAAGGCGCAATCACATCAGATAAGAGAGCCGAGAGAAATAAACAGCAGAAACATGAG	1894	; Sequence 1, Application US/09825147			
QY	561	ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer	580	; Patent No. 6767736			
Db	1895	ACCACAGACGATCTCAGTATGCTCGTGGGTGGTCAAGGTTGAAAAACAGAGTACAGTCC	1954	; GENERAL INFORMATION:			
QY	581	IleGluSerLysLeuAspCysLeuLeuAspIleTyGlnGlnValLeuArgLysGlySer	600	; APPLICANT: Hu, Yi			
Db	1955	ATAGAATCCAGCTGACCTGCTTACTAGACATCTATCAACAGTCTCTTCGGAAGGCTCT	2014	; APPLICANT: Kieke, James Alvin			
QY	601	AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer	620	; APPLICANT: Turner, C. Alexander Jr.			
Db	2015	GCCTCAGCCCTCGCTTGGCTTCATTCAGATCCCACTTTTGAATGTGAACAGACATCT	2074	; APPLICANT: Nehls, Michael C.			
QY	621	AspTyRcLysSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys	640	; APPLICANT: Friedrich, Glenn			
Db	2075	GACTATCAAGCCCTGTGGATAGCAAGATCTTTTCGGGTTCCGACAAACAGTGGCTGC	2134	; APPLICANT: Zambowicz, Brian			
QY	641	LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn	660	; APPLICANT: Zambowicz, Brian			
Db	2135	TTATCCAGATCAACTAGTGCACACATCTCGAGAGGCTGCAGTTCAATTCGACGCCAAAT	2194	; TITLE OF INVENTION: Polynucleotides Encoding the Same			
QY	661	GluPheSerAlaGlnThrPheTyRAlaLeuSerProThrMetHisSerGlnAlaThrGln	680	; FILE REFERENCE: LEX-0160-USA			
Db	2195	GAGTTACAGTCCCGACATTTCTACGGCGCTTAGCGCTTACTATGCACAGTCAAGCAACACAG	2254	; CURRENT APPLICATION NUMBER: US/09/825,147			
QY	681	ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln	700	; PRIOR FILING DATE: 2001-04-03			
Db	2255	GTGCCAATTAAGTCAAGCGATGGCTCAGCAGTGGCAGCACCACCAACCATTTGCCAAACCAA	2314	; PRIOR APPLICATION NUMBER: US 60/194,255			
QY	701	IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro	720	; NUMBER OF SEQ ID NOS: 3			
Db	2315	ATAAATACGGCACCCAGCCAGCAGCCCAACACTTTACAGATCCCACTCTCTCTCCCA	2374	; SOFTWARE: FastSeq for Windows Version 4.0			
QY	721	AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu	740	; SEQ ID NO 1			
Db	2375	GCCATCAGCAATCTGCCAGCCAGAACTCTGCACCTTAACCTCGCAGGCTTACAGGAA	2434	; LENGTH: 2772			
QY	741	SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln	760	; TYPE: DNA			
Db	2435	AGCATTTCTGACGTCACCACTGCTGTTTCCCTCCCAAGGAAATGTTTCAGGTTGCACAG	2494	; ORGANISM: homo sapiens			
QY	761	SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu	780	US-09-825-147-1			
				Alignment Scores:			
				Pred. No.: 0			
				Score: 4527.50			
				Percent Similarity: 99.00%			
				Best local Similarity: 98.89%			
				Query Match: 4			
				DB: 1			
				US-09-810-796-4 (1-897) x US-09-825-147-1 (1-2772)			
QY	1	MetLysAspValGluSerGlyArgGlyValLeuLeuAsnSerAlaAlaAargGly	20	Db	106	ATGAAGGATGTGAGTCCGGCCGGGCGAGGGTGTCTGTAACCTCGGAGCGCCGAGGGGC	165
QY	21	AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu	40	Db	166	GACGCTCTACTCTGGGACACCGCGCGGCCACCTCGGTGGCGCGCGGTGGCTG	225
QY	41	ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer	60				

Db 226 AGGGAGAGCCGGGGAGCAGGGGGCCCGATGAGCCTGCTGGGAAAGCCGCTCTCT 285  
Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgValGlnAsnTyrLeu 80  
Db 286 TACACGAGTAGCAGAGCTGCCGGCGCAAGCTCAAGTACCGCGGGTGCAGAACTACCTG 345  
Qy 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100  
Db 346 TACAACGTGCTGGAGAGACCCCGCGCTGGGGGTTTCATCTACACGCTTTCGTTTTCTC 405  
Qy 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu 120  
Db 406 CTGGTCTTGGTGTCTGATTTGTGAGTGTTCCTACCATCCCTGAGCACAAATGT 465  
Qy 121 AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe 140  
Db 466 GCCTCAAGTTGCTCTGATCTCGAGTTCGTGATGATTCGTCCTTTGGTTGGAGTTC 525  
Qy 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160  
Db 526 ATCATTCGAATCTGCTCGCGGTTCGTGTCGATATAGAGGATGCAAGGAAGACTG 585  
Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180  
Db 586 AGGTTTGTCTGAAAGCCCTTCGTGTATAGATACCATTTGTTCTTATCGCTTCAATAGCA 645  
Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200  
Db 646 GTTGTCTGCAAAACTCAGGGTAATATTTTGGCCAGCTCTGCACTCAGAACTCCGT 705  
Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220  
Db 706 TTCTACAGATCTCCCGATGTCGCATGAGCCAGAGGGAGGCACCTTGGAAATTAAGT 765  
Qy 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTyrIleGlyPheLeu 240  
Db 766 GTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGTGTATAGGATTTTG 825  
Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260  
Db 826 GTTCTTATTTTTCGCTTCCTCTCTATCTGTTGGTGGAAAGAGTGCCTCAATAAGAGTT 885  
Qy 261 SerThrTyrAlaAspAlaLeuTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280  
Db 886 TCTACATATGAGATGCTCTCTGTTGGGGCACAAATACATTGCAACTATTGGCTATGGA 945  
Qy 281 AspLysThrProLeuThrTrpLeuGlyValArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300  
Db 946 GACAAACTCCCTTAACTTGGCTGGGAAGATTGCTTCTGCAGGCTTTGCACTCTCTGGC 1005  
Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320  
Db 1006 ATTTCTTTCTTGGACTTCTCGCGCATCTTGGCTCAGTTTTCATTAAGTACAA 1065  
Qy 321 GluGlnHisArgGlnLysPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340  
Db 1066 GAACAACACCGCAGAAACACTTTGAGAAAAGAGAAACCCAGCTGCCAACCTCATTCAG 1125  
Qy 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360  
Db 1126 TGTGTTTGGCGTAGTTACGACGTGATGAGAAATCTGTTTCATTTGCAACCTGGAAGCCA 1185  
Qy 361 HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyGluAlaSerSer 380  
Db 1186 CACTTGAAGGCTTGCACACCTGCAGCCCTACC----- 1218  
Qy 381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400  
Db 1219 AATCAGAAGCTAAGTTTTTAAGGAGCGAGTGCATGGCTAGCCCCAGGGGGCAGAGTATT 1278  
Qy 401 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 420

Db 1279 AAGGCCGACAAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCACCGACATCACACCGAG 1338  
Qy 421 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 440  
Db 1339 GGCAGTCCCAACCAAGTGCAGAGAGCTGGAGCTTCAACGACCGAACCGCTTCCGGCCC 1398  
Qy 441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460  
Db 1399 TCGTGCOCCTCAAAAGTTCTCAGCCAAAACAGTATAGATGCTGCACACGCGCTTGGC 1458  
Qy 461 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480  
Db 1459 ACTGATGATGATATGATGAAAAGAGTCCAGTGTGATGATCATCTAGTGGAGAGCTCACC 1518  
Qy 481 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 500  
Db 1519 CCACACTTAAACCTGTCATTTCGAGCTATCAGAAATATGAAATTTTCATGTTGCAAAACGG 1578  
Qy 501 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 520  
Db 1579 AAGTTTAAGGAAACATTAAGTCCATATGATGATAAAGATGTCAATTGAACAAATTTCTCT 1638  
Qy 521 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540  
Db 1639 GGTCACTCGACATGTTGTGTAGAAATTAAGCCCTTCAACACGCTGTGTGATCAAAATCTT 1698  
Qy 541 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560  
Db 1699 GGAAGAGGGCAATCACATCAGATAGAAAGAGCCGAGAGAAATAACACAGCAGAACATGAG 1758  
Qy 561 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 580  
Db 1759 ACCACAGACGATCTCAGTATGCTCGGTGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1818  
Qy 581 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 600  
Db 1819 ATAGATCCAAAGCTGGACTGCTACTAGACATCTATCAACAGGCTCTTCGGAAAGGCTCT 1878  
Qy 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620  
Db 1879 GCCTCAGCCCTCGCTTTGGCTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT 1938  
Qy 621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640  
Db 1939 GACTATCAAGCCCTGTGGATAGCAAGATCTTTGGGTTCGCGCACAAAAACAGTGGCTGC 1998  
Qy 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660  
Db 1999 TTATCCAGATCACTAGTGCACACATCTCGAGAGGCTGCAGTTCATTTCTGACGCCAAT 2058  
Qy 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680  
Db 2059 GAGTTCAGTGCCAGACTTCTACGCGCTTAGCCCTACTATGCAGTCAAGCAACACAG 2118  
Qy 681 ValProIleSerGlnSerAspGlySerAlaValAlaIleThrAsnThrIleAlaAsnGln 700  
Db 2119 GTGCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGCGAGCCACCAACACCATTTGCAAAACCAA 2178  
Qy 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro 720  
Db 2179 ATAAATACGGCACCCCAAGCCAGCAGCCCAACAATTTTACAGATCCCACTCTCTCCCA 2238  
Qy 721 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740  
Db 2239 GCCATCAAGCATCTGCCAGCCAGAAACTCTGCACCCCTAACCCCTGCAGGCTTACAGGAA 2298  
Qy 741 SerIleSerAspValThrThrCysLeuValIleAserLysGluAsnValGlnValAlaGln 760  
Db 2299 AGCATTTCTGACGTCAACCCCTGCTTGTTCCTTCCAGGAAAAATGTTTCAGGTTCACAG 2358  
Qy 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyLthrLeu 780  
Db 2359 TCNAATCTCAAGGACCGTTCTATGAGGAAAAGCTTTTGATGAGGAGGAGAAAACCTCTG 2418

QY 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800  
Db 2419 TTGTCGTCTCTCCATGGTCCGAGGACTTGGGCAAAATCTTTGTCTGTGCAAAACCTG 2478  
QY 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 820  
Db 2479 ATCAGTCCGACCGAGGAACCTGAATATACAACTTTTCAGGAGTGTAGTCAAGTGGCTCCAGA 2538  
QY 821 GlySerGlnAspPheTyrProLysTyrArgGluSerLysLeuPheIleThrAspGluGlu 840  
Db 2539 GGCACCCCAAGATTTTACCCCAATGAGGGAATCCAAATGTTTATAACTGATGAAGAG 2598  
QY 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 860  
Db 2599 GTGGGTCCGAGAGACAGACAGACACTTTTGTATGCCGACCCGAGCCCTGCCAGGGAA 2658  
QY 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 880  
Db 2659 GCTGCCTTTGCAATCAGACTCTCTAAGGACTGGAAGGTCAAGTCAATCATCTCAGAGCATTTGT 2718  
QY 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897  
Db 2719 AAGGAGGAGGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACCTGAAA 2769

RESULT 4  
US-09-825-147-3  
; Sequence 3, Application US/09825147  
; Patent No. 6767736  
; GENERAL INFORMATION:  
; APPLICANT: Hu, Yi  
; APPLICANT: Kieke, James Alvin  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Nehls, Michael C.  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 676736el Human Ion Channel Protein and  
; FILE OF INVENTION: Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0160-USA  
; CURRENT APPLICATION NUMBER: US/09/825,147  
; CURRENT FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: US 60/194,255  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 3111  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-825-147-3

Alignment Scores:  
Pred. No.: 0 Length: 3111  
Score: 4527.50 Matches: 887  
Percent Similarity: 99.00% Conservative: 1  
Best Local Similarity: 98.89% Mismatches: 0  
Query Match: 98.68% Indels: 9  
DB: 4 Gaps: 1

US-09-810-796-4 (1-897) x US-09-825-147-3 (1-3111)  
QY 1 MetLysAspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaArgGly 20  
Db 165 ATGNAGATGTGAGTGGGCGGGGAGGGTGTCTGCTGAACCTCGGACCGCGAGGGGC 224  
QY 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrIleuGlyGlyGlyGlyLeu 40  
Db 225 GACGGCTGTACTGTCTGGGACCCGCGGCGCACGCTCGGTGGCGCGCGGTGCCCTG 284  
QY 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60  
Db 285 AGGAGAGGCCCGCGGGGAGAGAGGCGGCGGAGTGTCTGTTGGGAGGCCCTCTCT 344

QY 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgValGlnAsnTyrLeu 80  
Db 345 TACACAGTAGCCAGAGCTGCCGGCGCAACGTCAGTACCGGGGGTGCAGAACTACCTG 404  
QY 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100  
Db 405 TACACAGTGTGGAGAGACCCCGCGGTTCATCTACACGCTTTCGTTTCTCTC 464  
QY 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu 120  
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QY 121 AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe 140  
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QY 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160  
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QY 161 ArgPheAlaArgProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180  
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QY 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeu 200  
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QY 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240  
Db 825 GGTTCAGTGTGTTATGCTCACACAGGAATTAATCACAGCTTGTGTACATAGGATTTG 884  
QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260  
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QY 261 SerThrTyrAlaAspAlaLeuTrpTyrGlyThrIleThrLeuThrThrIleGlyTyrGly 280  
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QY 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300  
Db 1005 GACAAAACTCCCTTAACCTTGGCTGGGAAGATTTGTTTCTGCAGGCTTTGCACCTCTTGGC 1064  
QY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320  
Db 1065 ATTTCTTTTCTTTCGCTTCTGCGCGCATTTCTTGCTCAGGTTTGCATTTAAAGTACAA 1124  
QY 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaLeuIleGln 340  
Db 1125 GAACAACACCCCGAGAAACACTTTGAGAAAAGAGAAAGAACCCAGCTGCAACTCATTCAG 1184  
QY 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360  
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QY 361 HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyGluAlaSerSer 380  
Db 1245 CACTTGAAGGCTTTGCAACCTGCGAGCCCTTACC----- 1277  
QY 381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400  
Db 1278 AATCAGAGCTAAGTTTTAAGGAGCGAGTGCATGCTAGCCCCAGGGCCAGAGTATT 1337  
QY 401 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 420  
Db 1338 AAGAGCCGACAAAGCCTCAGTAGGTGACAGGAGGTCCTCCCAAGCACCGACATCACAGCCGAG 1397

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QY 421 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 440
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QY 441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460
Db 1458 TCGCTGGCGCTCAAAAGTTCTCAGCCCAAAACAGATGATAGATGCTGCACACAGCCCTTGGC 1517
QY 461 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480
Db 1518 ACTGATGATGATATGATCAAAAGGATGCGAGTGTGATGATCAGTGGAGACCTCACC 1577
QY 481 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 500
Db 1578 CCACACATTAAACCTGCTATTCGAGCTATCAGAATTATGAAATTTTCATGTTGCAAAACGG 1637
QY 501 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 520
Db 1638 AGTTTAAAGAAACATTAGCTCCATATGATGTAAAGATGTCATTGAACATATTTCTGCT 1697
QY 521 GlyHisLeuAspMetLeuLysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540
Db 1698 GGTCACTCGACATGTTGTAGATTTAAAGCCCTTCAACACAGCTGTTGATCAAAATTCCT 1757
QY 541 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560
Db 1758 GGAAAGGGCAAAATCACATCATGATGAAGAGCGGAGAGAAATTAACAGCAGAAATCAG 1817
QY 561 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 580
Db 1818 ACCACAGACGATCTCAGTATGCTCGGTGGGTGTCAGGTTTGAAGTTGAACAGTACAGTCC 1877
QY 581 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 600
Db 1878 ATAGAATCCAGCTGAGCTGCCTACTAGACATCTATCAACAGTCTCTTCGGAAGGCTCT 1937
QY 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620
Db 1938 GCCTCAGCCCTCGCTTGGCTTTCATTCAGATCCCACTTTTGAATGTGAACAGACATCT 1997
QY 621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640
Db 1998 GACTATCAAGCCCTGTGATAGCAAGATCTTTCGGGTTCGCGACAAAACAGTGGCTGC 2057
QY 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660
Db 2058 TTATCCAGATCAACTAGTGCCAAATCTCGAGAGGCTGCAGTTCTTCTGAGCGCAAT 2117
QY 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680
Db 2118 GAGTTTCAGTGGCCAGACTTCTACGCGCTTACGCTTACTATGACAGTCAAGCAACACAG 2177
QY 681 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 700
Db 2178 GTGCCAATTAGTCAAAAGGATGGCTCAGCAGTGGCAGCCACCAACCATTTGCAAAACCA 2237
QY 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro 720
Db 2238 ATAAATACGGCACCCCAAGCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2297
QY 721 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740
Db 2298 GCCATCAAGCATCTGCCAGGCGCAGAAACTCTGCACCCCTTAACCCCTGCAGGCTTACAGAA 2357
QY 741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760
Db 2358 AGCATTTCTGAGCTCACCACCTGCTTGTGCTCTCAAGGAAATTTTCAGGTTGCACAG 2417
QY 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780
Db 2418 TCAAAATCTCACCAGACCGTTCTATGAGAAAGCTTTGACATGGGAGGAGAACTCTG 2477
QY 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800
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Db 2478 TTGTCGTGTCCTCCATGGTCCGAAGACTTGGCAAAATCTTTGCTGTGCAAAACCTGT 2537
QY 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 820
Db 2538 ATCAGTTCGACCGAGGAACCTGAATATACAATTTTCAGGAGGTGAGTCAAGTGGCTCCAGA 2597
QY 821 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840
Db 2598 GGCAGCCAAAGATTTTACCCCAATGGAGGAAATCCAAATTTGTTTATAACTGATGAAGAG 2657
QY 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 860
Db 2658 GTGGTCCCGAAGACAGACAGACACTTTTGATGCCGACCCGACGCTGCCAGGGAA 2717
QY 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 880
Db 2718 GCTGCTTTGATCAGACTCTCTAAGGACTCGAAGGTCCAGATCATCTCAGAGCATTTGT 2777
QY 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897
Db 2778 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAA 2828

RESULT 5
US-09-492-361-1
; Sequence 1, Application US/09492361
; Patent No. 6794161
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE
; TITLE OF INVENTION: POTASSIUM CHANNELS
; FILE REFERENCE: 2815-127P
; CURRENT APPLICATION NUMBER: US/09/492.361
; CURRENT FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2335
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(2335)
; NAME/KEY: CDS
; LOCATION: (83)..(2170)
US-09-492-361-1

Alignment Scores:
Pred. No.: 1,91e-195 Length: 2335
Score: 2012.00 Matches: 437
Percent Similarity: 65.45% Conservative: 82
Best Local Similarity: 55.11% Mismatches: 136
Query Match: 43.85% Indels: 138
DB: Gaps: 16

US-09-810-796-4 (1-897) x US-09-492-361-1 (1-2335)
QY 8 ArgGlyArgValLeuLeuAsnSerAlaAlaAlaArgGlyAspGlyLeuLeuLeuGly 27
Db 127 CGGGGAGCGCCCGCGCGAGTAGTGGCGCTCAGCGC----- 165
QY 28 ThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyGlyLeuArgGluSerArgArgGlyLys 47
Db 166 ---CGTCAGAGCGAAACAGGGCGAGCGCGG-----CGGGGGCGG 201
QY 48 GlnGlyAla-ArgMetSerLeuLeuGlyLysProLeu----- 59
Db 202 CTCGCCGCGCGCTCTCGGCTCTCGGCGAGCCCTTCGCCGCGCGCGCGCCCTCCCTGG 261
QY 60 -----SerTyrThrSerSerGlnSerCysArgArgAsnValLys 73
Db 262 GCCGGGCTCCGGCTCGGGCTCGGCTCGGCGAGCGGCTCTCTCGGCGCGCGCACAGGCTA 321
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QY 73 rArgArgValGlnAsnTyrLeuTyrAsnValLeuGluAArgProArgGlyTrpAlaPheIl 93  
 Db 322 CGCGCGCTGAGAACTGGGTCTACAACTGCTGGAGCGGCCCGCGCTGGCGCTTCGT 381  
 QY 93 eTyrHisAlaPheValPheLeuValPheGlyCysLeuLeuLeuSerValPheSerTh 113  
 Db 382 CTACACAGCTCTTATATTTTGGTCTTTCAGCTGGCTGTGTGTGTGTGTGTGTGTGT 441  
 QY 113 rIleProGluHisThrLysLeuAlaSerSerCysLeuLeuLeuLeuLeuValMetIl 133  
 Db 442 TATCAGAGGACACGAACTTGGCAAGAGTGTCTCTCATCTTGGAAATCGTGATGAT 501  
 QY 133 eValValPheGlyLeuGluPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 153  
 Db 502 CGTGTCTTTCGCTTGGAGTACATCGTCCGGTCTGTGTGTGTGTGTGTGTGTGTGTGT 561  
 QY 153 rArgGlyTrpGlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrIl 173  
 Db 562 CCGAGGATGGCAGGTCGCTTCCGCTTTGCCAGAAAGCCCTTCTGTGTGTGTGTGTGTGT 621  
 QY 173 eValLeuIleAlaSerIleAlaValValSerAlaLysThrGlnGlyAsnIlePheAlaTh 193  
 Db 622 CGTGTCTGGGCTCGGTGGCGTTCATCGCGCGGTATACCCAGGCGCAACATCTTCGCCAC 681  
 QY 193 rSerAlaLeuArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgAr 213  
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 QY 213 sGlyGlyThrTrpLysLeuLeuGlySerValValTyrAlaHisSerLysGluLeuIleTh 233  
 Db 742 CGCGGCGACCTGAGAGTGTGTGGCTCAGTGTCTACGCGCATAGCAAGGAGTGTATCAC 801  
 QY 233 rAlaTrpTyrIleGlyPheLeuValLeuLeuPheSerSerPheLeuValTyrLeuValGl 253  
 Db 802 CGCTGTGTACATCGGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 861  
 QY 253 uLysAspAlaAenLysGluPheSerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleTh 273  
 Db 862 GAAGGACGCGCACTCGACTTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 921  
 QY 273 rLeuThrThrIleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSe 293  
 Db 922 ATTGACAACCATCGGTATGTGTGACAAAGACCGCACATCGCTGGGCGAGGCTCTGTGC 981  
 QY 293 rAlaGlyPheAlaLeuLeuGlyLysPhePheAlaLeuProAlaGlyIleLeuGlySe 313  
 Db 982 TGT 1041  
 QY 313 rGlyPheAlaLeuLysValGlnGluGlnHisArgGlnLysHisPheGluLysArgArgAs 333  
 Db 1042 CGGCTTTGGCTGAAGTCCAGGAGCAGCACCGGAGAGAGCACTTCGAGAAGCGGAGGAT 1101  
 QY 333 nProAlaAlaAsnLeuIleGlnCysValTrpArgSerTyrAlaAlaAsp---GluLysSe 352  
 Db 1102 GCGCGGACGCAACCTCATCCAGGCTGCTGGCGCTGTACTCCACGATATGAGCGGGC 1161  
 QY 352 rValSerIleAlaThrTrp----- 358  
 Db 1162 CTACCTGACAGCCACCTGT 1221  
 QY 358 ----- 358  
 Db 1222 CCTCTTGT 1281  
 QY 359 -----LysProHisLeuLysAlaLeuHisTh 367  
 Db 1282 GCGGGCGCGGTACCGAGCGAGCACCTCCCGTGTACCCCGCTGTGTGTGTGTGTGTGTGTGT 1341  
 QY 367 rCysSerProThrLysLysGluGlnGlyGluAlaSerSerSerGlnLysLeuSerPheTh 387  
 Db 1342 GCGGGGCGGACCTCTCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1392  
 QY 387 sGluArgValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGln-----Al 405

Db 1393 AGACGCGATCCGATGGGCGAGTCCAGCGGGAGCGGTCTCTTCAAAGCAGCAGCTGGC 1452  
 QY 405 aSerValGlyAspArgArgSerProSerThrAspIleThrAlaGluGly---SerProTh 424  
 Db 1453 ACTCTCAACAATGCGCACCTCCCAAGCAGCAGCGGTGGTGGTGGTGGTGGTGGTGGTGGT 1512  
 QY 424 rLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLe 444  
 Db 1513 CAAAGTGTCAAAAGAGCTGGAGCTTCAATGACCGCACCGCTTCCGGGCATCTCTGAGACT 1572  
 QY 444 uLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspAspVa 464  
 Db 1573 C-----AAACCCCGCACCTCTCTGCTGAGGATGCC---CCCTCAGAGGAAGT 1614  
 QY 464 lTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuLys 484  
 Db 1615 AGCAGAGGAGAGAGACTACCACTGTGAGCTCAGGTGGTGGACGACATCATCCCTGCTGTGNA 1674  
 QY 484 sThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPheLysGl 504  
 Db 1675 GACAGTCATCCGCTCCATCAGGATTTCTCAAGTTCTCTGTGTGGTGGCCMAAAGGAAATTC 1734  
 QY 504 uThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAs 524  
 Db 1735 GACACTGCGACCTTACGACGTGAAGGACGTCTATTGACGAGTACTCAGCAGGCGCACCTGGA 1794  
 QY 524 pMetLeuCysArgLysLeuLysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGl 544  
 Db 1795 CATGCTGGGCGGATCAAGAGCTGCAACTCGGTGGACCAAAATTTGTGGTGGGCGG--- 1852  
 QY 544 nIleThrSerAspLysSerArgGlu-----LysIleThrAlaGluHisGluTh 561  
 Db 1853 -----CCCGGGGACAGGAAGCGCGGAGAAAGGCGCAAAAGGCGCGCGAGGT 1908  
 QY 561 rThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSerIl 581  
 Db 1909 GGTGGATGAATCAGCATGATGGAGCGGTGGTCAAGTGGAGAGCAGAGTGTGAGTCCAT 1968  
 QY 581 eGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySerAl 601  
 Db 1969 CGAGCACAGCTGGACCTGCTGTGGCTTCTATTGCGGTGCTGTGGCTGTGGCACCTC 2028  
 QY 601 aSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSerAs 621  
 Db 2029 GGCC-----AGCCTGGCGCGCGTGAAGTGGCGCTTTCGACCCCGACATCCTCCGA 2082  
 QY 621 pTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCysLe 641  
 Db 2083 CTACACAGCCCTGTGACCAACGAGGACATCTCGTCTCCGACAGAGCGCTCAGC---AT 2139  
 QY 641 uSerArgSerThrSerAlaAsnIleSerArgLysLeuGlnPheIleLeuThrProAsnGl 661  
 Db 2140 CTCCCGCTCGCTCAGCACCAACATGAGCTGAGG----- 2173  
 QY 661 uPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGlnVa 681  
 Db 2173 ----- 2173  
 QY 681 lProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGlnIl 701  
 Db 2174 -----ACTTCTCAGAGGCGGCGAGCACA----- 2197  
 QY 701 eAsnThrAlaProLysProAlaAlaProThrThrLeu-GlnIleProProLeuProA 721  
 Db 2198 -CGGCGACCGCGCGCTGCGCTCCGACTGCGCTCTGAGGCGCTCCGAGCTCTCTCTCGT 2256  
 QY 721 lAlaLysHisLeuProArgProGluThrLeuHis 732  
 Db 2257 ACTTGAACTCACTCCCTCAGCGGGAGAGAGACCCAC 2291  
 RESULT 6  
 US-09-949-016-1823

```

; Sequence 1823, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1823
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-1823

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Db 1678 CTGCAAACTCGGTGGACCAAAATGTGGTTCGGGGG-----CCCGGGGACAGGAAGGCC 1731
Qy 552 ArgGlu-----LysIleThrAlaGluHisGluThrThrAspAspLeuSerMetLeu 568
Db 1732 CGGAGAGAGCGCAAGGGCCCTCCAGCCGAGGTGGTGAATGAATCAGATGATG 1791
Qy 569 GlyArgValValLysValGlnValGlnSerIleGluSerLysLeuAspCysLeu 588
Db 1792 GGACGGTGTTCAGGTGGAGAGCAGGTGAGTCCATCCAGCAGCAAGCTGGACTGCTG 1851
Qy 589 LeuAspIleThrGlnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAsp 608
Db 1852 TTGGCTTCTATTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1905
Qy 609 PheGlnIleProProPheGluCysGluGlnThrSerAspThrGlnSerProValAspSer 628
Db 1906 GTGCAAGTGGCGCTGTTTCGACCCCGACATCATCCCTCCGACTACACAGCCCTGTGGACAC 1965
Qy 629 LysAspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsn 648
Db 1966 GAGGACATCTCGTCTCGCACAGCAGCTCAGC---ATCTCCGCTCGGTGAGCAGCAAC 2022
Qy 649 IleSerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyr 668
Db 2023 ATGGACTGAGGG----- 2034
Qy 669 AlaLeuSerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGly 688
Db 2035 -----ACTTCTCAGAGGAGGGC 2052
Qy 689 SerAlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAla 708
Db 2053 AGCACA-----CGGCCAGCCCGCGGCTGGC 2079
Qy 709 AlaProThrThrLeuGlnIleProProLeuProAlaIleLysHisLeuProArgPr 728
Db 2080 GCTCCGACTGCTCTGAGGCTCCGGACTCTCTCGTACTTGAACCTCACTCCCTCACGG 2139
Qy 728 oGluThrLeuHis 732
Db 2140 GGAGAGACACCAC 2152
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## RESULT 7

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; Sequence 22, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blonar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2169
; TYPE: DNA
; ORGANISM: mouse
US-09-105-058C-22

Alignment Scores:
Pred. No.: 4,26e-175 Length: 2169
Score: 1813.00 Matches: 393
Percent Similarity: 65.68% Conservative: 72
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Best Local Similarity: 55.51% Mismatches: 153
Query Match: 39.52% Indels: 90
DB: 3 Gaps: 17

US-09-810-796-4 (1-897) x US-09-105-058C-22 (1-2169)

Qy 17 AlaAlaArgGlyAspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGly 36
Db 100 TCCACACGCGAGCGCGCTACTCATCGCGGCTCCGAGGCCCCCAAG-----CGC 150
Qy 37 GlyGlyGlyLeuArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGly 56
Db 151 GGCACGCGTTTGTAGCAAGCGCGAGCGCGCGCGCGGAGCC-----GGG 195
Qy 57 LysProLeuSerTyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgVal 76
Db 196 AAGCCC-----CCGAGGCGCAACGCTTCTACCGCAAGCTG 231
Qy 77 GlnAsnTyrLeuTyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAla 96
Db 232 CAGAAATTCCTCTACAACGTGTAGAGCGGCCCGCGCTGGCGGCTTCATCTACACGCC 291
Qy 97 PheValPheLeuLeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlu 116
Db 292 TACGTGTTCCTTTAGTCTTCTCCTGCTTGTGCTTTCTGTGTTTCCACCATCAAGGAG 351
Qy 117 HisThrLysLeuAlaSerSerCysLeuLeuLeuGluPheValMetIleValValPhe 136
Db 352 TACGAGAAGAGCTCTGAGGGGCGCTCTACATCTTGGAAATCGTGACTATCGTGTATTC 411
Qy 137 GlyLeuGluPheIleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyr 156
Db 412 GGTCTGAGTACTTGTGAGGATCTGGGCTGCAGGCTGCTGTTCCGGTATCGAGGCTGG 471
Qy 157 GlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIle 176
Db 472 AGGGGAGGCTCAAGTTTGCAGAACCGTCTCTGTGTGATGTGATATATCATGGTCTGAT 531
Qy 177 AlaSerIleAlaValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeu 196
Db 532 GCCTCCATTGCTGTGCTGGTGTGCTGCCAGGGCAATGCTTTGGCCACATCTGCGCTT 591
Qy 197 ArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyThr 216
Db 592 CGGAGCTTGGGTTCTTTCGAAATCTTGGATGATCCGTATGGACCGGAGGGTGGCACC 651
Qy 217 TrpLysLeuLeuGlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyr 236
Db 652 TGGAAAGCTCTGGGATCGGTAGTCTACGCTCACAGCAAGGAGCTGGTGACTGCTGGTAC 711
Qy 237 IleGlyPheLeuValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAla 256
Db 712 ATTGGCTTCTCTGCTCATCTCGGCTCATCTTCTGGTGTACTTGGCAGAAAAGGGTGAG 771
Qy 257 AsnLysGluPheSerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThr 276
Db 772 AATCACCACCTTGACACCTACGAGATGCACTCTGTGGGGTCTGATCACCCTGCACGACC 831
Qy 277 IleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPhe 296
Db 832 ATTGGCTACGGGGACAAAGTACCCCTCAGACCTGGAAACCGGGAGGCTGTGGCAGCCCTTT 891
Qy 297 AlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAla 316
Db 892 ACCCTCATTTGGTGTCTGTTCTTCTGCTTCTTCTGTCATTTTGGGATCGGGCTTGCC 951
Qy 317 LeuLysValGlnGluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAla 336
Db 952 CTGAAAGTCCAAAGAGCAGCATCGCAAAAAACACTTTGAGAAACCGCGGAAACCTCTCGGCA 1011
Qy 337 AsnLeuIleGlnCysValTrpArgSerTyrAlaAlaAsp----- 349
Db 1012 GGTCTGATCCAGTCTGCTGGAGATTCTATGCTACTAACTCTCTCAGCACCGACCTGCAC 1071
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Qy 350 -----GluYSerValSerIleAlaThrTrpLys-----ProHis 361  
Db 1072 TCCAGTGGCAGTACTACGAGCGGACAGTCTGTCCTCCCATGTACAGACTCATCCACCT 1131  
Qy 362 LeuYsAlaLeuHisThrCysSerProThrLysLysGluGlnGly----- 376  
Db 1132 CTGAACACGCTGGAGCTGCTGAGGAATCTCAAGAGCAAAATCTGACCTCACCTTCAGGAAG 1191  
Qy 377 -----GluAlaSerSerGlnLysLeuSerPheLysGluArgValArgMet 392  
Db 1192 GAGCACACGAGCCATCACCAGTCAAGAGTCACTTTCAAGATCGTGTC---TTC 1248  
Qy 393 AlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAsp-----Arg 410  
Db 1249 TCCAGCCCCGAGGATGCTGCCAAGGAAAGGGTCTCCCCAGCGCCAGACGGTCCGG 1308  
Qy 411 ArgSerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSerTrp 430  
Db 1309 CGGTCCCCAGTGGGATCAGAGTCTTGATGACAGCCGAGCAAGGTGCCCAAGAGCTGG 1368  
Qy 431 SerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerSerGlnProLys 450  
Db 1369 AGCTTGTGACCGGACGCGCACAGCCAGGCTTTCGCATCAAGGGTGTGCTATCCCGG 1428  
Qy 451 ProValIleAspAlaAspThrAlaLeuGlyThrAspValTyrAspGluLysGlyCys 470  
Db 1429 CAGAATTCAGAAGCAAGCTCCCT---GGGAGGACATCGTAGAGCAACAAGAGCTGT 1485  
Qy 471 GlnCysAspValSerValGluAspLeuThrProProLeuLysThrValIleArgAlaIle 490  
Db 1486 AACTGCGAGTTGTGACTGAAGATCTTACCCCTGGCCTCAAGTTAGCATCAGAGCTGTG 1545  
Qy 491 ArgIleMetLysPheHisValAlaLysArgLysPheLysGluThrLeuArgProTyrAsp 510  
Db 1546 TGTGTATGCGGTCTTGTATATCAAGCAAGTTCAAGAGAGTCTGCGCCCATATGAT 1605  
Qy 511 ValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMetLeuLysArgIleLys 530  
Db 1606 GTGATGGACGTCATCGAAGACGACTCGGCTGGACACTTGGATATGTTGTCGCGCATCAAG 1665  
Qy 531 SerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLysLys 550  
Db 1666 AGCTGTCAGTCCAGAGTGGACAGATTTGTGGGGGGGGCCCAACAATAAAGGAT---AAG 1722  
Qy 551 SerArgGluLysIleThrAlaGluHisGluThrThrAspAspLeuSerMetLeuGlyArg 570  
Db 1723 GATCGCACCAAGGCCAGCGGAACGAGGTGCCCCGAAGACCCAGCATGATGGGACGG 1782  
Qy 571 ValLysValGluLysGlnValGlnSerIleGluSerLysLeuAspCysLeuLeuAsp 590  
Db 1783 CTTGGGAAGTGGAGAAACAGTCTTGTCATGGAAAGAGCTCGACTTCTTGTGTAGC 1842  
Qy 591 IleTyrGlnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPheGln 610  
Db 1843 ATCTATACACAG-----AGAATGGC----- 1863  
Qy 611 IleProProPheGluCys-----GluGlnThrSerAsp 621  
Db 1864 ATCCACACGAGAGACAGAGCCCTATTTTGGGGCCAGAGGACCTGAGCCGGCACCCACC 1923  
Qy 622 TyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys--- 640  
Db 1924 TACCACAGCCCGAGGACAGCGGTGAC-----CATGCAGACAAGCATGGCTGTATC 1974  
Qy 641 -----LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThr 658  
Db 1975 ATTAAGATCGTCCGCTCCACAGCTCT----- 2001  
Qy 659 ProAsnGluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisGlnAla 678  
Db 2002 -----ACGGGCGCAGGAGNACTACGAGCACCACCCAGCCATC-----CCCCCT 2043

Qy 679 ThrGlnValProfileSerGlnSer 686  
Db 2044 GCCCAGTGTCTCTCCCTCCACCTCG 2067

## RESULT 8

US-09-177-650-95  
; Sequence 95, Application US/09177650  
; Patent No. 6413719  
; GENERAL INFORMATION:  
; APPLICANT: Leppert, Mark F.  
; APPLICANT: Singh, Nanda  
; APPLICANT: Charlier, Carole  
; TITLE OF INVENTION: KCNQ3 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE  
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)  
; FILE REFERENCE: 2323-134  
; CURRENT APPLICATION NUMBER: US/09/177,650  
; CURRENT FILING DATE: 1998-10-23  
; EARLIER APPLICATION NUMBER: 60/063,147  
; EARLIER FILING DATE: 1997-10-24  
; NUMBER OF SEQ ID NOS: 129  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 95  
; LENGTH: 3237  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (128)..(2917)  
US-09-177-650-95  
Alignment Scores:  
Pred. No.: 4,08e-174 Length: 3237  
Score: 1806.50 Matches: 435  
Percent Similarity: 56.43% Conservative: 105  
Best Local Similarity: 45.45% Mismatches: 232  
Query Match: 39.37% Indels: 186  
DB: 3 Gaps: 25  
US-09-810-796-4 (1-897) x US-09-177-650-95 (1-3237)

Qy 17 AlaAlaArgGlyAspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGly 36  
Db 227 TCCACCCGGGACGGGGCGCTGCTGATCGCGGCTCCGAGGCCCCCAAG-----CGC 277  
Qy 37 GlyGlyGlyLeuArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGly 56  
Db 278 GGCAGCATCTTCAGCAAACTCGCGCGGGCGGGCGGGCGCC-----GGG 322  
Qy 57 LysProLeuSerTyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgVal 76  
Db 323 AAGGCC-----CCCAAGCGCAACGGCTTCTACCGCAAGCTG 358  
Qy 77 GlnAsnTyrLeuTyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAla 96  
Db 359 CAGAAATTCCTCTACAACGTCTGAGCGGGCGGGCGGGCTGCTCATCTACACGCC 418  
Qy 97 PheValPheLeuLeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlu 116  
Db 419 TACGTGTTCCTCTCTGGTTTCTCCTGCTGCTGCTGTGTGTGTGTGTTCACCATCAAGGAG 478  
Qy 117 HisThrLysLeuAlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPhe 136  
Db 479 TATGAGAAGAGCTCGGAGGGGGCCCTTACATCTCTGGAAATCGTGACTATCGTGTGTGTT 538  
Qy 137 GlyLeuGluPheIleIleArgIleTyrSerAlaGlyCysCysCysArgTyrArgGlyTrp 156  
Db 539 GGCCTGAGTACTTCGTGCGGATCTGGCGAGCTGCTGCTCGCGGCTGCTGCTGCTGCTG 598  
Qy 157 GlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIle 176  
Db 599 AGGGGGCGGCTCAAGTTTGGCCGGAACCGGTTCTGTGTGATGTGATCATCATCGTGTCTCATC 658

177 AlaSerIleAlaValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeu 196  
178 GCTTCCATTGGGTGGCGCGCTCCAGGGCAACGTCTTGGCACTTGGCGTC 718  
197 ArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgGlyGlyThr 216  
719 CGAGAGCTTGGCTCTCTGCAGATTCTGGGATGATCGCATGGACCGCGGGAGGAC 778  
217 TrpLysLeuLeuGlySerValValTyrAlaHisSerLysGlnLeuIleThrAlaTrpTyr 236  
779 TGAAGCTGTGGCTCTGTCTGTATGCCACAGCAAGAGAGCTGTCACTGTCTGTATC 838  
237 IleGlyPheLeuValLeuPheSerSerPheLeuValTyrLeuValGluLysAspAla 256  
839 ATCGGCTCTCTGTCTATCTCGCTGTCTGTGTGTCTGTGTGTGTGTGTGTGTGTGT 898  
257 AsnLysGluPheSerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThr 276  
899 AACGACCACTTGTACACCTAGCGGATGCACCTCTGTGTGGGCTGTATCAGCTGAC 958  
277 IleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPhe 296  
959 ATTGGCTACGGGGACAGTACCTGAGACCTGGAACCGGAGCTCTTGGGCAACCTTC 1018  
297 AlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAla 316  
1019 ACCCTCATCTGGGTCTCTCTTCTGGCTGCTCTGAGGATCTTGGGCTGTGGTTGCC 1078  
317 LeuLysValGlnGlnGlnHisArgGlnLysHisPheGluLysArgAsnProAlaAla 336  
1079 CTGAGGTTTACGAGCAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1138  
337 AsnLeuIleGlnCysValTyrArgSerTyrAlaAlaAsp----- 349  
1139 GGCCTGATCCAGTCGGCTGGAGATTACGCCACCAACCTCTCGCGCAGACCTGAC 1198  
350 -----GluLysSerValSerIleAlaThrTrpLys----- 359  
1199 TCACGTGGCAGTACTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1258  
360 -----ProHisLeuLysAlaLeuHisThrCysSerProThr 371  
1259 ACCTACGGGGCTCCAGACTTATCCCGCTGAAACACGCTGGAGCTCTGAGGAACCTC 1318  
372 LysLysGluGlnGlyGluAla----- 378  
1319 AAGAGTAAATCTGGACTCGCTTTCAGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1378  
379 -----SerSerSerGlnLysLeu 384  
1379 GGCAGCGCTGCAGAGGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1438  
385 SerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGln 404  
1439 AGTTTGAAGATGTGTCTCTTCTCAGGCGGCGGCTGTGTGTGTGTGTGTGTGTGTGTGT 1495  
405 AlaSerValGlyAsp-----ArgArgSerProSerThrAspIleThrAlaGluGlySer 422  
1496 TCCCCCGAGCGCCAGACTGTAGCGGCTCACCAGCGCGCAGCAGCAGCTTCAGGAGCAG 1555  
423 ProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgProSerLeu 442  
1556 CCCAGCAAGTGTCAGAGCTGTAGCTTTCGGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 1615  
443 ArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAsp 462  
1616 CGCATCAAGGGTCCCGCTCAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1672  
463 AspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThrProPro 482  
1673 GACATTGTGATGACAGAGCTGCTCCCTGCGAGTTTGTGACCGGAGGAGGAGGAGGAGGAG 1732  
483 LeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPhe 502

1733 CTCAAAGTCAGCATCAGAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1792  
503 LysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAlaGlyHis 522  
1793 AAGGAGAGCTCGCGCTTACGACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1852  
523 LeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyLys 542  
1853 CTGGACATCTGTCTCCGAATTAAAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1912  
543 GlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlnThrThr 562  
1913 GGCCAGCGCATCAGGAC---AAGGACCGCACCAAGCGCGCGCGGAGCGGAGCTGCC 1969  
563 AspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSerIleGlu 582  
1970 GAGGACCCAGCATGATGGAGCGCTCGGGAGGTGGAGAGGAGGAGGAGGAGGAGGAGGAG 2029  
583 SerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySerAlaSer 602  
2030 AAGAAGCTGGACTTCTGTGTGAATATCTATATGAG---CGGATGGGC----- 2074  
603 AlaLeuAlaLeuAlaSerPheGlnIleProPheGluCys----- 616  
2075 -----ATCCCCCGACAGACCGGAGCGCTACTTTGGGGCC 2110  
617 -----GluGlnThrSerAspTyrGlnSerProValAspSerLysAspLeuSerGly 633  
2111 AAGAGCGGAGCGCGCGCGCTTACACAGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2161  
634 SerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIleSerArgGlyLeu 653  
2162 CATGTGACAGGAGCGCTGCTGTCAAGATCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2218  
654 GlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAlaLeuSerProThr 673  
2218 ----- 2218  
674 MetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySerAlaValAlaAla 693  
2218 ----- 2218  
694 ThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAlaProThrLeu 713  
2219 -----CAGAAGAACTTCTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2257  
714 GlnIleProPro-----ProLeuProAlaIleLysHis 724  
2258 CAGTGTCCGCTCCACTCTGTGACGACGACGACGACGACGACGACGACGACGACGACGAC 2316  
725 LeuProArg-----ProGluThr-----LeuHis-ProAsnProAlaGlyLeuGlnI 740  
2317 CTCCCCGTGGGAGCACCGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2376  
740 uSerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaG 760  
2377 GTCTGTCTGCGCTTACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 2436  
760 nSerAsnLeuThrLys-----AspArgSerMetArgLysSerPheAspMetGlyGly 778  
2437 CACCGCGGCTGAGCG 2481  
778 uThrLeuLeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValG 798  
2482 CACGTCCATCTCCATCCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2541  
798 nAsnLeuIleArgSerThrGluLeuAsnIleGlnLeuSerGlySerGlySerGlySer 818  
2542 CAGCATCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2601  
818 ySerArgGlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAs 838









Db 892 ACCCTCATTTGGTCTGCTCTTTCTTCTTCCGGCTGGCATTTTGGGATCCGGCTTTGCC 951  
Qy 317 LeuysValGlnGluGlnHiArgGlnLysHisPheGluLysArgArgAsnProAlaAla 336  
Db 952 CTGAAGTCCAAAGAGCAGCATCGGCAAAACACATTTTGAGAAACGGCGGAACCCCTGCGCA 1011  
Qy 337 AsnLeuLleGlnCysValTrrArgSerTyrAlaAlaAsp----- 349  
Db 1012 GGTCTGATCCAGTCTGCTGGAGATTCTATGCTACTAACTCTCAACCGACCGACTGAC 1071  
Qy 350 -----GluLysSerValSerLleAlaThrTrpLys----- 359  
Db 1072 TCCAGTGGCAGTACTACGAGCGNACAGTCACTGTCCCATGTACAGCTCACAACCTCAA 1131  
Qy 360 -----ProHisLeuLysAlaLeuHisThrCysSerProThr 371  
Db 1132 ACCTATGGGGCTCCAGACTCATCCACTCTGAACACAGCTGGAGCTGCTGAGGAATCTC 1191  
Qy 372 LysLysGluGlnGlyGluAlaSerSerSerGlnLysLeuSerPheLysGluArgValArg 391  
Db 1192 AAGACAAATCTGGA-----CTCACCTTCAGGAAGGCCACAG 1230  
Qy 392 -----MetAlaSerProArgGlyGlnSerLleLysSerArgGlnAlaSerValGly 408  
Db 1231 CCAGAGCCATCACCAAGCCCCGAGCATGCTGCCAAGGGNAGGGGTCTCCCCAGGCC 1290  
Qy 409 Asp-----ArgArgSerProSerThrAspLleThrAlaGluLysProThrLysVal 426  
Db 1291 CAGACGGTCCGGCGTCCCGCAGTCCGATCAGAGTCTTTGTATGACAGCCCGCAGCAAGGTG 1350  
Qy 427 GlnLysSerTrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSer 446  
Db 1351 CCCAAGAGCTGGAGCTTTGGTGACCGCAGCGCACACGCCAGCGCTTCCGCATCAAGGGT 1410  
Qy 447 SerGlnProLysProValLleAspAlaAspThrAlaLeuGlyThrAspValTyrAsp 466  
Db 1411 CTGTCATCCCGCAGAAATTCAGAAGACAGCCCTCCCTGGGAGGACATCTGAGAGAC 1470  
Qy 467 GluLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuLysThrVal 486  
Db 1471 AACAGAGCTGTAACTGCGAGTTTGTGACTGAAGATCTTACCCCTGGCGCTCAAGTVAGC 1530  
Qy 487 IleArgAlaLleArgLleMetLysPheHisValAlaLysArgLysPheLysGluThrLeu 506  
Db 1531 ATCAGAGCGTGTGTATGCGGTCTTGTATCTAAGCGAAAGTTCAAGAGAGTCTG 1590  
Qy 507 ArgProTyrAspValLysAspValLleGluGlnTyrSerAlaGlyHisLeuAspMetLeu 526  
Db 1591 CGCCATATGATGTATGACGCTCATCGACAGTACTCGGCTGGACACTTGGATATGTTG 1650  
Qy 527 CysArgLleLysSerLeuGlnThrArgValAspGlnLleLeuGlyLysGlyGlnLleThr 546  
Db 1651 TCCCGCATCAAGAGCTGCAGACACAGAGTGACAGATTGTGGGCGGGGCCCAACAATA 1710  
Qy 547 SerAspLysLysSerArgGluLysLleThrAlaGluHisGluThrThrAspAspLeuSer 566  
Db 1711 ACGGAT---AAGGATCGACCAAGAGCCCGGCGGAAACGGAGCTGCCCGAAGACCCACG 1767  
Qy 567 MetLeuGlyArgValLysValGluLysGlnValGlnSerLleGluSerLysLeuAsp 586  
Db 1768 ATGATGGACCGCTTGGGAGGTGGAGAAACAGGCTTGTCTCATGGAAAGAGCTCGAC 1827  
Qy 587 CysLeuLeuAspLleTyrGlnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeu 606  
Db 1828 TTCTTGTGGAGCATCTATACAG-----AGAATGGGCATCCAACACGACGACAGACAG 1881  
Qy 607 AlaSerPheGlnLleProProPheGluCysGluGlnThrSerAspTyrGlnSerProVal 626  
Db 1882 GCCTATTTTGGGCGCAAG-----GAGCCTGAGCGCGCACCCACCTTACACAGCCACAG 1935  
Qy 627 AspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys-----LeuSerArg 643  
Db 1936 GACAGCCGTGAC-----CATGCAGACAGCATGGCTGTATCATTAAGATCTCCGC 1986

Qy 644 SerThrSerAlaAsnLleSerArgGly-----LeuGln 654  
Db 1987 TCCACAGCTCTACGG--GCCAGAGGAACACTACGACGACACCCCGACCCATCCCCCTGCC 2044  
Qy 655 PheIleLeuThrProAsnGluPheSerAlaGlnThr----- 666  
Db 2045 AGTGTCTCTCCCTCCACCTCGTGGCGGCGAGACCCACGCGCATCGCCACCTCCCTGTGG 2104  
Qy 667 -----PheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGlnVal 681  
Db 2105 GAGACCATGGCTCACTGTAGCATCCACCACTCCCTGCACACGAGCGGTGCTGTCTG 2164  
Qy 682 ProLysSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrLleAlaAsnGlnLle 701  
Db 2165 CCT-----ACGTTGGGGCAACACAGAGCCAGTACCCAGTTCTTGA 2203  
Qy 702 Asn---ThrAlaProLysProAlaAlaProThrThrLeu 713  
Db 2204 GGCTGGAGGGCACCCCGCTGACGGCCCTCTGAGGCTG 2242

## RESULT 12

US-09-105-058C-26  
; Sequence 26, Application US/09105058C  
; Patent No. 6403360

## GENERAL INFORMATION:

; APPLICANT: Blonar, Michael A.  
; APPLICANT: Dworetzky, Steven  
; APPLICANT: Grikoff, Valentin K.  
; APPLICANT: Levesque, Paul C.  
; APPLICANT: Little, Wayne A.  
; APPLICANT: Neubauer, Michael G.  
; APPLICANT: Yang, Wen-Pin

; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME  
; FILE REFERENCE: 3053-4052

; CURRENT APPLICATION NUMBER: US/09105,058C

; CURRENT FILING DATE: 1998-06-26

; PRIOR APPLICATION NUMBER: US 60/055,599

; PRIOR FILING DATE: 1997-08-12

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 26

; LENGTH: 2565

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-105-058C-26

## Alignment Scores:

Pred. No.:	3e-154	Length:	2565
Score:	1611.00	Matches:	392
Percent Similarity:	55.43%	Conservative:	108
Best Local Similarity:	43.46%	Mismatches:	244
Query Match:	35.11%	Indels:	158
DB:	3	Gaps:	28

US-09-810-796-4 (1-897) x US-09-105-058C-26 (1-2565)

Qy 3 AspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaAargGlyAspGly 22  
Db 91 GACCTGGAGCAA-----GTCACCTTGGCGTCCGGCGCGGAGCCGACAAAGACGGG 141  
Qy 23 LeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeuArgGlu 42  
Db 142 ACCCTGTCTGTG-----GAGGGCGCGCGCGCGGACGAGGGG 177  
Qy 43 SerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLys---ProLeuSerTyr 61  
Db 178 CAGCGGAGGACCCCGCAGGGC-----ATCGGGCTCTCTGGCCCAAGACCCCGCTGAGCCGC 231  
Qy 62 ThrSerSerGlnSerCysArgArgAsnValLysTyrArgValGlnAsnTyrLeuTyr 81  
Db 232 CCAGTCAAG-----AGAAACACGCCCAAGTACCGCGCGCATCCAAACTTTGATCTAC 282





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Db 2263 ---CGAATCTCCCGGCGAG-----AGAGTAGCATC 2292
Qy 774 AspMetGlyGluThrLeuLeuSerValCysProMetValProLysAspLeuGlyLys 793
Db 2293 ACGGAGACAGTGACACACCTCTGTCCCTG----- 2322
Qy 794 SerLeuSerValGlnAsnLeuLeuArgSerThrGluGluLeuAsnIleGlnLeuSerGly 813
Db 2323 ---ATGTCGGTCAACAC-----GAGGAGCTGGAGAGGTCTCCAAGTGGC 2364
Qy 814 SerGluSerSerGlySerArgGlySerGlnAspPheTyrPro-----LysTyr 829
Db 2365 TTCACATCTCCAGCAGACAGATGATTATGTTCGCGCCCAATGGGGGTGCGAGCTGG 2424
Qy 830 ArgGluSerLysLeuPheIleThrAspGluValGlyProGluGluThrGluThrAsp 849
Db 2425 ATGAGGAGAGCGGTACCTCGCCGAG-----GGTGAGACGACACACAGACGGAC 2475
Qy 850 ThrPhe 851
Db 2476 CCCTTC 2481

RESULT 13
US-09-177-650-6
; Sequence 6, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; TITLE OF INVENTION: AND OTHER EPILEPSIES
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09177,650
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 50/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 2914
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)..(2634)
; FEATURE:
; NAME/KEY: allele
; LOCATION: (840)
; OTHER INFORMATION: The polymorphism of a T to a C at this position
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (947)
; OTHER INFORMATION: The missense mutation from a G to a T occurs at
; FEATURE:
; NAME/KEY: allele
; LOCATION: (678)
; OTHER INFORMATION: This position is polymorphic for C or T.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (750)
; OTHER INFORMATION: This position is polymorphic for T or C.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1089)
; OTHER INFORMATION: This position is polymorphic for G or C.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (2598)
; OTHER INFORMATION: This position is polymorphic for T or C.

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US-09-177-650-6
Alignment Scores:
Pred. No.: 3,77e-154 Length: 2914
Score: 1611.00 Matches: 392
Percent Similarity: 55.43% Conservative: 108
Best Local Similarity: 43.46% Mismatches: 244
Query Match: 35.11% Indels: 158
DB: 3 Gaps: 28

US-09-810-796-4 (1-897) x US-09-177-650-6 (1-2914)
Qy 3 AspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaAlaAraGlyAspGly 22
Db 163 GACGTGGAGCAA-----GTCACCTTGGCGTCGGGGCGGAGCGACAAAGACGGG 213
Qy 23 LeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeuArgGlu 42
Db 214 ACCCTGTGCTG-----GAGGGCGGCGGCGGCGACGAGGGG 249
Qy 43 SerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLys---ProLeuSerTyr 61
Db 250 CAGCGGAGGACCCCGCAGGGC-----ATCGGGGTCTCTGGCCAAAGACCCCGCTGAGCCGC 303
Qy 62 ThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeuTyr 81
Db 304 CCAGTCAAG-----AGAAACACAGCCCAAGTACCGGCGCATCCAAACTTTGATCTAC 354
Qy 82 AsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeuLeu 101
Db 355 GACCCCTGGAGAGACCGCGGGCTGGCGCTGTTTACACACGGCTGGTGTCTCTGATT 414
Qy 102 ValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeuAla 121
Db 415 GTCTCGGGGTGCTTGTATTCCTGGCTGTCTCGACCATTCAGGAGATATGAGACTGTCTCG 474
Qy 122 SerSerCysLeuLeuLeuLeuGluPheValMetIleValPheGlyLeuGluPheIle 141
Db 475 GGAGACTGGCTTCTGTACTGGAGACATTTGCTATTTTCATCTTTGGAGCGAGTTTCT 534
Qy 142 IleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeuArg 161
Db 535 TTGAGGATCTGGCTGTCTGGATGTCTCGATACAAAGCTGGCGGGCGGCTGAGG 594
Qy 162 PheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAlaVal 181
Db 595 TTGCGCAGGAAGCCCTGTGTCATCTGTGACATCTTTGTGCTGATTGCTCTGTGCGCATG 654
Qy 182 ValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArgPhe 201
Db 655 GTTCTGTGGGAACCAAGGCAATGTTCTGGCCACCTCC---CTGCGAAGCTCGGCTTC 711
Qy 202 LeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTyrLeuLeuGly 221
Db 712 CTGAGATCTTCGTCATCTGCGATGCGGATGACCGAGAGGTGGCACCTGGAAGCTTCTGGGC 771
Qy 222 SerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeuVal 241
Db 772 TCAGCCATCTGTGCCACAGCAAAAGAACTCATCACGCGCTGGTACATCGGTTTCTGTACA 831
Qy 242 LeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAla----- 256
Db 832 CTCATCTCTTCTTCATTTCTGTCTACCTGTGTGAGAAAGACGTCCAGAGGTGGATGCA 891
Qy 257 -----AsnLysGluPheSerThrTyrAlaAspAlaLeuTyrTyrGlyThr 271
Db 892 CAGGAGAGGAGATGAAGAGGAGTTTGACACCTATGACATGCTGTGTGGGGCGCTG 951
Qy 272 IleThrLeuThrThrIleGlyTyrGlyAspLysThrProLeuThrTyrLeuGlyArgLeu 291
Db 952 ATCACACTGGCCACCATTTGCTATGGACAGACACCCAAACGCTGGGAGGCGGCTGTG 1011
Qy 292 LeuSerAlaGlyPheAlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeu 311

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Db 1012 ATTGGCGCCACCTTTCTCTAATGGGTCTCTCTTTTGGCCCTCCAGGGGCGATCCTG 1071  
Qy 312 GlySerGlyPheAlaLeuLysValGlnGlnHisArgGlnLysHisPheGluLysArg 331  
Db 1072 GGGTCGGGGCTGGCCCTCAAGGTGAGGAGCAACACCGTTCAGAAAGCACTTTGAGAAAGG 1131  
Qy 332 ArgAsnProAlaAlaAsnLeuLeuGlnCysValTrpArgSerTrpAlaAlaAspGluLys 351  
Db 1132 AGGAAGCCAGCTGTGAGCTCATTCAGCTCCCTGGAGGTATTATGTACCAACCCCAAC 1191  
Qy 352 SerValSer---IleAlaThrTrpLysProHisLeuLysAlaLeuHisThrCysSerPro 370  
Db 1192 AGGATTGACCTGGTGGCGACATGGAGA---TTTATGAATCAGTCTCTTTTCTTCTTC 1248  
Qy 371 ThrLysLysGluGlnGlnGluAlaSerSerSerGlnLysLeuSerPheLysGluArgVal 390  
Db 1249 TTCAGGAAGAACAGCTGGAGGAGCATCCAGCCAAAGCTTCTCTGGATCGGGTT 1308  
Qy 391 ArgMetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAspArg 410  
Db 1309 CGCTTTCTAATCTCTGGTGGATGACTATAA-----GGAAAGCTA 1350  
Qy 411 ArgSerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSerTrp 430  
Db 1351 TTTACCCCTCTGAATGTAGATGCCATAGAAAGTCTCTTAAAGAACCAAGCCTGTT 1410  
Qy 431 SerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLys----- 445  
Db 1411 GGCTTAAACAATAAGAGCGTTTCGCGACGCTTCGCGATGAAAGCCTACGCTTTCTGG 1470  
Qy 446 --SerSerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspAspVal 464  
Db 1471 CAGAGTTCTGAA-----GATCCCGGACAGT-----GACCCCATG 1506  
Qy 465 TyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThrProLysLys 484  
Db 1507 GCGGAAGACAGGGGTATGGGAATGACTTCCCATCGAAGACATGATCCCGACCTGGAAG 1566  
Qy 485 ThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPheLysGlu 504  
Db 1567 GCGCCCATCCGAGCGGTGAGAAATCTCAATTCGCTCTTATAAATAAATAATCAAGGAG 1626  
Qy 505 ThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAsp 524  
Db 1627 ACTTTGAGGCTTACGATGTGAAGATGCTGATTGAGCAGTATTCTGCGGGCATCTCGAC 1686  
Qy 525 MetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGln 544  
Db 1687 ATGCTTTCCAGGATAAAGTACTCTTCAGACGAGAATAGATATGATTTTCCACCCCTGGACCT 1746  
Qy 545 IleThrSerAspLysSerArg----- 552  
Db 1747 CCTCCACGCCAAACACACAGAGTCTCAGAAAGGTCAGCATTCACCTTCCATCCCGAG 1806  
Qy 553 -----GluLysIleThrAlaGluHisGluThr-----AspAspLeu 565  
Db 1807 CAATCTCCAGGAATGAACATATGTAGCCAGACCATCCATCAGAAATCGAAGACCAA 1866  
Qy 566 SerMetLeuGlyArgValLysValGlnLysGlnValGlnSerIleGluSerLysLeu 585  
Db 1867 AGCATGTGGGAAGCTTTGTAAGTGTGAAGACAGGTTTCAGGACATGGGGAAGAAGCTG 1926  
Qy 586 AspCysLeuLeuAspIleTyrGlnGlnValLeuArg----- 597  
Db 1927 GACTTCTCTGGATATGCATGCACATGCACATGGAAACGGTTGCAGGTGCAGGTACGGAG 1986  
Qy 598 -----LysGlySerAlaSerAlaLeuAlaLeuAlaSerPheGlnIleProPro 613  
Db 1987 TATTACCAACCAAGGACCTCTCTG-----CCA 2016  
Qy 614 PheGluCysGluGlnThrSerAspTyrGlnSerProValAspSerLysAspLeuSerGly 633

Db 2017 GCTGAAGCAGAGAAGAAGGAGGAGCAACAGGTATTTC-----GATTTGAAAACCATCATCTGC 2073  
Qy 634 SerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIleSerArgGlyLeu 653  
Db 2074 AACTATTCTGAGACAGGCCCCCGGAACCACTTACAGCTTCCAC----- 2118  
Qy 654 GlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAlaLeuSerProThr 673  
Db 2119 -----CAGGTGACCATTTGACAAAGTCAGCCCTATGGGTTTTTGGCACATGACCTT--- 2169  
Qy 674 MetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySerAlaValAlaAla 693  
Db 2170 -----GTGAACCTGCCCGGAGGGGAGCCAGTCTCTGGAAGGTTTCAGGCA 2214  
Qy 694 ThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAlaProThrLeu 713  
Db 2215 ACT-----CCTCTTCTCAGCAACACGTATGTG 2244  
Qy 714 GlnIleProProLeuProAlaIleLysHisLeuProArgProGluThrLeuHisPro 733  
Db 2245 GAGAGGCCACCGTCTCTGCTTCTTCTGACTCTTCTGACTCCCGAGTGAGTGGCAC--- 2301  
Qy 734 AsnProAlaGlyLeuGlnGluSerIleSerAspValThrThrCysLeuValAlaSerLys 753  
Db 2302 TCCAGGCTGACCTGCGAGGCCCTCTACTCGGAC----- 2334  
Qy 754 GluAsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMetArgLysSerPhe 773  
Db 2335 ---CGAATCTCCCCCGGAG-----AGACGTAGCATC 2364  
Qy 774 AspMetGlyGlyGluThrLeuLeuSerValCysProMetValProLysAspLeuGlyLys 793  
Db 2365 ACGGACAGACGTGACACACCTCTGTCTCTG----- 2394  
Qy 794 SerLeuSerValGlnAsnLeuIleArgSerThrGluGluLeuAsnIleGlnLeuSerGly 813  
Db 2395 ---ATGTCGGTCAACCA-----GAGGAGCTGAGAGGTCTCCNAAGTGC 2436  
Qy 814 SerGluSerSerGlySerArgGlySerGlnAspPheTyrPro-----LysTrp 829  
Db 2437 TTCAGCATCTCCAGGACAGACAGATGATTATGTTCGGCCCCCAATGGGGTCCGAGCTGG 2496  
Qy 830 ArgGluSerLysLeuPheIleThrAspGluGluValGlyProGluGluThrGluThrAsp 849  
Db 2497 ATGAGGGAAGAAGCGGTACTCTCGCGAG-----GGTGAGACGGACACAGACCGGAC 2547  
Qy 850 ThrPhe 851  
Db 2548 CCCTTC 2553

RESULT 14  
US-09-177-650-90  
; Sequence 90, Application US/09177650  
; Patent No. 6413719  
; GENERAL INFORMATION:  
; APPLICANT: Leppert, Mark F.  
; APPLICANT: Singh, Nanda  
; APPLICANT: Charlier, Carole  
; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE  
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)  
; TITLE OF INVENTION: AND OTHER EPILEPSIES  
; FILE REFERENCE: 2323-134  
; CURRENT APPLICATION NUMBER: US/09/177,650  
; CURRENT FILING DATE: 1998-10-23  
; EARLIER APPLICATION NUMBER: 60/063,147  
; EARLIER FILING DATE: 1997-10-24  
; NUMBER OF SEQ ID NOS: 129  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 90  
; LENGTH: 2814  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:

; NAME/KEY: CDS  
; LOCATION: (202)..(2811)  
US-09-177-650-90

## Alignment Scores:

Pred. No.: 1,74e-150 Length: 2814  
Score: 1575.00 Matches: 387  
Percent Similarity: 55.48% Conservative: 114  
Best Local Similarity: 42.86% Mismatches: 243  
Query Match: 34.33% Indels: 160  
DB: 3 Gaps: 27

US-09-810-796-4 (1-897) x US-09-177-650-90 (1-2814)

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Db 340 GACCTGGAGCAA-----GTCACCTTGGCGCTAGGGCGCGGAGCGCAAGACGGG 390  
Qy 23 LeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeuArgGlu 42  
Db 391 ACCCTGTCTGTG-----GAGGGCGGTGGCGCGAAGAGGGG 426  
Qy 43 SerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLys---ProLeuSerTyr 61  
Db 427 CAGAGGAGGACCCCGCAGGGC-----ATCGGGCTCTCGCAAGACCCCTGAGCGGC 480  
Qy 62 ThrSerSerGlnSerCysArgAsnValLysTyrArgArgValGlnAsnTyrLeuTyr 81  
Db 481 CCAGTCAAG-----AGGAACAACGCCAAGTACAGCGCATCCAACTTTGATCTAT 531  
Qy 82 AsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeuLeu 101  
Db 532 GACGCCCTGGAGAGACCGCGGGCTGGCGGTCTCTACCAACGCGCTTGTCTCTGATT 591  
Qy 102 ValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeuAla 121  
Db 592 GTCTGGGATGCTGATTCGGCGTCTACCACTTCAAGGAATATGAGACTGTGTCT 651  
Qy 122 SerSerCysLeuLeuLeuGluPheValMetIleValAlaPheGlyLeuGluPheIle 141  
Db 652 GGAGACTGGCTTGTCTCGTGGAAACATTTGCTATTTTTCATCTTTGGAGCTGAGTTGCT 711  
Qy 142 IleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeuArg 161  
Db 712 TTGAGGATCTGGCTGCGAGGATGTGTCTGCGATACAAAGGCTGGCGTGGCGCTAAAG 771  
Qy 162 PheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAlaVal 181  
Db 772 TTTGCCAGGAAGCCCTGTGATGTGGACATCTTCGTACTGATGCTCTGTGCCAGTG 831  
Qy 182 ValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArgPhe 201  
Db 832 GTTGGCGTGGGAACACGAGCAATGCTTGTGGCCACCTCC---CTGGGAAGCTTCGCTTC 888  
Qy 202 LeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeuGly 221  
Db 889 CTGCAGATCTCGCGATCTTCGATGTGATAGGAGGGGTGGCCACCTGCGAAGCTCTCGGGC 948  
Qy 222 SerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeuVal 241  
Db 949 TCGGCTATCTGTGCCCAAGCAAGAACTCATCTGCTGCTGATAGGCTTCTTGACA 1008  
Qy 242 LeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAla----- 256  
Db 1009 CTCATCTCTTCTTCTTCTTCTGCTACCTGGTGAGAGGATGTGCCAGAAATGGATGCC 1068  
Qy 257 -----AsnLysGluPheSerThrTyrAlaAspAlaLeuTrpTrpGlyThr 271  
Db 1069 CAAGGAGAGGAGATGAAGGAGGAGTTTGAGACCTATGAGATGCTCTGTGTGGGGCGCTG 1128  
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Qy 292 LeuSerAlaGlyPheAlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeu 311  
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Db 1369 AGGTGGATCTGTGTGGCAACCTCGAGATCTTAT---GAATCAGTTGTCTCTTCCCATTC 1425  
Qy 371 ThrLysLysGlnGlnGlyAlaSerSerSerClnLysLeuSerPheLysGluArgVal 390  
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Qy 411 ArgSerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSerTrp 430  
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Db 1924 CCATCCACTCCAAACATAAAGAGTCTCAGAAAGGAGGACGAGCATTTACCTACCCATCCAG 1983  
Qy 557 -----AlaGluHisGluThrThrAspAspLeu 565  
Db 1984 CAGTCTCCAGGAATGAACCATATGTAGCCAGGCGAGCCACCATCAGAAACTGAAGACCA 2043  
Qy 566 SerMetLeuGlyArgValValLysValGluLysGlnValGlnSerIleGluSerLysLeu 585  
Db 2044 AGCATGATGGGAAGTTTGTAAAGTTGAAAGACAGAGTTTATGATGATGATGATGATGATG 2103  
Qy 586 AspCysLeuLeuAspIleTyrGlnGlnValLeuArg----- 597  
Db 2104 GACTTCCTGGGACATGTCATATGTCATATGAGCAAGCTTACAGGTACATGTGCTACCTGAG 2163  
Qy 598 -----LysGlySerAlaSerAlaLeuAlaLeuAlaSerPheGlnIleProPro 613  
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Qy 633 ySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIleSerArgGlyLe 653
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Qy 653 uGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAlaLeuSerProTh 673
Db 2311 AGAGTTGGCCCTTACGGG-----TTTTTGGACATGATCCT-- 2346
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Db 2347 -----GTGAACCTGACCGAGGGGACCCAGCTTCTACAAAGGC 2384
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; Sequence No. 5, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blumar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNO POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; FILE REFERENCE: 3053-4052
; CURRENT APPLICATION NUMBER: US/09/105.058C
; PRIOR FILING DATE: 1998-06-26
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
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; LENGTH: 900
; TYPE: DNA
; ORGANISM: mouse
; FEATURE:
; OTHER INFORMATION: 900 nucleotides of murine KCNQ2
US-09-105-058C-5

Alignment Scores:
Pred. No.: 1,08e-113 Length: 900
Score: 1207.50 Matches: 227
Percent Similarity: 83.88% Conservative: 28
Best Local Similarity: 74.67% Mismatches: 40
Query Match: 26.32% Indels: 9
DB: 3 Gaps: 2

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Qy 76 ValGlnAsnTyrLeuTyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHis 95
Db 49 CTGCAGAAATTCCTCTCAACAGCTAGAGCGGCCCGCGCTGGCGTTCATCTACCAC 108
Qy 96 AlaPheValPheLeuValPheGlyCysLeuIleLeuSerValPheSerThrIlePro 115
Db 109 GCCTACGTTGTTCTTTAGTCTTCTCTGCTTCTTCTGTTTTCACCATCAAG 168
Qy 116 GluHisThrLysLeuAlaSerSerCysLeuLeuIleLeuGluPheValMetIleValVal 135
Db 169 GAGTACGAGAAGAGCTCTGAGGGGGCCCTCTACATCTTGGAAATCGTACTATCGTGTA 228
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Qy 236 TyrIleGlyPheLeuValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAsp 255
Db 529 TACATTGGCTTCCTCTGCTCATCTCCCTGCTCATTTCTGGTGTACTTTGGCAGAAAAGGT 588
Qy 256 AlaAsnLysGluPheSerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThr 275
Db 589 GAGNATGACCATTTGACACCTACGAGATGCACTCTGTGGGTCTGATCACCTGACG 648
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Qy 336 AlaAsnLeuIleGlnCysValTyrArgSerTyrAlaAlaAspGluLysSerValSerIle 355  
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Qy 356 ---AlaThrTyr 358  
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Job time : 407.267 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 3, 2005, 06:10:16 ; Search time 9703.68 Seconds  
(without alignments)  
4479.159 Million cell updates/sec

Title: US-09-810-796-4

Perfect score: 4588

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database :

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3: gb.in.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.scs.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	4588	100.0	2694	6 AX322509	AX322509 Sequence
2	4588	100.0	3137	6 AR430568	AR430568 Sequence
3	4588	100.0	3137	6 AX056817	AX056817 Sequence
4	4588	100.0	3137	9 AF202977	AF202977 Homo sapi

5	4574	99.7	3074	6 AR393778	AR393778 Sequence
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7	4574	99.7	3074	6 AX456864	AX456864 Sequence
8	4574	99.7	3074	9 AF249278	AF249278 Homo sapi
9	4527.5	98.7	2772	6 AR565635	AR565635 Sequence
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11	4527.5	98.7	3111	6 AR565636	AR565636 Sequence
12	4527.5	98.7	3111	6 AX268476	AX268476 Sequence
13	4407	96.1	3718	6 BD275572	BD275572 Homo sapi
14	4389	95.7	2832	9 AF263835	AF263835 Homo sapi
15	4288	93.5	3108	10 AF263836	AF263836 Mus muscu
16	2613	57.0	1552	6 CO720576	CO720576 Sequence
17	2012	43.9	2335	6 AX032994	AX032994 Sequence
18	2012	43.9	2335	6 AX456863	AX456863 Sequence
19	2012	43.9	2335	9 AF105202	AF105202 Homo sapi
20	1971	43.0	1508	9 BC050689	BC050689 Homo sapi
21	1832.5	39.9	4165	10 AF087453	AF087453 Rattus no
22	1819.5	39.7	7420	9 HSKCNQ2	Y15065 Homo sapien
23	1815	39.6	2613	10 AF490773	AF490773 Mus muscu
24	1813	39.5	2169	6 AR213255	AR213255 Sequence
25	1813	39.5	2169	6 BD074166	BD074166 KCNQ pota
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32	1805	39.3	3287	6 AR213254	AR213254 Sequence
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35	1800.5	39.2	3232	6 BD086323	BD086323 KCNQ2 and
36	1792.5	39.1	3232	9 AF033348	AF033348 Homo sapi
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45	1749	38.1	2899	10 AB000496	AB000496 Mus muscu

#### ALIGNMENTS

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LOCUS AX322509 2694 bp linear PAT 07-JAN-2002  
DEFINITION Sequence 1 from Patent WO0192526.  
ACCESSION AX322509  
VERSION AX322509.1 GI:18093555  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
Dworetzky,S.I., Ramanathan,C.S., Trojnecki,J.T., Boissard,C.G. and Gribkoff,V.K.  
Human kcnq5 potassium channel, methods and compositions thereof  
Patent: WO 0192526-A 1 06-DEC-2001;  
Bristol-Myers Squibb Company (US)  
LOCATION/Qualifiers  
1. .2694  
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Score: 4588.00 Matches: 897  
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
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QY	21	AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu	40
DB	61	GACGCCCTGCTACTCTGGCAGCCCGCGGCCACGCTTGTGTGGCGGGGGTGGCTG	120
QY	41	ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer	60
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QY	301	IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln	320
DB	901	ATTTCTTTTGTGACCTTCTCTGGCGGCAATTTCTGGCTCAGGTTTGTCAATTAAGTAC	960
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Qy 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro 720
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Qy 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800
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RESULT 2
LOCUS AR430568 3137 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6649371.
ACCESSION AR430568
VERSION AR430568.1 GI:40191384
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3137)
AUTHORS Jentsch,T.J.
TITLE Potassium channel KCNQ5 and sequences encoding the same
JOURNAL Patent: US 6649371-A 1 18-NOV-2003;
FEATURES
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ORIGIN

Alignment Scores:
Pred. No.: 2,766-298 Length: 3137
Score: 4588.00 Matches: 897
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-810-796-4 (1-897) x AR430568 (1-3137)

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REFERENCE 1  
AUTHORS Jentsch, T.J.  
TITLE Novel potassium channels and genes encoding these potassium  
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Patent: WO 0077035-A 1 21-DEC-2000;  
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## ORIGIN

## Alignment Scores:

Pred. No.: 2,766-298 Length: 3137  
Score: 4588.00 Matches: 897  
Percent Similarity: 100.00% Conservative: 0  
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DB: 6 Gaps: 0

US-09-810-796-4 (1-897) x AX056817 (1-3137)

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ORIGIN			
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Score:		4588.00 Matches: 897	
Percent Similarity:		100.00% Conservative: 0	
Best Local Similarity:		100.00% Mismatches: 0	
Query Match:		100.00% Indels: 0	
DB:		9 Gaps: 0	
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Db	601	TTTCTACAGATCCTCCGATGTCGATGGACCGAAGGGAGGCACCTTGGAATTTACTG	660	Db	1681	ACCACAGACGATCTCAGTATGCTCGTCGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC	1740
Qy	221	GlySerValValTyraHisSerLysGluLeuIleThrAlaTrpTyIleGlyPheLeu	240	Qy	581	IleGluSerLysLeuAspCysLeuLeuAspIleTyGlnGlnValLeuArgLysGlySer	600
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Qy	301	IleSerPheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln	320	Qy	661	GluPheSerAlaGlnThrPheTyraLeuSerProThrMetHisSerGlnAlaThrGln	680
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REFERENCE
1
Lerche,C., Scherer,C., Seeborn,G., Busch,A. and Steinmeyer,K.
Potassium channel protein kmq5, a target for diseases of central
nervous system and cardiovascular system
Patent: WO 0170811-A 1 27-SEP-2001;
Aventis Pharma Deutschland GmbH (DE)
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REFERENCE

AUTHORS Argentero, T.M. and Sheldon, J.H.  
TITLE Methods of selecting compounds for modulation of bladder function  
JOURNAL Patent: WO 0232960-A 5 25-APR-2002;  
Wyeth (US)

FEATURES

source

Location/Qualifiers

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Db 575 GCCTCAAGTTGCCTCTGATCTGGAGTTCGTGATGATGTCTGCTTTGGTTGGAGTTC 634  
Qy 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160  
Db 635 ATCATTCGAATCTGTCTGCGGGTTCGTTGTGATATAGAGATGCAAGGAGAGACTG 694  
Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180  
Db 695 AGGTTTGCTCGAAAGCCCTCTCTGTGTATATAGATACCATTTCTTATCGCTTCAATAGCA 754  
Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200  
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Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220  
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Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320  
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Qy 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360  
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Qy 381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400  
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Qy 561 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 580  
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Qy 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620



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Db 515 CTTGCTTTGGTTGCTTGAATTTGTCAAGTGTCTTCTACCATCCCTGAGCACAAAATTG 574  
Qy 121 AlaSerSerCysLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe 140  
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Db 2015 GCCTCAGCCCTCGCTTTTGGCTTCATTCAGATCCCACTTTTGAATGTGAACAGACATCT 2074  
Qy 621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640  
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Qy 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780  
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QY	821	GlySerGlnAspPheTyrProLysTyrArgGluSerLysLeuPheIleThrAspGluGlu	840	Db	466	GCCTCAAGTTGCTTGTGATCTCTGGAGTTCGTGATGATGATGCTGCTTTGTTGTTGGAGTTC	525
Db	2675	GGCAGCCAGATTTTACCCCAATGAGGGAATCCAAATGTTTATTAACATGATGAAGAG	2734	QY	141	IleIleAraGlleTyrSerAlaGlyCysCysCysArgTyrArgGlyTyrGlnGlyArgLeu	160
QY	841	ValGlyProGluGluThrGluThrAspThrPheAspAlaProGlnProAlaAraGlu	860	Db	526	ATCATTCGAATCTGGTTCGGGGTGTCTGTGTGATATAGAGATGGCAAGAGACTG	585
Db	2735	GTGGGTCCGGAAGACAGACAGACACATTTTGTATCCGACCGCAGCTGCGAGGAA	2794	QY	161	ArgPheAlaAraGlyLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla	180
QY	861	AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys	880	Db	586	AGGTTTGTCTGAAAGCCCTTCTGTGTATAGATACCATTTGTTTATTCGCTTCAATAGCA	645
Db	2795	GCTGCTTTGCATCAGATCTCTTAAGACTGGAAGGTTCAGATCATCTCAGACATTTGT	2854	QY	181	ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg	200
QY	881	LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLysLeu	897	Db	646	GTGTGTTTCTGCAAAACTCAGGGTAATATTTTGCACGTCTGCACCTCAGAAGTCTCCGT	705
Db	2855	AGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAA	2905	QY	201	PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu	220
Db	2855	AGGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAA	2905	Db	706	TTCTTACAGATCTCCGATGCTGTCATGTCGGAAGGATGCCAATAAAGAGTTT	765
RESULT 9					221	GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaThrTyrIleGlyPheLeu	240
LOCUS	AR565635	2772 bp	DNA	linear	766	GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTATAGGATTTTGT	825
DEFINITION	Sequence 1 from patent US 6767736.				241	ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe	260
ACCESSION	AR565635				826	GTTCCTTATTTTTCGTCCTTCTGTCATCTGTCGGAAGGATGCCAATAAAGAGTTT	885
VERSION	AR565635.1	GI:53981668			261	SerThrTyrAlaAspAlaLeuTrpGlyThrIleThrLeuThrThrIleGlyTyrGly	280
KEYWORDS	Unknown.				886	TCTACATATGCAGATGCTCTCTGGTGGGCAACAATTAATGACAACTATTGGCTATGGA	945
ORGANISM	Unknown.				281	AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly	300
REFERENCE	1 (bases 1 to 2772)				946	GACAAACTCCCTTAACTTGGCTGGGAAGATTCCTTCTGAGGCTTTCGACTCTCTTGGC	1005
AUTHORS	Hu, Y., Kieke, J.A., Turner, C.A. Jr., Nehls, M.C., Friedrich, G.,				301	IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln	320
TITLE	Zamrowicz, B. and Sands, A.T.				1006	ATTTCCTTCTTTCGACTCTCTGCGGCACTTCTTGGCTCAGGTTTTCATTAAGAGTACAA	1065
JOURNAL	Human ion channel protein and polynucleotides encoding the same				321	GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln	340
FEATURES	Patent: US 6767736-A 1 27-JUL-2004;				1066	GAACAACACCGCCAGAAACACTTTGAGAAAGAGAACCCAGCTCCCAACTCATTCAG	1125
FEATURES	Location/Qualifiers				341	CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro	360
source	1. .2772				1126	TGTGTTTGGGTAGTTACGACGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA	1185
ORIGIN	/organism="unknown"				361	HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyAlaSerSer	380
Alignment Scores:	2.67e-294	Length:	2772		1186	CACTTGAAGGCTTGCACACTGCGAGCCCTTACC	1218
Pred. No.:	4527.50	Matches:	887		381	SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle	400
Score:	99.00%	Conservative:	1		1219	AATCAGAAAGCTTAAAGGCTTTAAGGACGAGTGGCATGCTAGCCAGGCGCCAGAGTATT	1278
Percent Similarity:	99.00%	Mismatches:	0		401	LysSerArgGlnAlaSerValGlyAspArgSerProSerThrAspIleThrAlaGlu	420
Best Local Similarity:	98.89%	Indels:	9		1279	ARGAGCCGACAGCCTCAGTAGGTGACAGGAGGTCCCAAGCACCAGCATCACAGCCGAG	1338
Query Match:	98.68%	Gaps:	1		421	GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro	440
DB:	6				1339	GGCAGTCCACCAAGTGCAGAAAGCTGGAGCTTCAACGACCCGAAACCCGCTTCGGGCC	1398
US-09-810-796-4 (1-897) x AR565635 (1-2772)					441	SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly	460
QY	1	MetLysAspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaAraGly	20	QY	1399	TGCTTGGCCCTCAAAAGTTCTCAGCCAAAACCAAGTATAGTATGCTGACACAGCCCTTGGC	1458
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QY	21	AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu	40	QY	1459	ACTGATGATGATATGATGAAAAAGGATGCCAGTGTGATGATCATGCTGGAAGACTCACC	1518
Db	166	GACGGCTGTACTGTCTGGGACCCGCGGCGCACGCTCGGTGGCGGCGGTGGCCTG	225	QY	481	ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg	500
QY	41	ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer	60	QY	1519	CCACCACCTTAAACCTGCTCATTCGACCTATCAGAAATTTGAAATTTTCATGTTTGCAAAACGG	1578
Db	226	AGGAGAGCCCGCGGCGCAGCAGGCGCGCGATGAGCCTGCTGGGGAAGCGCTCTCT	285				
QY	61	TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu	80				
Db	286	TACACGATAGCAGAGTCGCGCGCAACGTCGAAGTACCGCGGGGTGCAGAACTACCTG	345				
QY	81	TyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu	100				
Db	346	TACAACTGCTGGAGACCCCGCGGTGGCGGTTCATCTACCACTGCTTCTGTTTCTC	405				
QY	101	LeuValPheGlyCysLeuLeuSerValPheSerThrIleProGluHisThrLysLeu	120				
Db	406	CTTGCTTTGGTTGCTTGTATTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	465				
QY	121	AlaSerSerCysLeuLeuLeuLeuPheValMetIleValValPheGlyLeuGluPhe	140				



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Db 2719 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAA 2769
RESULT 10
AX268474 2772 bp DNA linear PAT 29-OCT-2001
LOCUS AX268474
DEFINITION Sequence 1 from Patent WO0175108.
ACCESSION AX268474
VERSION AX268474.1 GI:16541652
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Hu, Y., Kiecke, J. A., Turner, A. C., Nehls, M. C., Friedrich, G. B.,
Zambrowicz, B. A. and Sands, A. T.
TITLE Human ion channel protein and polynucleotides encoding the same
JOURNAL Patent: WO 0175108-A 1 11-OCT-2001;
Lexicon Genetics Incorporated (US)
FEATURES
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1. .2772
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Score: 4527.50 Matches: 887
Percent Similarity: 99.00% Conservative: 1
Best Local Similarity: 98.89% Mismatches: 0
Query Match: 98.88% Indels: 9
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ACCESSION AR565636  
VERSION AR565636.1 GI:53981669  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 3111)  
AUTHORS Hu,Y., Kieke,J.A., Turner,C.A. Jr., Nehis,M.C., Friedrich,G.,  
Zambrowicz,B. and Sands,A.T.  
TITLE Human ion channel protein and polynucleotides encoding the same  
JOURNAL Patent: US 6767736-A 3 27-JUL-2004;  
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QY	601	AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProPheGluCysGluGlnThrSer	620
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QY	621	AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAenSerGlyCys	640
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DEFINITION	Sequence 3 from Patent WO0175108.		
ACCESSION	AX268476		

VERSION	AX268476.1	GI:16541653
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Hu, Y., Kieke, J.A., Turner, A.C., Nehls, M.C., Friedrich, G.B., Zambrowicz, B. and Sands, A.T. Human ion channel protein and polynucleotides encoding the same Patent: WO 0175108-A 3 11-OCT-2001; Lexicon Genetics Incorporated (US) Location/Qualifiers 1. 3111 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	
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JOURNAL		
FEATURES		
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ORIGIN		
Alignment Scores:	3.16e-294	Length: 3111
Pred. No.:	4527.50	Matches: 887
Score:	99.00%	Conservative: 1
Percent Similarity:	98.89%	Mismatches: 0
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Db	525	GCTCAAGTTCCTTGTGATCCTCGAGTTCGTGATGATTCGTCTTTCGTTTGGAGTTC 584
QY	141	IleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu 160
Db	585	ATCATTCGAATCTGTCTGCGGGTTCCTGTTGTTCATATAGAGGATGCGAAGGAACTG 644
QY	161	ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db	645	AGGTTTGTTCGAAAGCCCTTCGTGTTATAGATACCATTTGTTCTTATCGCTTCAATAGCA 704
QY	181	ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db	705	GTTGTTTCTGCAAAACACTCAGGGTAATATTTTTCACAGCTCTGCACTCAGAGTCTCGT 764
QY	201	PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrThrLysLeuLeu 220
Db	765	TTCTACAGATCTCTCGCATGCTGGCATGGTGGCATGGACCGAGGGGAGGCACCTTGGAAATTA 824

QY 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240  
DB 825 GGTTCAGTGGTTTATGCTTCACAGCAAGAAATTAATCACAGCTGTGTCATAGGATTTTGT 884  
QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260  
DB 885 GTTCTTAATTTTTCGTCCTTCTGTCATCTGGTGGAAAGGATGCAATAAAGAGTTT 944  
QY 261 SerThrTyrAlaAspAlaLeuTrpGlyThrIleThrLeuThrIleGlyTyrGly 280  
DB 945 TCTACATATGCAGATGCTCTCTGGTGGGCAACATTAATTCACAACTATTGGCTATGGA 1004  
QY 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300  
DB 1005 GACAAACTCCCTTAACCTGGCTGGGAAGATTGCTTCTGCAGGCTTTGCACCTCCCTGGC 1064  
QY 301 IleSerPheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320  
DB 1065 ATTTCCTTTCTTGCACTTCTCGCCGCAATCTTGCTCAGGTTTGGCAATTAAGATGCA 1124  
QY 321 GluGlnHisArgGlnLysPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340  
DB 1125 GAACAACACCCAGCAACACTTTGAGAAAGAGAACCCAGCTGCCCACTCATTCAG 1184  
QY 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360  
DB 1185 TGTGTTTGGCGTAGTTACGAGCTGATGAGAAATCTGTTTCATTTGCAACCTGGAAGCCA 1244  
QY 361 HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyAlaSerSer 380  
DB 1245 CACTTGAAGGCTTGCACACCTGCGCCCTACC----- 1277  
QY 381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400  
DB 1278 AATCAGAGCTAAGTTTAAAGAGCGAGTGGCGATGGCTAGCCCGAGGGCCAGAGTATT 1337  
QY 401 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 420  
DB 1338 AAGAGCCGACAAAGCCTCAGTAGTGACAGAGGTCCTCCCAAGCAGCAGATCACAGCCGAG 1397  
QY 421 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgTrpArgPheArgPro 440  
DB 1398 GCGAGTCCCAACCAAGTCAGAAAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1457  
QY 441 SerLeuArgLeuLysSerSextGlnProLysProValIleAspAlaAspThrAlaLeuGly 460  
DB 1458 TCGCTGCGCCTCAAAAGTTCTCAGCCAAACAGTGATAGATGCTGACACAGCCCTTGGC 1517  
QY 461 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480  
DB 1518 ACTGATGATGATATGATGAAAGGATGCCAGTGTGATGATCATCAGTGAAGACCTCACC 1577  
QY 481 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 500  
DB 1578 CCACACCTTAAACACTGTCATTCGAGCTATCAGAAATTAAGAAATTTGATGTCGCAAAACGG 1637  
QY 501 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 520  
DB 1638 AAGTTTAAGGAAACATTACGTCATATGATGTAAAGATGTCATTGAACAATATTCGCT 1697  
QY 521 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540  
DB 1698 GGTCACTCGGACATGTTGTTAGAAATTAAGAGCCTTCAAAACGCTGTTGATCAAAATTCCT 1757  
QY 541 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560  
DB 1758 GGAAAGGCGCAATCACATCAGATGAAGAGAGCCGAGAGAAATAACAGCAGAAATCAG 1817  
QY 561 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 580  
DB 1818 ACCACAGAGCATCTCAGTATGCTCGGTGGGTGGTCAAGGTTGAAGAAACAGGTACAGTCC 1877  
QY 581 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 600

DB 1878 ATAGAATCCAAAGCTGGACTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAGAGCTCT 1937  
QY 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620  
DB 1938 GCCTCAGCCCTCGTGTGGCTTCATTCAGATCCCACTTTGAATGTGAACAGACATCT 1997  
QY 621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640  
DB 1998 GACTATCAAGCCCTGTGGATAGCAAGATCTTTCCGGTTCGCAACAAACAGTGGCTGC 2057  
QY 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660  
DB 2058 TTATCCAGATCAACTAGTGCCAAATCTCGAGAGGCTTCAGAGTTCATTTCTCAGCCCAAT 2117  
QY 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680  
DB 2118 GAGTTCAGTGCCAGACTTTCTACGCGCTTAGCCCTACTATGCAGTCAAGCAACACAG 2177  
QY 681 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 700  
DB 2178 GTGCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGCAGCCACCAACCATTTGCAAAACCA 2237  
QY 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro 720  
DB 2238 ATAAATACGGCACCAAGCCAGCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA 2297  
QY 721 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740  
DB 2298 GCCATCAAGCATCTGCCAGGCCCAAACTCTGCACCTTAACCTTGAGGCTTACAGGA 2357  
QY 741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760  
DB 2358 AGCATTTCTGACGTCACCACTGCTGTTGCCCTCCAAGGAAATGTTTTCAGGTTGCACAG 2417  
QY 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780  
DB 2418 TCNAATCTCAACAGGACCGTTCTATGAGGAAAGCTTTTGACATGGGAGGAGAACTCTG 2477  
QY 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800  
DB 2478 TTGTCTGCTGTCCTCCATGGTCCGAGGACTTGGCAAAATCTTTGCTGTGCAAAACCTG 2537  
QY 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 820  
DB 2538 ATCAGGTCCAGCCAGGAACTGAATATACAACCTTTTCCAGGAGTGAGTCAAGTGGCTCCAG 2597  
QY 821 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840  
DB 2598 GGCAGCCAAAGATTTTACCCTCAATGGAGGAAATCCAAATTTGTTTAACTGATGAAGAG 2657  
QY 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 860  
DB 2658 GTGGGTCCGAGAGAGACAGACAGACACTTTTGTGCGCAGCCAGCAGCTTCCAGGGA 2717  
QY 861 AlalaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 880  
DB 2718 GCTGCTTTGCATCAGACTCTTAAGGACTGGAAGTCAAGTCAATCATCTCAGAGCATTTGT 2777  
QY 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897  
DB 2778 AAGCAGGAGAAAGTACAGATGCCCTCAGTTCGCTCATGTCAAACTGAAA 2828

RESULT 13

BD275572 3718 bp DNA linear PAT 17-JUL-2003  
LOCUS BD275572

DEFINITION Novel Human Voltage-Gated Potassium Channel.

ACCESSION BD275572

VERSION BD275572.1 GI:33085340

KEYWORDS JP 2002543768-A/2.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

[illegible]

QY	617	GluGlnThrSerAspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGln	636
Db	1833	GAACAGACATCTGACTATCAAAAGCCCTGTGGATAGCAAAAGATCTTTCCGGTTCCGCACAA	1892
QY	637	AnSerGlyCysLeuSerArgSerThrSerAlaAanlleSerArgGlyLeuGlnPheIle	656
Db	1893	AAACGTGGCTGCTTATCCAGATCAACTAGTGCACATCTCAGAGGCTCGAGTTCATT	1952
QY	657	LeuThrProAsnGluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMethIser	676
Db	1953	CTGACGCCAAATGAGTTCAGTGCCCGAGACTTTCTACGCGCTTAGCCCTACTATGCACAGT	2012
QY	677	GlnAlaThrGlnValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThr	696
Db	2013	CAAGCAACACACAGGTGCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACC	2072
QY	697	IleAlaAnGlnIleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIlePro	716
Db	2073	ATTGCAAAACCAANTANATAGCGCACCCAGCCAGCCAGCCCAACAACTTTACAGATCCCA	2132
QY	717	ProProLeuProAlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAla	736
Db	2133	CTCTCTCTCCAGCCATCAAGCATCTGCCAGCCAGAAACTCTGCACCCCTAACCCCTGCA	2192
QY	737	GlyLeuGlnGluSerIleSerAspValThrThrCysLeuValAlaSerIysGluAsnVal	756
Db	2193	GGCTTACAGGAAGCATTTCTGACGTCAACCTCCCTCTGTTGGCTTCCAGGAAATGTT	2252
QY	757	GlnValAlaGlnSerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGly	776
Db	2253	CAGTTGCACAGTCAAAATCTCACCAGGACCGTTCTATGAGGAAGCTTTGACATGGGA	2312
QY	777	GlyGluThrLeuLeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSer	796
Db	2313	GGAGAACTCTGTTGTTCTGTCTGTCTGCCATGGTGGCCGAGGACTTGGGCAATCTTTGTCT	2372
QY	797	ValGlnAsnLeuIleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSer	816
Db	2373	GTGCAAAACCTGATCAGGTGCGACCCAGGAACCTGAATATACAACTTTCAGGAGTGAATCA	2432
QY	817	SerGlySerArgGlySerGlnAspPheTyrProLysTyrArgGluSerLysLeuPheIle	836
Db	2433	AGTGCTTCAGAGGAGCCAGATTTTACCCCAATGAGGGAATCCAAATGTTTATA	2492
QY	837	ThrAspGluGluValGlyProGluThrGluThrAspThrPheAspAlaAlaProGln	856
Db	2493	ACTGATGAAGAGGTGGTCCCGAAGAGACAGACAGACACTTTTGTATGTCGCCACCGCAG	2552
QY	857	ProAlaArgGluAlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSer	876
Db	2553	CCTGCCAGGGAAGCTGCCTTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCT	2612
QY	877	GlnSerIleCysLysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeu	896
Db	2613	CAGACATTTGTAGGAGGAGGAGAAAGTACAGATGCCCTCAGCTTCCCTCATGTCAAACTG	2672
QY	897	Lys 897	
Db	2673	AAA 2675	
RESULT 14			
AF263835			
LOCUS			
DEFINITION	Homo sapiens voltage-gated potassium channel KCNQ5 (KCNQ5) mRNA,	2832 bp	PRI 01-JUN-2000
ACCESSION	AF263835		
VERSION	AF263835.1	GI:81322996	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		

REFERENCE	1	(bases 1 to 2832)	
AUTHORS		Kniazeva,M. and Han,M.	
TITLE		A new gene of the voltage-gated potassium channel KCNQ family, KCNQ5, is a candidate gene for retinal disorders	
JOURNAL		Unpublished	
REFERENCE	2	(bases 1 to 2832)	
AUTHORS		Kniazeva,M. and Han,M.	
TITLE		Direct Submission	
JOURNAL		Porter Biosciences Bldg., Boulder, CO 80309, USA	
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		/tissue_type="brain; retina"	
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CDS	<1..2586	/gene="KCNQ5"	
		/note="member of the KCNQ family"	
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ORIGIN			
Alignment Scores:			
Pred. No.:	5,53e-285	Length:	2832
Score:	4389.00	Matches:	856
Percent Similarity:	99.65%	Conservative:	2
Best Local Similarity:	99.42%	Mismatches:	3
Query Match:	95.66%	Indels:	0
DB:	9	Gaps:	0
US-09-810-796-4 (1-897) x AF263835 (1-2832)			
QY	37	GlyGlyLeuArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGly	56
Db	1	GGCGGTGGCTTGAGGAGAGCGCGCGGCGAAGCAGCGGCGCGCGATGAGCCTGCTGGGG	60
QY	57	LysProLeuSerTyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgVal	76
Db	61	AAGCGCTCTCTTACACGAGTAGCAGAGCTGCGCGCGCAACGTCAGTACGCGCGGTG	120
QY	77	GlnAsnTyrLeuTyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAla	96
Db	121	CAGAACTACCTGTACACGCTGCTGAGAGAGACCCCGCGCGCTTTCATCCACACGCT	180
QY	97	PheValPheLeuLeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlu	116
Db	181	TTCTGTTTCTCTCTGCTTTGCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	240
QY	117	HisThrLysLeuAlaSerSerCysLeuLeuIleLeuGluPheValMetIleValPhe	136



Db 241 CACACAAAATTGGCCTCAAGTTGCCTCTTGATCCTGGAGTTCGTGATGATGTCGTCTTT 300  
 Qy 137 GlyLeuGluPheIleIleAglIleTrpSerAlaGlyCysCysArgTyrArgGlyTyr 156  
 Db 301 GGTGGAGTTTCATCATCTCGAATCTGGTCTCGCGGTTGCTGTGTGATATAGAGATGG 360  
 Qy 157 GlnGlyArgLeuAArgPheAlaAArgLysProPheCysValIleAspThrIleValLeuIle 176  
 Db 361 CAAGGAAGACTGAGGTTTGCTCGAAGGCCCTTTTGTGTATAGATACCAATGTTCTTATC 420  
 Qy 177 AlaSerIleAlaValSerAlaIlyThrGlnGlyAsnIlePheAlaThrSerAlaLeu 196  
 Db 421 GCTTCAATAGCAGTGTGTTCTGCAAAACTCAGGGTAATATTTTGGCAGCTCTGCACTC 480  
 Qy 197 ArgSerLeuAArgPheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThr 216  
 Db 481 AGAAGTCTCCGTTTCTACAGATCTCCGCATGGTGGCATGGAGCGGAGGCAC 540  
 Qy 217 TrpLysLeuLeuGlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyr 236  
 Db 541 TGGAAATTAATCTGGGTTCAAGTGTGTATGCTCACAGCAAGGAATTAATCACAGCTTGTGAC 600  
 Qy 237 IleGlyPheLeuValIlePheSerSerPheLeuValTyrLeuValGluLysAspAla 256  
 Db 601 ATAGGATTTTGGTCTTATTTTTCGTTCTTCTTCTGTTCTATCTGGTGGAAAGATGCC 660  
 Qy 257 AsnLysGluPheSerThrTyrAlaAspAlaLeuTrpIleThrIleThrLeuThr 276  
 Db 661 NATAAAGATTTTCTACATATGATGATGCTCTCTGGTGGGCACAAATTAATACATTTGACAACT 720  
 Qy 277 IleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPhe 296  
 Db 721 ATTGGCTATGGAGACAAACTCCCTTAACCTGGCTGGGAAGATTGCTTTCTGAGGCTTT 780  
 Qy 297 AlaLeuLeuGlyIleSerPheAlaLeuProAlaGlyIleLeuGlySerGlyPheAla 316  
 Db 781 GCACCTCTTGGCATTTCTTCTTCTGACATCTCTGCGGCATTTCTGGCTCAGGTTTTCGA 840  
 Qy 317 LeuLysValGlnGluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAla 336  
 Db 841 TTAAGAGTACAAGAACACACCGCCAGAACACTTTTGAAAGAAAGAAAGAACCCAGCTGCC 900  
 Qy 337 AsnLeuIleGlnCysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAla 356  
 Db 901 AACCTATTCACTGTGTGTGGCTAGTTACGCGAGCTGATGAGAAATCTGTTCCATTGCA 960  
 Qy 357 ThrTrpLysProHisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGly 376  
 Db 961 ACCTGGAAGCCACACTTGAAGGCTTTGCACACCTGCGAGCCCTTACCAGAAAGAACCAAGGG 1020  
 Qy 377 GluAlaSerSerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArg 396  
 Db 1021 GAAGCATCAAGCAGTCAAGAGCTAAGTTTAAAGAGCGAGTGGCATGGCTAGGCCAGG 1080  
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 Db 1141 ATCACCCGAGGCGCTCCACCAAGTGCAGAAAGCTGGAGCTTCAACGACCCGAC 1200  
 Qy 437 ArgPheArgProSerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAsp 456  
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 Qy 457 ThrAlaLeuGlyThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerVal 476  
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 Qy 477 GluAspLeuThrProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHis 496  
 Db 1321 GAAGACCTCACCCACCACTTAAACCTGATTCAGCTATCAGATTAATGAAATTTTCAT 1380

Qy 497 ValAlaLysArgLysPheLysGluThrLeuArgProTyrAspValLysAspValIleGlu 516  
 Db 1381 GTTGCAAAACGGAAGTTTAAAGAAACATTAGCTCATATGATGTAAAGATGTCATTGAA 1440  
 Qy 517 GlnTyrSerAlaGlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgVal 536  
 Db 1441 CAATATCTCTGCTGCTCACTCGACATGTTGTAGATTTAAAGCCTTCAACACAGTGT 1500  
 Qy 537 AspGlnIleLeuGlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThr 556  
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 Db 1561 GCAGAAATGACAGACACAGACGATCTCATGATGCTCGGTGCTCAAGGTTGAAAAA 1620  
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 Db 1621 CAGGTACATGCTCATAGATCCAAAGCTGACTGCTACTAGACATCTATCAACAGGCTCTT 1680  
 Qy 597 ArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCys 616  
 Db 1681 CGAAAGGCTCTGCTCTCAGCCCTCGCTTGGCTTCAATCCAGATCCACCTTTTGAATGT 1740  
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 Db 1741 GAACACATCTGACTATCAAAAGCCTGTGGATAGCAAAAGATCTTTTCGGGTTCCGACAA 1800  
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 Qy 657 LeuThrProAsnGluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSer 676  
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 Qy 677 GlnAlaThrGlnValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThr 696  
 Db 1921 CAAGCAACACAGGTGCTCAATTAGTCAAAAGCGATGGCTCAGCATGTGTAGCCACCAACC 1980  
 Qy 697 IleAlaAsnGlnIleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIlePro 716  
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QY 857 ProAlaArgGluAlaAlaPheAlaSerArgSerLeuArgThrGlyArgSerArgSerSer 876  
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QY 897 lys 897  
 Db 2581 AAA 2583

RESULT 15  
 AF263836 3108 bp mRNA linear ROD 01-JUN-2000  
 DEFINITION Mus musculus voltage-gated potassium channel KCNQ5 (Kcnq5) mRNA,  
 partial cds.

ACCESSION AF263836  
 VERSION  
 KEYWORDS AF263836.1 GI:8132998

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 3108)  
 AUTHORS Kniazeva, M. and Han, M.  
 TITLE A new gene of the voltage-gated potassium channel KCNQ family,  
 KCNQ5, is a candidate gene for retinal disorders

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 3108)

AUTHORS Kniazeva, M. and Han, M.

TITLE Direct Submission

JOURNAL Submitted (04-MAY-2000) MCB, University of Colorado at Boulder,  
 Porter Biosciences Bldg., Boulder, CO 80309, USA

FEATURES Location/Qualifiers

1..3108

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/db\_xref="taxon:10090"

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/tissue\_type="brain"

/dev\_stage="9-11 weeks"

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<1..2638

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 channel KCNQ5; member of the KCNQ family"

/codon\_start=2

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 SAAPKPAAPTLQIPPLLSAIKHLSPRLSNPLGLOESI SDVTTCIVASKESVQFA  
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ORIGIN

Alignment Scores:

Pred. No.:

3.84e-278 Length: 3108

Score: 4288.00 Matches: 837  
 Percent Similarity: 96.92% Conservative: 13  
 Best Local Similarity: 95.44% Mismatches: 27  
 Query Match: 93.46% Indels: 0  
 Gaps: 10

US-09-810-796-4 (1-897) x AF263836 (1-3108)

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 QY 40 LeuArgGluSerArgArgGlyGlyGlnGlyAlaArgMetSerLeuLeuGlyLysProLeu 59  
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Db	962	GCTGCTGGCTAGTATGAGCTGATGAAATCTCTTCCATTGCAACCTGGAAG	1021
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Db	1022	CCACATCTGAAGGCTTTGCACACCTGCAGCCCTACCAAGAAAGAACAGGGGGAGGATCA	1081
Qy	380	SerSerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSer	399
Db	1082	ACGAGTCAGAGCTTGAGCTTTAAGAGCGAGTAGCGATGCTAGCCCAAGGGGCCAGAGC	1141
Qy	400	IleLysSerArgGlnAlaSerValClyAspArgArgSerProSerThrAspIleThrAla	419
Db	1142	ATTAAGACGACAGACATGATAGTGGTACAGAGATCCCGAGCATGTGACATCAGCTGCC	1201
Qy	420	GluGlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArg	439
Db	1202	GAGGGCAGCCCCACCAGAGTCCAGNAGAGTTGGAGCTTCAACGACCGAACCCTTCAGG	1261
Qy	440	ProSerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeu	459
Db	1262	CCCTCACTAGCGCTCAAGAGTTCCAGGCCAAGCCAGTGTAGACGCGACACAGCCCTT	1321
Qy	460	GlyThrAspAspValTyAspGluLysGlyCysGlnCysAspValSerValGluAspLeu	479
Db	1322	GGCATTGATGATGTGTATGATGAGAAAGATGCCAGTGTGACGTCTGTGTGGAGACCTC	1381
Qy	480	ThrProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLys	499
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Qy	500	ArgLysPheLysGluThrLeuArgProTyAspValLysAspValIleGluGlnTySer	519
Db	1442	CGGAAGTTTAAAGAAACATTCAGCCCATATGATGATAAGATGTCTTGAACATACTCT	1501
Qy	520	AlaGlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIle	539
Db	1502	GCTGGTCACCTGACATGCTTTGTAGATAAAGCCITTCAGACACGCGTGTGATCAAAAT	1561
Qy	540	LeuGlyLysGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHis	559
Db	1562	CTTTGGAAGAGCAAAATGACGTGAGATAAGAGAGCCGAGAGAAATTAACAGCAAGAC	1621
Qy	560	GluThrThrAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGln	579
Db	1622	GAGACACATGACCCAGCATGCTCGCCCGGTTGTGAGGTTGAGAAACAGGTCCAG	1681
Qy	580	SerIleGluSerLysLeuAspCysLeuLeuAspIleTyGlnGlnValLeuArgLysGly	599
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Qy	600	SerAlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThr	619
Db	1742	TCTGCCCTCCGCCCTCATCTGGGATCTTTTCAGATCCCGCTTTTGAATGTGAACAGAC	1801
Qy	620	SerAspTyGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGly	639
Db	1802	TCTGACTATCAAGTCTGTGGATAGCAAGACCTGCTGGCTCAGCACAAAAACAGCGGC	1861
Qy	640	CysLeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrPro	659
Db	1862	TGTTTAAAGAGGTGAGCGAGTCCCAACATCTCAAGAGCGCTGCGATTCCTTAACACCA	1921
Qy	660	AsnGluPheSerAlaGlnThrPheTyAlaLeuSerProThrMetHisSerGlnAlaThr	679
Db	1922	AATGAGTTCAGTGTCTGACATTTCTATGGGCTTAGCCCTACTATGACAGCCAAAGCTACC	1981
Qy	680	GlnValProIleSerGlnSerAspGlySerAlaValAlaIleThrAsnThrIleAlaAsn	699
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Qy	700	GlnIleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeu	719

Search completed: April 3, 2005, 16:35:43  
Job time : 9768.68 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 2, 2005, 23:56:51 ; Search time 1122.13 Seconds  
(without alignments)  
4732.082 Million cell updates/sec

Title: US-09-810-796-4

Perfect score: 4588

Sequence: 1 MKOVESGRVLLNSAARG.....SICKAGESTDALSLPHVKLK 897

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=N Geneseq.16Dec04 -QWTF=fastap -SUPFIX=ring -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09810796.cgn.1.1128.@runat.31032005.141120.18189 -NCPU=6 -ICPU=3  
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOC  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq.16Dec04:

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- 2: geneseqn1990s.\*
- 3: geneseqn2000s.\*
- 4: geneseqn2001as.\*
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- 6: geneseqn2002as.\*
- 7: geneseqn2002bs.\*
- 8: geneseqn2003as.\*
- 9: geneseqn2003bs.\*
- 10: geneseqn2003cs.\*
- 11: geneseqn2003ds.\*
- 12: geneseqn2004as.\*
- 13: geneseqn2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4588	100.0	2694	AAS14652	Aas14652 Human CDN
2	4588	100.0	2694	AAD27192	Aad27192 Human pot
3	4588	100.0	3137	AAC85414	Aac85414 Human KCN
4	4584	99.9	3071	AAS14651	Aas14651 Human CDN
5	4574	99.7	3074	AH49499	Aah49499 Human KCN

6	4574	99.7	3074	10	ADB78684	Adb78684 Human pot
7	4527.5	98.7	2667	4	AAS14653	Aas14653 Human CDN
8	4527.5	98.7	2772	5	AAH43633	Aah43633 Human ion
9	4527.5	98.7	3111	5	AAH43634	Aah43634 Human ion
10	4407	96.1	3718	3	AAC64371	Aac64371 Human KCN
11	2012	43.9	2335	3	AA47618	Aa47618 KCNQ4 Pot
12	2012	43.9	2335	10	AD31698	Ad31698 Human 323
13	1832.5	39.9	5595	13	ADSI7851	Adsi7851 Rattus no
14	1820.5	39.7	7407	10	ADB78687	Adb78687 Human pot
15	1819.5	39.7	7407	10	ADB78685	Adb78685 Human pot
16	1819.5	39.7	7407	10	ADB78688	Adb78688 Human pot
17	1819.5	39.7	7407	10	ADB78686	Adb78686 Human pot
18	1819.5	39.7	7407	10	ADB78683	Adb78683 Human pot
19	1819.5	39.7	7411	10	ADD39557	Add39557 Human tum
20	1819.5	39.7	7420	11	ADN38963	Adn38963 Cancer/an
21	1819.5	39.7	7420	11	ADP65810	Adp65810 Human mRN
22	1819.5	39.7	7420	11	ADP65731	Adp65731 Human pot
23	1819.5	39.7	7420	12	ADL06495	Adl06495 Human tum
24	1819.5	39.7	7863	10	ADJ56529	Adj56529 Human CDN
25	1813	39.5	2169	2	AAJ26588	Aax26588 Nucleotid
26	1812.5	39.5	2565	2	AAJ81548	Aax81548 Human bra
27	1812.5	39.5	3195	5	AAJ74831	Aax74831 DNA encod
28	1806.5	39.4	3237	2	AAJ57145	Aax57145 Human mut
29	1805	39.3	3287	2	AAJ26587	Aax26587 Nucleotid
30	1800.5	39.2	3232	2	AAJ57057	Aax57057 Human KCN
31	1800.5	39.2	3232	10	AAJ58489	Aad58489 Human pot
32	1800.5	39.2	3232	13	ADSI7844	Adsi7844 Human KCN
33	1797.5	39.2	7413	5	AAJ74832	Aas74832 DNA encod
34	1792.5	39.1	3232	5	AAJ74830	Aas74830 DNA encod
35	1784.5	38.9	3029	2	AAJ81547	Aax81547 Human bra
36	1772.5	38.6	4512	10	ADJ56528	Adj56528 Rat cDNA
37	1769.5	38.6	2273	2	AAJ57140	Aax57140 Mouse KCN
38	1667.5	36.3	125910	3	AAJ64370	Aac64370 Human KCN
39	1633.5	35.6	1848	12	ADH51119	Adh51119 Potassium
40	1633.5	35.6	1848	12	ADM77995	Adm77995 KCNQ2-15b
41	1626.5	35.5	1878	12	ADH51117	Adh51117 Potassium
42	1626.5	35.5	1878	12	ADM77993	Adm77993 KCNQ2-15b
43	1614.5	35.2	1932	12	ADH51115	Adh51115 Potassium
44	1614.5	35.2	1932	12	ADM77991	Adm77991 KCNQ2-15b
45	1611	35.1	2565	2	AAJ26596	Aax26596 Nucleotid

ALIGNMENTS

RESULT 1

AAS14652	
ID	AAS14652 standard; cDNA; 2694 BP.
XX	
AC	AAS14652;
XX	
DT	18-DEC-2001 (first entry)
XX	
DE	Human cDNA encoding a voltage gated potassium channel hKCNQ5-1.
XX	
KW	Human; ss; voltage-gated potassium channel; hKCNQ5-1; nootropic;
KW	cerebroprotective; neurotropic; analgesic; vision disorder;
KW	central nervous system disorder; epilepsy; migraine; hearing disorder;
KW	psychotic disorder; seizure; learning disorder; memory disorder; stroke;
KW	pain; gene therapy; splice variant.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	1..2994
FT	/*tag= a
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WO200170759-A1.

27-SEP-2001.

20-MAR-2001; 2001WO-US009328.

XX

PR 21-MAR-2000; 2000US-0190954P.  
XX (ICAG-) ICAGEN INC.  
XX Jegla TJ;  
XX WPI; 2001-611467/70.  
DR P-PSDB; AAU09020.  
XX Polypeptides and polynucleotides of potassium channel KCNQ5 for  
PT identifying a compound modulating ion flux in eukaryotic cell or cell  
PT membrane expressing the protein, comprises KCNQ approximately alpha-subunits.  
XX Claim 5; Page 62-63; 78pp; English.  
XX The invention relates to an isolated polypeptide comprising an alpha-  
XX subunit of a KCNQ potassium channel, with a subsequence having 65%  
XX sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence  
XX and forms a KCNQ potassium channel having the characteristic of voltage-  
XX gating with at least an additional KCNQ alpha-subunit. Also included in  
XX the scope of the invention are the nucleic acids encoding hKCNQ5  
XX (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression  
XX vectors encoding them, antibodies against them, the use of 3-dimensional  
XX computer modelling to identify molecules that bind to a KCNQ containing  
XX potassium channel and modulate ion flux through the channel. The KCNQ  
XX polypeptide is useful for identifying a compound that increases or  
XX decreases ion flux through a potassium channel expressed in an eukaryotic  
XX host cell or cell membrane. The compound (and the KCNQ nucleic acid when  
XX used in gene therapy) is useful as a pharmaceutical agent for treating  
XX diseases involving abnormal ion flux, such as disorders of the central  
XX nervous system, such as epilepsy, migraines, hearing and vision problems,  
XX psychotic disorders, seizures, learning and memory disorders, stroke and  
XX pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a  
XX human tissue and the use of a nucleotide sequence of KCNQ5 to search  
XX computer databases to find variants of the sequence which are associated  
XX with disease states, is useful for screening mutations of KCNQ5. The  
XX present sequence is a splice variant of hKCNQ5 encoding hKCNQ5-1  
XX  
SQ Sequence 2694 BP; 714 A; 671 C; 669 G; 640 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 0 Length: 2694  
Score: 4588.00 Matches: 897  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-09-810-796-4 (1-897) x AAS14652 (1-2694)

QY 121 AlaSerCysLeuLeuLeuLeuLeuLeuLeuValMetIleValValPheGlyLeuGluPhe 140  
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QY 141 IleIleArgIleTrpSerAlaGlyCysCysArgTrpArgGlyTrpGlnGlyArgLeu 160  
DB 421 ATCATTTCGAATCTGGTCTCGGGTTGCTGTCGATATAGAGGATGCGCAAGAGACTG 480  
QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180  
DB 481 AGGTTTGGCTCGAAAGCCCTCTGTGTATAGATACCATTTGTTCTTATCGCTTCATAGCA 540  
QY 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200  
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QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220  
DB 601 TTCTACAGATCTCCGTCATGGTGGCATGGACCCGAGGGAGGACCTTGGAAATTTACTG 660  
QY 221 GlySerValValTyrAlaHisSerLysGluLeuLeuThrAlaTrpTyrIleGlyPheLeu 240  
DB 661 GGTTCAGTGGTTTATGCTCAGCAAGGAATTAATCAGAGCTTGGTACATAGGATTTTG 720  
QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaLeuLysGluPhe 260  
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QY 261 SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280  
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QY 281 AsplysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300  
DB 841 GACAAACTCCCTTAAGTGGCTGGGAAGATTCCTTCTGACGGCTTTCACCTCTTGGC 900  
QY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320  
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DB 1081 CACTTGAAGGCTTTGCAACCTCTGAGCCCTTACCAGAAAGAACCAAGGGGAGCATCAAGC 1140  
QY 381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400  
DB 1141 AGTCAGAGCTTAAGTCTTAAAGAGCGAGTGCGCATAGCTAGCCCCAGGGGCGCAGATTT 1200  
QY 401 LysSerArgGlnAlaSerValGlyAspArgSerProSerThrAspIleThrAlaGlu 420  
DB 1201 AAGAGCCGACAAAGCTCAGTAGGTGACAGGAGGTCCCAAGCACCAGCATCACAGCCGAG 1260  
QY 421 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 440  
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QY 501 LysPheLysGluThrLeuArgProFyrAspValLysAspValIleGluGlnFyrSerAla 520  
Db 1501 AAGTTTAAAGAAACGTTACGTCATATGATGTAAAGATGTCATTGAACAATATTCGCT 1560  
QY 521 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540  
Db 1561 GGTCACTCGCATCTGTTGTAGATTTAAAGCCCTTCAACACACGCTGTTGATCAAAATCTT 1620  
QY 541 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560  
Db 1621 GGAAAGGGCAAAATCACATCAGATCAGATGAAGAGCCGAGAGAAATTAACACAGCAATGAG 1680  
QY 561 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 580  
Db 1681 ACCACAGACGATCTCAGTATGCTCGGTGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740  
QY 581 IleGluSerLysLeuAspCysLeuLeuAspIleFyrGlnGlnValLeuArgLysGlySer 600  
Db 1741 ATAGAGTCCAAGCTGAGCTGCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800  
QY 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620  
Db 1801 GCCTCAGCCCTCGCTTGGCTTCATTCAGATCCCACTTTTGAATGTGAACACAGACATCT 1860  
QY 621 AspFyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640  
Db 1861 GACTATCAAGCCCTGTGGTAGCAAGATCTTTCGGGTTCCGACAAAAACAGTGGCTGC 1920  
QY 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660  
Db 1921 TTATCCAGATCAACTAGTGCACCAATCTCGAGAGGCTCGAGTTCATTCAGCGCAAAAT 1980  
QY 661 GluPheSerAlaGlnThrPheFyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680  
Db 1981 GAGTTCAGTGCCACAGCTTCTACGCGTCTAGCCCTTACTATGCACAGTCACAGCAACACAG 2040  
QY 681 ValProIleSerGlnSerAspGlySerAlaValAlaIleThrAsnThrIleAlaAsnGln 700  
Db 2041 GTGCCAATTAGTCAAGGCGATGGCTCAGCAGTGGGAGCCACCAACACCATTTGCCAAACCA 2100  
QY 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro 720  
Db 2101 ATAATACGGCACCCCAAGCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2160  
QY 721 AlalleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740  
Db 2161 GCCATCAAGCATCTGCCCGAGCCAGAAACTCTGCACCCCTTAACCCCTGCAGGCTTACAGGA 2220  
QY 741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760  
Db 2221 AGCATTTCTGAGTCAACACCTGCTTGTTCCTCAAGGAAATGTTTCAGTTGTCACAG 2280  
QY 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780  
Db 2281 TCAATCTCACCAGGACCGTCTATGAGGAAAGCTTTTGACATGGGAGGAGAACTCTG 2340  
QY 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800  
Db 2341 TTGTCGTCTGTGCCATGTCGCGAGGACTTGGGCAAAATCTTTGCTGTGTGCAAAACCTG 2400  
QY 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 820  
Db 2401 ATCAGTTCGACGAGGAACCTGNATATACATTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2460  
QY 821 GlySerGlnAspPheFyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840  
Db 2461 GGCACCAAGATTTTTTACCCCAATGGAGGGAATCCAAATGTTTATTAACATGATGAAGAG 2520  
QY 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaIleProGlnProAlaArgGlu 860

Db 2521 GTGGTCCCGAAGAGACAGACAGACACTTTTGTATGCCGACCCGACGCTGCCAGGAA 2580  
QY 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 880  
Db 2581 GCTGCCCTTTCATCAGACTCTCTAAGGACTGGAAGTCAACGATCATCTCAGAGCATTTGT 2640  
QY 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897  
Db 2641 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAA 2691  
RESULT 2  
RAD27192  
ID AAD27192 standard; cDNA; 2694 BP.  
XX  
AC AAD27192;  
XX  
DT 09-APR-2002 (first entry)  
XX  
DE Human potassium channel polypeptide, KCNQ5 cDNA.  
XX  
KW Human; potassium channel polypeptide; KCNQ5; pain; migraine; stroke;  
KW dementia; trauma; epilepsy; seizure; amyotrophic lateral sclerosis; ALS;  
KW multiple sclerosis; MS; Parkinson's disease; ataxia; depression;  
KW anxiety disorder; bipolar disorder; sleep disorder; eating disorder;  
KW addiction; myokymia; Alzheimer's disease; age-associated memory loss;  
KW learning deficiency; cognitive disorder; motor disease; neuron disease;  
KW neuropsychological disorder; neuropsychological disorder; asthma;  
KW neuron cell death; brain tumour; gene therapy; antisense therapy;  
KW synaptic transmission; electrical excitability; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1. 2694  
FT /tag= a  
FT /product= "Human KCNQ5 protein"  
XX  
PN WO200192526-A1.  
XX  
PD 06-DEC-2001.  
XX  
PF 24-MAY-2001; 2001WO-US017314.  
XX  
PR 26-MAY-2000; 2000US-0207389P.  
XX  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX  
PI Dworetzky SI, Ramanathan CS, Trojnak JT, Boissard CG;  
PI Gribkoff VK;  
XX  
DR WPI; 2002-122069/16.  
XX  
PT P-PSDB; AAE16599.  
XX  
DR Novel potassium channel polypeptide, KCNQ5 and polynucleotide encoding  
XX it, for diagnosing, treating and identifying modulators useful in  
XX treating neurological, neuropsychological and neuropsychological  
XX diseases.  
XX  
PS Claim 3; Fig 1; 128pp; English.  
XX  
XX The invention relates to potassium channel polypeptides referred to as  
XX KCNQ5 and nucleic acid molecules encoding such polypeptides. KCNQ5  
XX polypeptides are useful for identifying compounds that modulate their  
XX biological activity. The compounds identified and KCNQ5 polynucleotides  
XX are useful for treating acute and chronic pain, migraine, acute stroke,  
XX dementia, trauma, epilepsy, seizure, amyotrophic lateral sclerosis (ALS),  
XX multiple sclerosis (MS), Parkinson's disease, ataxia, anxiety disorders,  
XX depression, bipolar disorders, sleep disorders, eating disorders,  
XX addiction, myokymia, Alzheimer's disease, age-associated memory loss,  
XX learning deficiencies, cognitive disorders and motor neuron diseases. The  
XX nucleic acid molecules of the invention are further useful for treating  
XX neuropsychological, neuropsychological disorders, asthma, neuron cell

CC death and brain tumours. They are also used in gene therapy and antisense  
CC therapy. KNO5 polypeptides modulate synaptic transmission and electrical  
CC excitability in the brain and are useful for generating antibodies. They  
CC are also useful to affinity purify biological effectors from biological  
CC materials e.g. disease tissues or cells. The present sequence is human  
CC KNO5 cDNA  
XX  
SQ Sequence 2694 BP; 714 A; 671 C; 669 G; 640 T; 0 U; 0 Other;

Alignment Scores:		Length:	2694
Pred. No.:	0	Matches:	897
Score:	4588.00	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	6	Gaps:	0
DB:			
US-09-810-796-4 (1-897) x AAD27192 (1-2694)			
QY	1	MetLysAspValGluSerGlyArgGlyValLeuLeuAanSerAlaAlaAargGly	20
DB	1	ATGAAGGATGTGGAGTCGGGCGGGCAGGGTGTCTGAACTCGGCAGCCGCCAGGGGC	60
QY	21	AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu	40
DB	61	GACGGCTGTACTCTGTGGACACCGCGGGCCAGCTTGTGGGGCGGGTGGCTG	120
QY	41	ArgGluSerArgArgGlyGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer	60
DB	121	AGGGAGAGCGCGGGCGAAGCAGGGGCGCGGATGAGCTGCTGGGGAAGCCGCTCTCT	180
QY	61	TyrThrSerSerGlnSerCysArgArgAanValLysTyrArgGlyValGlnAanTyrLeu	80
DB	181	TACACGAGTAGCAGAGCTGCGGGCGCAACGTCAGTACCGCGGGTGCAGACTACCTG	240
QY	81	TyrAanValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu	100
DB	241	TACACGCTGTGAGAGACCCCGCGCTGGGGTTCATCTACCAGCTTCGTTTCTCTC	300
QY	101	LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu	120
DB	301	CTTGTCTTTGGTGTCTGATTTGTGAGTTCCTGAGTTCGATGATGCTCTTTGGTGGAGTTC	360
QY	121	AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe	140
DB	361	GCCTCAAGTGTCTCTTGATCTCTGAGTTCGATGATGCTCTTTGGTGGAGTTC	420
QY	141	IleIleArgIleTrpSerAlaGlyCysCysCysArgTyrArgGlyTrpGlnGlyArgLeu	160
DB	421	ATCATTGGAATCTGTCTCGGGTGTCTGTTCGATATAGAGGATGCGCAAGGAAGACTG	480
QY	161	ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla	180
DB	481	AGGTTCGTGCAAGGCCCTCTGTGTATAGATACCATTTCTTATCGCTTCATAGCA	540
QY	181	ValValSerAlaLysThrGlnGlyAanIlePheAlaThrSerAlaLeuArgSerLeuArg	200
DB	541	GTGTTCGCAAAAACCTCAGGGTAATATTTTGGCCAGCTCTGCACTCAGAAAGTCTCCGT	600
QY	201	PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu	220
DB	601	TTCTCAGATCTCCGCGATGTGGCGCATGGACCGAAGGGGAGGCACTTGGAAATACTG	660
QY	221	GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu	240
DB	661	GGTTCAGTGTATGCTACACAGGAAGTAATACAGCTTGGTACAGATTTTGT	720
QY	241	ValLeuIlePheSerPheLeuValTyrLeuValGluLysAspAlaSerLysGluPhe	260
DB	721	GTTCCTTATTTTTCGTCTTCTCTGTCTATCTCGTGGAAAAGGATGCCAATAAGAGTTT	780
QY	261	SerThrTyrAlaAspAlaLeuTrpGlyThrIleThrLeuThrThrIleGlyTyrGly	280

DB	781	TCTACATATGCAGATGCTCTCTGTGGGGGCACAAATTACATTGACAACTATTGGCTATGCA	840
QY	281	AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly	300
DB	841	GACAAACCTCCCTTACCTTGGCTGGGAAGATTGCTTTCTTGACGGCTTTCATCTCTTGGC	900
QY	301	IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln	320
DB	901	ATTCTCTTTCTTGGCACTTCTCGCGGCATTCTTGGCTCAGGTTTTCATATAAAGTACAA	960
QY	321	GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln	340
DB	961	GAACAACACCGCCAGAAACACTTTGAGAAAAGAGAACCCAGCTGCCAACCTCATTCAG	1020
QY	341	CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro	360
DB	1021	TGTGTTTGGCTAGTTACGAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA	1080
QY	361	HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyGluAlaSerSer	380
DB	1081	CACCTTGAAGGCTTGCACACCTGCAGCCCTTACCAGAAAAGAACAGGGGAAGCATCAAGC	1140
QY	381	SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle	400
DB	1141	AGTCAGAGCTAAGTTTAAAGGAGCGAGTCGCGATGCTAGCCCGAGGGCCAGAGTATT	1200
QY	401	LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu	420
DB	1201	AAAGCGCAGACAGCCTCAGTAGGTGACAGGAGTCCCAAGCACCCGACATCACAGCCGAG	1260
QY	421	GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro	440
DB	1261	GGCAGTCCCAAGAGTGCAGAGAGCTGGAGCTTCAACACCGAACCCGCTTCGCGCCC	1320
QY	441	SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly	460
DB	1321	TCGCTGCGCCTCAAAAGTTCTCAGCCCAAAACAGTAGTAGTGTGACACAGCCCTTGC	1380
QY	461	ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr	480
DB	1381	ACTGATGATGATATGATGAAAAGGATGCGCAGTGTGATGTATCATGTGGAAGACCTCAC	1440
QY	481	ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg	500
DB	1441	CCACCACTTAAACTGTCTCGAGCTATCAGAAATTAAGAAATTTCAATTTGCAAAACGG	1500
QY	501	LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla	520
DB	1501	AAGTTTAAAGGAACGTTACGTCCTCCATATGATGTAAGATGTCATTGAAACAATATCTGCT	1560
QY	521	GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu	540
DB	1561	GGTCATCTGGACATGTTGTGTAGAAATTAAGAGCCTTCAACACAGCTGTGTGATCAATCTT	1620
QY	541	GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu	560
DB	1621	GGAAAGGGCAATTCATCAGATAGAGAGCCGAGAGAAATAACAGCAGAACATGAG	1680
QY	561	ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer	580
DB	1681	ACCACAGCATCTCAGTATGCTCGTGGTGGTCAAGGTTGAAAACACAGGTACAGTCC	1740
QY	581	IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer	600
DB	1741	ATAGAGTCCAAAGCTGGACTGCTACTAGACATATCAACAGGTCCTTCGGAAGGCTCT	1800
QY	601	AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProPheGluCysGluGlnThrSer	620
DB	1801	GCTTCAGCCCTCGCTTGGCTTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT	1860
QY	621	AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAanSerGlyCys	640
DB	1861	GACTATCAAGCCCTGTGGATAGCAAGATCTTTGGGTTCCGCACAAAAACAGTGGCTGC	1920



Qy 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660  
 Db 1921 TTATCCAGTCAACTAGTGCACCAATCTCGAGAGCGCTCGCATTCATTCTGACGCCAAT 1980  
 Qy 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680  
 Db 1981 GAGTTCACTGCCAGACTTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACAG 2040  
 Qy 681 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 700  
 Db 2041 GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACCATTTGCCAACCAA 2100  
 Qy 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro 720  
 Db 2101 ATAAATACGGCACCACCAAGCCAGCCCAACATTTTACAGATCCCACTCTCTCCCA 2160  
 Qy 721 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740  
 Db 2161 GCCATCAAGCATCTGCCCAGGCCAGAACTCTGCACCCCTAACCTTGCAGGCTTACAGGA 2220  
 Qy 741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760  
 Db 2221 AGCATTTCTGAGCTCACCACCTGCCTCTGTGCTCCCAAGGAAATGTTTCAGTTGCACAG 2280  
 Qy 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780  
 Db 2281 TCAATCTCACCAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAACTCTG 2340  
 Qy 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800  
 Db 2341 TTGTCGTCTGTCCCATGTCGCCGAGGACTTGGCAAAATCTTTGTCTGTGCAAAACCTG 2400  
 Qy 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGlySerGlySerArg 820  
 Db 2401 ATCAGTTCGACCGAGGAACTGAATATACAACTTTTCAGGAGTGAGTCAAGTGGCTCCAGA 2460  
 Qy 821 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840  
 Db 2461 GGCAGCCCAAGATTTTATACCCCAATGGAGGAAATCCAAATTTGTTTATAACTGATGAAGAG 2520  
 Qy 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 860  
 Db 2521 GTGGTCCCGAGAGACAGACAGACACTTTTGTATGCCCGCACCCGCTGCACGGGA 2580  
 Qy 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 880  
 Db 2581 GCTGCTTTTGCATCAGACTCTCTAAGGACTGGAAGTCAAGTATCATCTCAGAGCATTTGT 2640  
 Qy 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897  
 Db 2641 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAA 2691  
 RESULT 3  
 AAC85414  
 ID AAC85414 standard; cDNA; 3137 BP.  
 XX  
 AC AAC85414;  
 XX  
 DT 20-APR-2001 (first entry)  
 XX  
 DE Human KCNQ5 potassium channel subunit coding sequence.  
 XX  
 KW Human; KCNQ5; heteromeric channel; chromosome 6; Parkinson's disease;  
 KW central nervous system; CNS; Alzheimer's disease; anxiety; ataxia;  
 KW CNS damage; trauma; stroke; neurodegenerative illness; schizophrenia;  
 KW compulsive behaviour; dementia; depression; Huntington's disease; mania;  
 KW memory impairment; memory dysfunction; spinal cord damage; phobia;  
 KW pick's disease; psychosis; stroke; tremor; seizure; convulsion; epilepsy;  
 KW ds.  
 XX  
 OS Homo sapiens.  
 XX

EH Key Location/Qualifiers  
 FT CDS 1..2694  
 FT /\*tag= a  
 FT /product= "KCNQ5 subunit"  
 XX  
 PN WO200077035-A2.  
 XX  
 PD 21-DEC-2000.  
 XX  
 PF 29-MAY-2000; 2000WO-DK000289.  
 XX  
 PR 11-JUN-1999; 99DK-00000828.  
 XX  
 PA (NEUR-) NEUROSEARCH AS.  
 XX  
 PI Jentsch TJ;  
 XX  
 DR WPI: 2001-080678/09.  
 XX  
 DR P-PSDB; AAB47046.  
 XX  
 PT Novel genes encoding KCNQ5 potassium channel subunits, useful for  
 PT treating Alzheimer's disease, anxiety, ataxia, stroke, dementia,  
 PT depression, Huntington's disease, schizophrenia and Parkinson's disease.  
 XX  
 PS Claim 2; Page 44-48; 50pp; English.  
 XX  
 CC This sequence encodes the human KCNQ5 protein. The KCNQ5 protein forms  
 CC heteromeric channels with other KCNQ channel subunits, in particular  
 CC KCNQ3 and KCNQ4. The KCNQ5 gene has been localised to the long arm of  
 CC chromosome 6 (6q14). Chemicals which have the ability to bind to KCNQ5  
 CC are useful for diagnosis, treatment, prevention or alleviation of  
 CC diseases related to diseases or adverse conditions of the central nervous  
 CC system (CNS), including affective disorders, Alzheimer's disease,  
 CC anxiety, ataxia, CNS damage caused by trauma, stroke or neurodegenerative  
 CC illness, cognitive deficits, compulsive behavior, dementia, depression,  
 CC Huntington's disease, mania, memory impairment, memory disorders, memory  
 CC dysfunction, motion disorders, motor disorders, neurodegenerative  
 CC diseases, Parkinson's disease and Parkinson-like motor disorders,  
 CC phobias, pick's disease, psychosis, schizophrenia, spinal cord damage,  
 CC stroke, tremor, seizures, convulsions and epilepsy  
 XX  
 SQ Sequence 3137 BP; 865 A; 749 C; 745 G; 778 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 0 Length: 3137  
 Score: 4588.00 Matches: 897  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 4 Gaps: 0  
 US-09-810-796-4 (1-897) x AAC85414 (1-3137)  
 Qy 1 MetLysAspValGluSerGlyValArgValLeuLeuAanSerAlaAlaAargGly 20  
 Db 1 ATGAAGATGTGGAGTCGGCCGGGCGAGGTGCTGTAACCTCGCAGCGCCAGGGGC 60  
 Qy 21 AspGlyLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40  
 Db 61 GACGGCTGTCTACTGTGGGCACCCGCGCGCCACGCTCGTGGCGGGGTGGCTG 120  
 Qy 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuLeuLysProLeuSer 60  
 Db 121 AGGAGAGACCGCCGGGCAAGCAGGGGCCCGGATGAGCTGCTGGGGAACCGCTCTCT 180  
 Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80  
 Db 181 TACACGAGTACCCAGAGCTGCCGGCGCAACGTCAAGTACCCGGCGGTGCAGAACTACCTG 240  
 Qy 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100  
 Db 241 TACAACTGTCTGGAGAGACCCCGGGCTGGGGCGTTTCATCTACCAACGCTTTCGTTTTCTC 300



Db 2461 GGCACCCAGATTTTACCCCAATGGAGGAATCCAAATTTGTTATTAACCTGATGAAGAG 2520  
QY 841 ValGlyProGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 860  
Db 2521 GTGGTCCCGAAGACAGACAGACACACTTTTGATGCGCACCGCAGCCTGCCAGGGA 2580  
QY 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 880  
Db 2581 GCTGCTTTGTCATCAGACTCTCTAAGGACTGGAAGTCCAGCATCATCTCAGAGCATTTGT 2640  
QY 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897  
Db 2641 AAGCGAGGAGAAAGTACAGATGCCCTCAGCTTGCTCTATGTCAAACTGAAA 2691

## RESULT 4

AA14651  
ID AA14651 standard; cDNA; 3071 BP.  
XX  
AC AA14651;  
XX  
DT 18-DEC-2001 (first entry)  
XX  
DE Human cDNA for voltage gated potassium channel hKCNQ5.  
XX  
KW Human; ss; voltage-gated potassium channel; hKCNQ5; nootropic;  
KW cerebroprotective; neurotropic; analgesic; vision disorder;  
KW central nervous system disorder; epilepsy; migraine; hearing disorder;  
KW psychotic disorder; seizure; learning disorder; memory disorder; stroke;  
KW pain; gene therapy.  
XX

XX Homo sapiens.

XX WO200170759-A1.

XX 27-SEP-2001.

XX 20-MAR-2001; 2001WO-US009328.

XX 21-MAR-2000; 2000US-0190954P.

XX (ICAG-) ICAGEN INC.

XX Jegla TJ;

XX WPI; 2001-611467/70.

XX Polypeptides and polynucleotides of potassium channel KCNQ5 for  
PT identifying a compound modulating ion flux in eukaryotic cell or cell  
PT membrane expressing the protein, comprises KCNQ approximately a- subunits.

XX Claim 5; Page 61-62; 78pp; English.

XX The invention relates to an isolated polypeptide comprising an alpha-  
CC subunit of a KCNQ potassium channel, with a subsequence having 65%  
CC sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence  
CC and forms a KCNQ potassium channel having the characteristic of voltage-  
CC gating with at least an additional KCNQ alpha-subunit. Also included in  
CC the scope of the invention are the nucleic acids encoding hKCNQ5  
CC (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression  
CC vectors encoding them, antibodies against them, the use of 3-dimensional  
CC computer modelling to identify molecules that bind to a KCNQ containing  
CC potassium channel and modulate ion flux through the channel. The KCNQ  
CC polypeptide is useful for identifying a compound that increases or  
CC decreases ion flux through a potassium channel expressed in an eukaryotic  
CC host cell or cell membrane. The compound (and the KCNQ nucleic acid when  
CC used in gene therapy) is useful as a pharmaceutical agent for treating  
CC diseases involving abnormal ion flux, such as disorders of the central  
CC nervous system, such as epilepsy, migraines, hearing and vision problems,  
CC psychotic disorders, seizures, learning and memory disorders, stroke and  
CC pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a  
CC human tissue and the use of a nucleotide sequence of KCNQ5 to search  
CC computer databases to find variants of the sequence which are associated  
CC with disease states, is useful for screening mutations of KCNQ5. The

CC present sequence is a representative cDNA for hKCNQ5

XX Sequence 3071 BP; 849 A; 734 C; 737 G; 750 T; 0 U; 1 Other;

## Alignment Scores:

Pred. No.: 0 Length: 3071  
Score: 4584.00 Matches: 896  
Percent Similarity: 99.89% Conservative: 0  
Best Local Similarity: 99.89% Mismatches: 1  
Query Match: 99.91% Indels: 0  
DB: 4 Gaps: 0

US-09-810-796-4 (1-897) x AA14651 (1-3071)

QY 1 MetLysAspValGluSerGlyArgValLeuLeuAanSerAlaAlaArgGly 20  
Db 10 ATGAAGGATGTGGAGTCGGGCGGCGCAGGGTGTCTGTAACCTGGCAGCGCCAGGGGC 69  
QY 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40  
Db 70 GACGGCCTGTCTACTGTGGGCACCGCGCGCCACGCTTGGTGGCGGGGGTGGCGCTG 129  
QY 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60  
Db 130 AGGAGAGCCCGCGGCGCAAGCAGGGGCGCCGAGCTGCTGGGAAGCCGCTCTCT 189  
QY 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80  
Db 190 TACACGAGTACCCAGAGCTGCGGCGCAACGTCAGTACCGCGGGTGCAGAACTACCTG 249  
QY 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100  
Db 250 TACAACGTGTGTGGAGAGACCCCGCGGCTGGGCGTTCATCTACCAAGCTTTCGTTTTCTC 309  
QY 101 LeuValPheGlyCysLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120  
Db 310 CTGTCTTTGGTGTCTGATTTTGTGAGTGTTTCTACCATCCCTTGACACACAAATATG 369  
QY 121 AlaSerSerCysLeuLeuLeuPheValMetIleValValPheGlyLeuGluPhe 140  
Db 370 GCCTCAAGTTGCTCTTGATCCTCGAGTTCTGTGATGATTGCTCTTTGGTTGGAGTTC 429  
QY 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu 160  
Db 430 ATCATTCGAATCTGTCTGTGGGTTGTCTGTATAGAGGATGTCAGAGGAACTG 489  
QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180  
Db 490 AGGTTTGCTCGAAAGCCCTTCTGTATATAGTACCATTTGTTTATCGCTTCAATAGCA 549  
QY 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200  
Db 550 GTTGTCTCTGCAAAACTCAGGGTAATATTTTGGCAGCTCTGCACTCAGAAGTCTCCGT 609  
QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220  
Db 610 TTCCTACAGATCTCTCCGATGTCGCGATGACCGAGGGGAGGACACTTGGAAATTTACTG 669  
QY 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTrpIleGlyPheLeu 240  
Db 670 GGTTCAGTGGTTTATGCTCACAGCAAGAAATTAATCATCAGCTTGGTACATAGGATTTTG 729  
QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260  
Db 730 GTTCTTATTTTTCGTCCTTCTCTGTCATCTGTGGTGGAAAGGATGCCAATAAGAGTTT 789  
QY 261 SerThrTyrAlaAspAlaLeuTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280  
Db 790 TCTACATATGAGATGCTCTCTGTGGGGCAACAATTACATTCACAACTATTGTGGCTATGA 849  
QY 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300  
Db 850 GACAAAACTCCCTAACTTGGCTGGGAAGATTTGCTTTCTGCAAGGCTTTGCACTCTCTG 909

QY	301	IleSerPheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln	320
Db	910	ATTTCCTTTCTTGACATCTCCGCGCATCTTGGCTCAGGTTTGGCATTAAGAATACAA	969
QY	321	GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln	340
Db	970	GAACAACACCCGACAGAACACTTTTGAGAAAAGAGAACCCGCTGCGCAACCTCATTCAG	1029
QY	341	CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro	360
Db	1030	TGTGTTTGGCGTAGTTTACGACCTGATGAGAAATCTGTTCCATTCGAACCTGGAAGCCA	1089
QY	361	HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyAlaSerSer	380
Db	1090	CACTTGAAGGCTTGACACACCTGCAGCCCTACCAAGAAAGAACCAAGGGAGCATCAAGC	1149
QY	381	SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle	400
Db	1150	AGTCAGAAGCTAAAGTTTAAAGAGGAGTGGCGATGGCTAGCCCGAGGGCCAGATATT	1209
QY	401	LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu	420
Db	1210	AAAGCCCAACAGCTCAGTAGTCACAGGAGGTCCCAAGCACCACATCACAGCCGAG	1269
QY	421	GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro	440
Db	1270	GGCAGTCCCAACAAAGTCAGAAAGAGCTGGAGCTTCAACGACCGAACCCGCTCCGGCCC	1329
QY	441	SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly	460
Db	1330	TCGCTGCGGCTCAAAAGTTCTCAGCCAAACACAGTGATAGATGCTGACACAGCCCTTGGC	1389
QY	461	ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr	480
Db	1390	ACTGATGATGATATGATGAAAGAGATGCCAGTGTGATGTATCATGTGGAAGACCTACC	1449
QY	481	ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg	500
Db	1450	CCACCACTTAAAGTGTGCTATCGAGCTATCAGAAATATGAATTTCAATTTGTCAAAACGG	1509
QY	501	LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla	520
Db	1510	AACTTTAAGGAACRTTACGTCCATATGATGTAAGATGTCAATTGAACAATATTCTGCT	1569
QY	521	GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu	540
Db	1570	GGTCATCTGGACATGTTGTGTAGAAATTAAGAGCCITTCAAACACGCTGTTGATCAATTTCT	1629
QY	541	GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu	560
Db	1630	GGAAAGGGCAANTCAGATAGAGAGAGCCGAGAGAAATAACAGCAGAACATGAG	1689
QY	561	ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer	580
Db	1690	ACCACAGCATCTCAGTATGCTCGGTGCGGTGCTCAAGGTTGAAAACAGGTACAGTCC	1749
QY	581	IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer	600
Db	1750	ATGAAATCCAAAGCTGGACTCCCTACTAGACATTTATCAACAGTCTCTCGGAAGGCTCT	1809
QY	601	AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer	620
Db	1810	GCCTCAGCCCTCGCTTTGGCTTCATTCAGTTCCTCCACTTTTGAATGTGAACAGACATCT	1869
QY	621	AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys	640
Db	1870	GACTATCAAGCCCTGTGGATAGCAAGATCTTTTCGGGTTCCGACAAAACAGTGGCTGC	1929
QY	641	LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn	660
Db	1930	TTATCCAGATCAACTAGTGCCACATCTCCGAGAGGCTGCAGTTCAATCTGACGCCAAAT	1989
QY	661	GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln	680
Db	1990	GAGTTTCAGTGGCCAGACTTTCTACGCGCTTAGCCCTACTATGCAAGTCAAGCAACACAG	2049
QY	681	ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln	700
Db	2050	GTGCCAAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACCATTCGCAACCAA	2109
QY	701	IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro	720
Db	2110	ATAAATACGGCACCCCAAGCAGCAGCCCAACACTTTCAGATCCCACTCTCTCCCA	2169
QY	721	AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu	740
Db	2170	GCATCAACATCTGCCAGGCGCAGAACTCTGCACCTTAACCTGCGAGGCTTACAGGAA	2229
QY	741	SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln	760
Db	2230	AGCATTTCTGAGCTCACCACTCCCTTGTGCTTCAAGGAAAATGTTTCAGGTTGCACAG	2289
QY	761	SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu	780
Db	2290	TCAAACTCTACCAAGGACCGTCTATGAGGAAAAGCTTTGACATGGAGGAGAAACTCTG	2349
QY	781	LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu	800
Db	2350	TTGCTGCTGTGCCATGGTGGCAAGGACTTGGGCAAAATCTTTGCTGTGCAAAAACCTG	2409
QY	801	IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGlySerSerGlySerArg	820
Db	2410	ATCAGGTCGACCCGAGGAACATGATATACAACTTTCAGGGAGTGAGTCAAGTGGCTCCAG	2469
QY	821	GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu	840
Db	2470	GGCAGCCCAAGATTTTACCCTCAATGGAGGAATCCAAATTTGTTATACTGATGAAGAG	2529
QY	841	ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu	860
Db	2530	GTGGGTCCCAAGAGACAGACAGACACTTTTGTGTCGCCACCGCAGCTGCCAGGAA	2589
QY	861	AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys	880
Db	2590	GCTGCTTTGTCATCAGACTCTCTAAGGACTGGAAGGTACGATCATCTCAGAGCAATTGT	2649
QY	881	LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys	897
Db	2650	AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTTCATGTCACAACTGAAA	2700
RESULT 5			
ID	AAH49499	standard; DNA; 3074 BP.	
AC	AAH49499;		
DT	11-DEC-2001	(first entry)	
XX	Human KCNQ5 DNA.		
DE	KCNQ5; potassium channel protein; human; neurological; cardiovascular;		
KW	anticonvulsant; excitability modulator; membrane potential; neuron;		
KW	voltage-dependent KCNQ5 potassium channel; cardiomyocyte; epilepsy;		
KW	screening; central nervous system disease; cardiovascular disease; ds.		
OS	Homo sapiens.		
XX	Key	Location/Qualifiers	
FT	CDS	110..2908	
FT	ET	/*tag= a	
XX	XX	/product= "KCNQ5"	
PN	DE10013732-Al.		
XX	27-SEP-2001.		



QY	521	GlyHisLeuAspMetLeuCysArgIleIysSerLeuGlnThrArgValAspGlnIleIeu	540
DB	1775	GGTCATCTGGACATGTTGTGAGAAATTAAGAGCCTTCAACACGCTGTGTGATCAAAATTCCTT	1834
QY	541	GlyIysGlyGlnIleThrSerAspIlyIysSerArgGluIuLysIleThrAlaGluHisGlu	560
DB	1835	GGAAAAAGGGCAATACATCAGATAGAAAGAGCCGAGAGAAATTAACACGACAGACATGAG	1894
QY	561	ThrThrAspAspLeuSerMetLeuGlyArgValValIysValGluIuLysGlnValGlnSer	580
DB	1895	ACCACAGACATCTCAGTATGCTCGGTGGGTCAAGGTTGAAAAACAGGTACAGTCC	1954
QY	581	IleGluSerIysLeuAspCysLeuLeuAspIleIleThrGlnGlnValIleuArgIysGlySer	600
DB	1955	ATGAAATCCAAAGTGGACCTGCTTACAGATCATTATCAACAGGTCTCTCGGAAGGCTCT	2014
QY	601	AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer	620
DB	2015	GCCTCAGCCCTCGCTTGGCTTCATTTCCAGATCCCACTTTTGAATGTGAACAGACATCT	2074
QY	621	AspTyrGlnSerProValAspSerIysAspLeuSerGlySerAlaGlnAsnSerGlyCys	640
DB	2075	GACTATCAAGCCCTGTGGATAGCAAGATCTTTCCGGTTCGCGCAACAAACAGTGGCTGC	2134
QY	641	LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn	660
DB	2135	TTATCCAGATCAACTAGTGCACACATCTCGAGAGGCTCGAGTTCATTTGACGCCAAAT	2194
QY	661	GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln	680
DB	2195	GAGTTCAGTGCACAGACTTTCTACGGCGCTTAGCGCTACTATGCACAGTCAAGCAACACAG	2254
QY	681	ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln	700
DB	2255	GTGGCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACCACTTGCNAACCAA	2314
QY	701	IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro	720
DB	2315	ATNAATACGGCACCCAGCCAGCAGCCCCAACACTTTACAGATCCGACTCTCTCTCCCA	2374
QY	721	AlaIleIysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu	740
DB	2375	GCCATCAAGCATCTGCCAGGCCAGAAACTCTGCACCTTAACCTCGAGGCTTACAGGAA	2434
QY	741	SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln	760
DB	2435	AGCATTTCTGACGTCAACACTGCTTGTTCCTTCCAAAGGAAATGTTCAAGTTGCACAG	2494
QY	761	SerAsnLeuThrLysAspArgSerMetArgIysSerPheAspMetGlyGlyGluThrLeu	780
DB	2495	TCAAAATCTCACCAGGACCGTCTTATGAGGAAAGCTTGCATGGGAGGAGAACTCTG	2554
QY	781	LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu	800
DB	2555	TTGTCTGTCTGTCCCATGTGCCAGAGACTTGGGCCAAATCTTGTCTGTGTGCAAAACCTG	2614
QY	801	IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg	820
DB	2615	ATCAGTGCACCGAGGAACTGAATATACAACTTTTCAGGGAGTGTAGTCAAGTGGCTCCAGA	2674
QY	821	GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu	840
DB	2675	GGCAGCCAAAGATTTTACCCCCAAATGGAGGGGAATCCAAATTTGTTTAACTGATGAAGAG	2734
QY	841	ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu	860
DB	2735	GTGGGTCCTCCGAGAGACAGACAGACACTTTTGTATGCGCACCGCAGCCTGCCAGGGAA	2794
QY	861	AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys	880
DB	2795	GCTGCTCTTGCATCACACTCTTAAGACTGGAAGGTCAAGATCACTCAGACATTTGT	2854

Qy	881	LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValysLeuIys	897
Db	2855	AAGCAGGAGAGAACTACAGATGCCCTCAGCTTGCTCATGTCAAACCTGAAA	2905
RESULT 6			
ADBB78684			
ID	ADB78684	standard; cDNA; 3074 BP.	
XX			
AC	ADB78684;		
XX			
DT	04-DEC-2003	(first entry)	
XX			
DE		Human potassium channel subunit mutant cDNA SEQ ID NO:55.	
XX			
KW		ss; gene; mutant; ion channel; ion channel subunit; ICS; nootropic;	
KW		neuroprotective; inotropic; antipyrctic; antiarrhythmic; antimigraine;	
KW		antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;	
KW		nephrotropic; antidiabetic; ophthalmological; epilepsy;	
KW		ion channel dysfunction; human.	
XX			
OS		Synthetic.	
OS		Homo sapiens.	
XX			
PN	WO2003008574-A1.		
XX			
PD	30-JAN-2003.		
XX			
PF	08-JUL-2002; 2002WO-AU000910.		
XX			
PR	18-JUL-2001; 2001AU-00006452.		
PR	05-MAR-2002; 2002AU-00000910.		
PR	13-MAY-2002; 2002AU-00002292.		
XX			
PA	{BION-} BIONOMICS LTD.		
PA	{WALL/} WALLACE R W.		
XX			
PI	Mulvey JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;		
PI	Berkovic SF, Scheffer IE;		
XX			
DR	WPI; 2003-239332/23.		
XX			
PT	Identifying predisposition to an ion channel dysfunction, such as		
PT	periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,		
PT	schizophrenia, anxiety and depression, by detecting encoding-gene		
PT	mutation events.		
XX			
PS	Claim 6; SEQ ID NO 55; 106pp; English.		
XX			
CC	The invention relates to a novel method for identifying a subject		
CC	predisposed to a disorder associated with ion channel dysfunction. The		
CC	method comprises ascertaining if at least one of the genes encoding ion		
CC	channel subunits (ICS) has undergone a mutation event so that a cDNA		
CC	derived from the subject has any of 134 nucleotide sequences. The method		
CC	of the invention has nootropic, neuroprotective, inotropic, antipyrctic,		
CC	antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,		
CC	neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and		
CC	ophthalmological activity. A polynucleotide of the invention acts as an		
CC	ion channel agonist, or ion channel antagonist. The methods, isolated		
CC	nucleic acids, polypeptides, antibody, selective agonist, antagonist or		
CC	modulator of an ion channel, cells and genetically modified non-human		
CC	animal, are useful for the diagnosis and treatment of epilepsy and/or a		
CC	disorder associated with ion channel dysfunction, such as hyper- or hypo-		
CC	kalemic periodic paralysis, myotonias, malignant hyperthermia,		
CC	myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's		
CC	disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,		
CC	depression, phobic obsessive symptoms, neuropathic pain, inflammatory		
CC	pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,		
CC	Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic		
CC	fibrosis, congenital stationary night blindness and total colour		
CC	blindness. The present sequence represents a mutant cDNA of the		
CC	invention. The sequence data for this patent is not represented in the		
CC	printed specification, but was obtained in electronic format directly		
CC	from wipo.int/pub/published pat sequences.		

XX Sequence 3074 BP; 787 A; 784 C; 789 G; 714 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 0 Length: 3074  
Score: 4574.00 Matches: 895  
Percent Similarity: 99.78% Conservatives: 0  
Best Local Similarity: 99.78% Mismatches: 2  
Query Match: 99.69% Indels: 0  
DB: 10 Gaps: 0

US-09-810-796-4 (1-897) x ADB78684 (1-3074)

QY 1 MetLysAspValGluSerGlyArgGlyArgValLeuLeuAAsnSerAlaAlaAlaArgGly 20  
DB 215 ATGAAGGATGTGGAGTCGGGCGGGGAGGGTGTCTGCTGAATCTGGCAGCCGCGGGGC 274  
QY 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40  
DB 275 GACGGCTGTCTACTGTGGGCACCCCGCGGCCACGCTTGGTGGCGGGCGGTGGCGCTG 334  
QY 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60  
DB 335 AGGGAGAGCCCGCGGGCAGAGCGGGGCGCGGATGAGCCTGCTGGGAAGCCGCTCTCT 394  
QY 61 TyrThrSerSerGlnSerCysArgArgAenValLysTyrArgValGlnAAsnTyrLeu 80  
DB 395 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAGAGTACCGCGGGTGCAGAACTACCTG 454  
QY 81 TyrAenValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100  
DB 455 TACAACGTGCTGGAGAGACCCCGCGGCTGGGGCTTCATCTACACGCTTTCGTTTTCTCTC 514  
QY 101 LeuValPheGlyCysLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120  
DB 515 CTGTGCTTTGGTTGCTGATTTTGTGAGTTTCTACCATCCCTGAGCACACAAATTTG 574  
QY 121 AlaSerSerCysLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe 140  
DB 575 GCCTCAAGTTGCTCTTGCATCTGGAGTTTGTGATGATTTGCTGTTTGGTTTGGAGTTT 634  
QY 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160  
DB 635 ATCATTCGAATCTGTCTCGGGTGTCTGTGTATAGATACCATTTGTTCTTCAATAGCA 694  
QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180  
DB 695 AGGTTTGTCTGAAAGCCCTTCTGTGTATAGATACCATTTGTTCTTCAATAGCA 754  
QY 181 ValValSerAlaLysThrGlnGlyAenIlePheAlaThrSerAlaLeuAArgSerLeuArg 200  
DB 755 GTTGTGTTCTGCAAAACTCAGGGTAATATTTTGTGCACGCTCTGCACTCAGAACTCTCGT 814  
QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgGlyGlyThrTrpLysLeuLeu 220  
DB 815 TTCTTACAGATCCTCCGATGTGGCATGGAGCCGAGGGAGGCATTTGGAATAATCTG 874  
QY 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240  
DB 875 GGTTCAGTGTGTTATGCTCACAGCAAGGAATTAATCACAGCTTGTGTACATAGGATTTTG 934  
QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAAsnLysGluPhe 260  
DB 935 GTTCTTATTTTTCGTTCTTCTCTATCTGTGTGGTGGAAAGGATGCGCAATAAAGAGTTT 994  
QY 261 SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280  
DB 995 TCTCATATGCGAGTGTCTCTGGTGGGGGCAAAATTTACATTGACAACTATTGGCTATGGA 1054  
QY 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300  
DB 1055 GACAAACTCCCTAACTTGGCTGGGAAGATTGCTTTCTGACAGGCTTTGCACTCTCTTGGC 1114

QY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320  
DB 1115 ATTTCTTTTTCGACATTTCTCGCGCATTTCTTGCTCAGGTTTTCGATTTAAAGATACAA 1174  
QY 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAAsnLeuIleGln 340  
DB 1175 GAACAAACACCCGAGAAACACTTTGAGAAAGAAGAAACCCAGCTGCCAACCTCAATTCAG 1234  
QY 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360  
DB 1235 TGTGTTTGGCGTAGTTTACGCAGCTGATGAGAAATCTGTTCATTGCAACCTGGAAGCCA 1294  
QY 361 HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyGluAlaSerSer 380  
DB 1295 CACTTGAAGGGCTTGCACACCTGCAGCCCTACCAAGAAGAACAAGGGGAAGCATCAAGC 1354  
QY 381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400  
DB 1355 AGTCGAAGCTTAAGTTTTAAGAGCGAGTGCATGCGCTAGCCCCAGGGGCCAGATATT 1414  
QY 401 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 420  
DB 1415 AAGAGCCGACAAAGCCTCAGTAGTGACAGGAGTCCCAAGCACCATCACAGCCGAG 1474  
QY 421 GlySerProThrLysValGlnLysSerTrpSerPheAAsnAspArgThrArgPheArgPro 440  
DB 1475 GGCAGTCCCAACCAAGTGCAGAAGAGCTGGAGCTTCAACAGCACCGGCTTCGCGGCC 1534  
QY 441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460  
DB 1535 TCGTTCGCCCTCAAAAGTTCTCAGCCAAACACGATGATAGATGCTGACACAGCCCTTGGC 1594  
QY 461 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480  
DB 1595 ACTGATGATGATATGATGAAAGAGTGCAGTGTGATGATATCAGTGGAGACCTCACC 1654  
QY 481 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 500  
DB 1655 CCACCACCTAAACTGTCTATTCGAGCTATCAGAAATTTATGAAATTTTCATGTTCAAAACGG 1714  
QY 501 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 520  
DB 1715 AAGTTTAAGGAACATTAACGTCATATGATGTAAAGATGTCATTGAACATATTTCTGT 1774  
QY 521 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540  
DB 1775 GGTCACTCGACATGTTGTTGTAGAAATTAAGCCCTTCAACACAGCTGTTGATCAAAATCTT 1834  
QY 541 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560  
DB 1835 GGAAAGGGGCAAAATCACATCAGATAAGAGAGCCGAGAGAAATAACACAGCAAGCATGAG 1894  
QY 561 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 580  
DB 1895 ACCACAGACGATCTCAGTATGCTCGTCCGGTGTGTCAGAGTTGAAAGAACAGGTACAGTCC 1954  
QY 581 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 600  
DB 1955 ATAGAATCCAAGCTGGACTGCTCTTACATCATCATCAACAGGTCCTTCGGAAGGCTCT 2014  
QY 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620  
DB 2015 GCCTCAGCCCTCGCTTGGCTTCATTCAGATCCCACTTCCTTTTGAATGTGAACAGACATCT 2074  
QY 621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAAsnSerGlyCys 640  
DB 2075 GACTATCAAGCCCTGTGGATGCAAGATCTTTCCGGGTTCCGCAACAAACAGTGGCTGC 2134  
QY 641 LeuSerArgSerThrSerAlaAAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660  
DB 2135 TTATCCAGATCAACTAGTGCACCATCTCCGAGAGGCGCTGCAGTTTCATTCTGACGCCAAT 2194  
QY 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680



Db 2195 GAGTTTCAGTCCAGACATTTTACGCGCTTATGACCTTACTATGCAGCTCAAGCAACACAG 2254  
Qy 681 ValProIleSerGlnSerAspGlySerAlaValAlaIleThrAsnThrIleAlaAsnGln 700  
Db 2255 GTGCCAATTAGTCAAGAGGATGGCTCAGCAGTGGCAGCCACCAACACATTTGCACCA 2314  
Qy 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro 720  
Db 2315 ATAAATACGGCACCCCAAGCAGCCCAACAACTTTACAGATCCCACTCTCTCTCCA 2374  
Qy 721 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740  
Db 2375 GCCATCAAGCATCTGCCAGGCCAGAACTCTGACACCTTAACCTTGAGGCTTACAGAA 2434  
Qy 741 SerIleSerAspValThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760  
Db 2435 AGCATTTCTGACGTCAACCTGCTTGTGCTCCCAAGGAAATGTTTCAGGTTGCACAG 2494  
Qy 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780  
Db 2495 TCAAAATCTCACCAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG 2554  
Qy 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800  
Db 2555 TTGTCGTCTGTGCCATGTGTCGAGGAGACTTGGGCAATCTTTGCTGTGTCGCAAACTG 2614  
Qy 801 IleArgSerThrGluLeuAsnIleGlnLeuSerGlySerGlySerGlySerArg 820  
Db 2615 ATCAGGTGACCGAGGAACTGAATATACAACTTTCAGGAGTGTAGTCAAGTGGCTCCAGA 2674  
Qy 821 GlySerGlnAspPheThrProLysThrArgGluSerLysLeuPheIleThrAspGluGlu 840  
Db 2675 GGCAGCCAGATTTTACCCCAATGGAGGAAATCAAATGTTTATTAACGTATGACAGAG 2734  
Qy 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 860  
Db 2735 GTGGTCCCGAGAGACAGACAGACACTTTTGTATGCCGACCGACCGCTGCCAGGAA 2794  
Qy 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 880  
Db 2795 GCTGCTCTTGCATCAGACTCTTACGAGTGTGAGGAGTCAATCATCTCAGAGCAATTTGT 2854  
Qy 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897  
Db 2855 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCTCATGTCAAACTGAAA 2905  
RESULT 7  
ID AAS14653 standard; cDNA; 2667 BP.  
XX AAS14653;  
XX AC AAS14653;  
XX 18-DEC-2001 (first entry)  
XX Human cDNA encoding a voltage gated potassium channel hKCNQ5-2.  
XX Human; ss; voltage-gated potassium channel; KCNQ5-2; nootropic;  
XX cerebroprotective; neurotropic; analgesic; vision disorder;  
XX central nervous system disorder; epilepsy; migraine; hearing disorder;  
XX psychotic disorder; seizure; learning disorder; memory disorder; stroke;  
XX pain; gene therapy; splice variant.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH 1..2967  
FT CDS /\*tag= a  
FT /product= "hKCNQ5-2"  
XX WO200170759-A1.  
XX 27-SEP-2001.

XX PF 20-MAR-2001; 2001WO-US009328.  
XX PR 21-MAR-2000; 2000US-0190954P.  
XX PA (ICAG-) ICAGEN INC.  
XX PI Jegla TJ;  
XX WPI; 2001-611467/70.  
DR P-PSDB; AAU09021.  
XX Polypeptides and polynucleotides of potassium channel KCNQ5 for  
PT identifying a compound modulating ion flux in eukaryotic cell or cell  
PT membrane expressing the protein, comprises KCNQ approximately a- subunits.  
XX Claim 5; Page 63-64; 78pp; English.  
XX The invention relates to an isolated polypeptide comprising an alpha-  
CC subunit of a KCNQ potassium channel, with a subsequence having 65%  
CC sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence  
CC and forms a KCNQ potassium channel having the characteristic of voltage-  
CC gating with at least an additional KCNQ alpha-subunit. Also included in  
CC the scope of the invention are the nucleic acids encoding hKCNQ5  
CC (including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression  
CC vectors encoding them, antibodies against them, the use of 3-dimensional  
CC computer modelling to identify molecules that bind to a KCNQ containing  
CC potassium channel and modulate ion flux through the channel. The KCNQ  
CC polypeptide is useful for identifying a compound that increases or  
CC decreases ion flux through a potassium channel expressed in an eukaryotic  
CC host cell or cell membrane. The compound (and the KCNQ nucleic acid when  
CC used in gene therapy) is useful as a pharmaceutical agent for treating  
CC diseases involving abnormal ion flux, such as disorders of the central  
CC nervous system, such as epilepsy, migraines, and memory disorders, stroke and  
CC psychotic disorders, seizures, learning and memory disorders, stroke and  
CC pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a  
CC human tissue and the use of a nucleotide sequence of KCNQ5 to search  
CC computer databases to find variants of the sequence which are associated  
CC with disease states, is useful for screening mutations of KCNQ5. The  
XX present sequence is a splice variant of hKCNQ5 encoding hKCNQ5-2  
SQ Sequence 2667 BP; 701 A; 667 C; 660 G; 639 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 0 Length: 2667  
Score: 4527.50 Matches: 887  
Percent Similarity: 99.00% Conservatives: 1  
Best Local Similarity: 98.89% Mismatches: 0  
Query Match: 98.68% Indels: 9  
DB: 4 Gaps: 1  
US-09-810-796-4 (1-897) x AAS14653 (1-2667)  
Qy 1 MetLysAspValGluSerGlyArgValLeuLeuAsnSerAlaAlaArgGly 20  
Db 1 ATGAAGGATGTGGAGTCGGCGCGGCGAGGTGCTGTAACCTCGGAGCGCGGCGGCG 60  
Qy 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeu 40  
Db 61 GACGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120  
Qy 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60  
Db 121 AGGGAGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180  
Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysValArgValGlnAsnTyrLeu 80  
Db 181 TACACGAGTAGCAGAGCTGCGGCGCAACGTCTAGTACCGCGGCGGCGGCGGCGGCG 240  
Qy 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100  
Db 241 TACAACGTGCTGAGAGAGACCCCGCGGCTGGGCGTTTCATCTACACGCTTTCGTTTCTC 300

Qy	101	LeuValPheGlyCysLeuIleuSerValPheSerThrIleProGluHisThrLysLeu	120
Db	301	CTTGCTTTGGTTGGTTGCTGATTTTGTACAGTGTCTTCTACCATCTCCGTGAGCACACAAATTG	360
Qy	121	AlaSerSerCysLeuLeuIleuLeuPheValMetIleValValPheGlyLeuGluPhe	140
Db	361	GCCTCAAGTGGCCCTTGGATCCTGGAGTTCGTGTGATGATTTGCTGCTTTGGTGTTCGAGATTC	420
Qy	141	IleIleArgIleTyrPheAlaGlyCysCysArgTyrArgGlyTyrIleGlnGlyArgLeu	160
Db	421	ATCATTCGAATCTGGTCTGCGGGTTGCTGTTGTCGATATAGAGGATGGCAAGAAAGACTG	480
Qy	161	ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla	180
Db	481	AGGTTTGTCTGAAAGCCCTTCTGTGTATAGATACCATTTCTTATCGCTTCAATAGCA	540
Qy	181	ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg	200
Db	541	GTTGTGTTCTCGAAAACCTCAGGGTAATATTTTCCACGCTCTGCATCAGAAGTCTCCGT	600
Qy	201	PheLeuGlnIleLeuArgMetValArgMetAspArgGlyGlyThrTrpLysLeuLeu	220
Db	601	TTCTCTACAGATCCTCGCATGGTGGCATGACCGAAGGGGAGGCGCATTTGGAAATTACTG	660
Qy	221	GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu	240
Db	661	GGTTTCAGTGGTTATGCTTCACAGCAAGGAATTAATCATCAGCTTGCTGATAGGATTTTGT	720
Qy	241	ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe	260
Db	721	GTTCTTATTTTTTGGTCTTCTCTGCTGGGCAAAAGGATGCCAATAAAGAGCTTT	780
Qy	261	SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly	280
Db	781	TCTACATATGAGATGCTCTCTGCTGGGCAAAATTCATTGACAACTATTTGGCTATGGA	840
Qy	281	AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly	300
Db	841	GACAAACTCCCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCATCTCTTGGC	900
Qy	301	IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln	320
Db	901	ATTTCTTTCTTTGACATCTCTGCGCGCATCTCTGGCTCAGGTTTTCATTAAAGATCAA	960
Qy	321	GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln	340
Db	961	GAACCAACACCGCCGAACAACCTTTGAGNAAAGAAAGAACCCAGCTGCCAACCTCATTCAG	1020
Qy	341	CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro	360
Db	1021	TGTGTTGGCGTAGTTTACGACGCTGATGAGAAATCTGTTTCCATTGCAACTGGAGGCCA	1080
Qy	361	HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyGluAlaSerSer	380
Db	1081	CACTTGAAGGCCTTGCACACCTGCAGGCCCTTACC-----1113	
Qy	381	SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle	400
Db	1114	AATCAGAAGCTAAGTTTTTAAGACGAGTGGCGATGGCTAGCCCGAGGGCCAGAGTATT	1173
Qy	401	LysSerArgGlnAlaSerValGlyAspArgSerProSerThrAspIleThrAlaGlu	420
Db	1174	AAGAGCCGACAAGCCTCAGTAGGTGACAGAGAGTCCCCAAGCACCGACATCAGACCGAG	1233
Qy	421	GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro	440
Db	1234	GGCAGTCCCAACCAAGTGCAGAAAGCTGGAGCTTCAACGACCGCAACCCCGCTTCCGGCCC	1293
Qy	441	SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly	460
Db	1294	TCGCTGGCCCTCAAAGATTCTACCCAAAACCAAGTAGATAGATGCTGACAGAGCCCTTGGC	1353
Qy	461	ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr	480

Db	2434	GGCAGCCAGATTTTACCCCAATGGAGGAATCCAAATGTTTATTAACGTATGAAGAG	2493
Qy	841	ValGlyProGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaAArgGlu	860
Db	2494	GTGGTCCCGAAGACAGACAGACACATTTTGTATGCCGACCGCAGCTGCCAGGAA	2553
Qy	861	AlaAlaPheAlaSerAspSerLeuA:qThrGlyArgSerArgSerGlnSerIleCys	880
Db	2554	GCTGCTTTGCATCAGACTCTTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT	2613
Qy	881	LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys	897
Db	2614	AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAA	2664
RESULT 8			
AAH43633			
ID	AAH43633 standard; cDNA; 2772 BP.		
XX			
AC	AAH43633;		
XX			
DT	21-JAN-2002 (first entry)		
XX			
XX	Human ion-channel forming protein ORF.		
XX			
KW	Ion-channel forming protein; voltage-gated potassium channel; fetal;		
KW	brain; thymus; prostate; heart; skeletal muscle; probe; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200175108-A1.		
XX			
PD	11-OCT-2001.		
XX			
PF	03-APR-2001; 2001WO-US010875.		
XX			
PR	03-APR-2000; 2000US-0194255P.		
XX			
PA	(LEXI-) LEXICON GENETICS INC.		
XX			
PI	Hu Y, Kieke JA, Turner AC, Nehls MC, Friedrich G, Zambrowicz B;		
PI	Sands AT;		
XX			
DR	WPI; 2001-656987/75.		
DR	P-PSDB; AAB47678.		
XX			
PT	New human ion channel protein and polynucleotides encoding the protein,		
PT	useful in diagnosing or treating diseases, in drug screening, and in		
PT	clinical trial monitoring.		
XX			
PS	Claim 1; Page 34-35; 41pp; English.		
XX			
CC	The sequences in AAH43633-34 encode a novel ion-channel forming protein.		
CC	The protein shares structural similarity with mammalian ion channel		
CC	proteins, particularly voltage-gated potassium channel proteins. The		
CC	protein is expressed in many human cell lines including fetal brain,		
CC	brain, thymus, prostate, heart and skeletal muscle. The novel protein can		
CC	be used in the diagnosis or treatment of diseases, in drug screening, and		
CC	in clinical trial monitoring. The oligonucleotides may be used as		
CC	hybridization probes for screening libraries, and assessing gene		
CC	expression patterns (particularly using a micro array or high throughput		
CC	chip format). The nucleic acids and novel protein can also be used in the		
CC	identification, selection and validation of novel molecular targets for		
CC	drug discovery, to screen collections of genetic material from patients		
CC	who have a particular medical condition, to identify mutations associated		
CC	with a particular disease, as a diagnostic or prognostic assay, and to		
CC	screen for drugs which can be used to treat symptomatic or phenotypic		
CC	manifestations of perturbing the normal function of novel human protein.		
CC	The polypeptides are further used in generating antibodies		
XX			
SQ	Sequence 2772 BP; 715 A; 700 C; 713 G; 644 T; 0 U; 0 Other;		
Alignment Scores:			
Pred. No.:		0	Length: 2772

Score:	4527.50	Matches:	887
Percent Similarity:	99.00%	Conservative:	1
Best Local Similarity:	98.88%	Mismatches:	0
Query Match:	98.68%	Indels:	9
DB:	5	Gaps:	1
US-09-810-796-4 (1-897) x AAH43633 (1-2772)			
Qy	1	MetLysAspValGluSerClyArgValLeuLeuAsnSerAlaAlaAahArgGly	20
Db	106	ATGAAGATGTGAGTGGGGCCGGGACAGGTGCTGCTGAACCTCGGACGCCCGAGGGC	165
Qy	21	AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu	40
Db	166	GACGGCTGCTACTGCTGGGCACCCGCGCGCCACGCTCGTGGGGGGCGGCTGCTG	225
Qy	41	ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuGlyLysProLeuSer	60
Db	226	AGGGAGAGCGCGGGGCAAGCAGGGGGCCCGAGTAGCTCTGCTGGGGAAGCGCTCTCT	285
Qy	61	TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu	80
Db	286	TACACGAGTAGCCAGAGCTGCCGGCCCAAGTCACGTACCGGGGGTGCAGAACTACCTG	345
Qy	81	TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu	100
Db	346	TACAACGTGCTGGAGAGACCCCGCGCTGGGGTTCATCTACCCACGCTTTCGTTTTTCTC	405
Qy	101	LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu	120
Db	406	CTTGTCTTGGTGTGCTTGATTTTGTGAGTGTTCAGTGTTCCTACCATCCCTGAGGACAC	465
Qy	121	AlaSerSerCysLeuLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe	140
Db	466	GCCTCAAGTTGCCTCTGTATCTCTGGAGTTCGTGATGATTGCTCTTGGTTGGAGTTC	525
Qy	141	IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu	160
Db	526	ATCATTCGAATCTGGTCTCGGGTTCGTGTGTGATATAGAGATAGGAGGAGAAAGACTG	585
Qy	161	ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla	180
Db	586	AGTTTGTCTGAAAGCCCTCTGTGTATAGATACCATTTGTTCTTATCGCTTCAATAGCA	645
Qy	181	ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg	200
Db	646	GTTCTTCTGCAAAACTCAGGGTAAATATTTTCCACGCTCGCACTCAGAAAGTCTCCGT	705
Qy	201	PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyThrTrpLysLeuLeu	220
Db	706	TTCTCTACAGATCTCCCGCATGGTCCCATGGACCGAAGGGGAGGCACCTTGGAAATTACTG	765
Qy	221	GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu	240
Db	766	GGTTCAGTGGTTTATGCTCACAGCAAGAAATTAATCACAGCTTGGTACATAGGATTTTG	825
Qy	241	ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe	260
Db	826	GTTCTTATTTTTCGTCCTCTCTATCTGTGTGGAAGAGTGAATTAAGAGTTT	885
Qy	261	SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly	280
Db	886	TCTCATCATGACAGATGCTCTCTGGTGGGGCACAAATTAATTGACAACTATTGGCTATGGA	945
Qy	281	AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly	300
Db	946	GACAAACTCCCTAACTGGCTGGGAAGATTGCTTTCTGCAAGCTTTGGCACTCCTTGGC	1005
Qy	301	IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln	320
Db	1006	ATTTCTTCTTTGACATCTCCCGCGCATTTCTTGGCTCAGGTTTGGATTAAGATACAA	1065
Qy	321	GluGlnHisArgGlnLysHisPheGluLysArgAsnProAlaAlaAsnLeuIleGln	340

Db 1066 GAAACACACCGCCAGAAACATTTTGAGAAAGAGAGAAACCCAGCTGCCAACTCATTCAG 1125  
Qy CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360  
Db 1126 TGTGTTGGCTAGTACGACGCTGATGAGAAATCTGTTTCATTTGCAACTGGAGGCCA 1185  
Qy HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGluAlaSerSer 380  
Db 1186 CACTTGAAGGCGCTTCACACCTCGACGCTTACC----- 1218  
Qy 381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400  
Db 1219 AATCAGAAGCTAAAGTTTAAAGAGCGAGTGGCATGGCTAGCCCCAGGGGCCAGAGTATT 1278  
Qy 401 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 420  
Db 1279 AAGAGCCGACCAAGCCTCAGTAGTGACAGGAGTCCCCAGCAGCAGCATCACAGCCGAG 1338  
Qy 421 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 440  
Db 1339 GGCAGTCCGCCCAACAGTGCAGAGAGCTGGAGCTTCAACGACCGAACCCGCTTCGCGGCC 1398  
Qy 441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460  
Db 1399 TCGCTGCCGCTCAAAAGTTCTCAGCCCAACAGGATGATGATGCTGCACAGCCCTTGGC 1458  
Qy 461 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480  
Db 1459 ACTGATGATGATATGATGAAAGAGATGCCAGTGTGATGATCATCAGTGGAGACCTCACC 1518  
Qy 481 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 500  
Db 1519 CCACCATTAAACTGTCTATTCGAGCTATCAGAATTATCAAAATTTTCATGTTGCAAAACGG 1578  
Qy 501 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 520  
Db 1579 AAGTTTAAAGGAAACATTAAGTCCATGATGATGATAAAGATGATGAAACAATATTCGCT 1638  
Qy 521 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540  
Db 1639 GGTCTATCGACATGTTGTAGATTAAGCCITTCAAACACGCTGTTGATCAAAATCTT 1698  
Qy 541 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560  
Db 1699 GGAAAGGCGCAATCACATCATGATAAGAGAGCCGAGAGAAATAACAGCAGAACATCAG 1758  
Qy 561 ThrThrAspAspLeuSerMetLeuGlyArgValLysValGluLysGlnValGlnSer 580  
Db 1759 ACCACAGACGATCTCAGTATGCTCGGTGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1818  
Qy 581 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 600  
Db 1819 ATAGATCAAGCTGAGCTGCTACTAGACATCATCAACAGGCTCTTCGGAAGGCTCT 1878  
Qy 601 AlaSerAlaLeuAlaLeuSerPheGlnIleProProPheGluCysGluGlnThrSer 620  
Db 1879 GCCTCAGCCCTCGCTTTCGCTTTCATTCAGATCCCACTTTTGAATGTGAACAGACATCT 1938  
Qy 621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640  
Db 1939 GACTATCAAGCCCTGTGATAGCAAGATCTTTCGGGTTCGCAACAAACAGTGGCTGC 1998  
Qy 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660  
Db 1999 TTATCCAGATCAACTAGTGCCAACTCTCGAGAGCCCTGCAGTTCATTCAGCGCAAT 2058  
Qy 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680  
Db 2059 GAGTTTCAGTCCGACACTTCTACGCGCTTAGCCCTTACTATGACAGTCAAGCAACACAG 2118  
Qy 681 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 700

Db 2119 GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACCATTTGCAAAACCA 2178  
Qy 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro 720  
Db 2179 ATAATAACGGCACCCAGCAGCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA 2238  
Qy 721 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740  
Db 2239 GCCATCAAGCATCTGCCAGGCCAGAACTCTGCACCCCTAAACCTTCAGGCTTACAGGA 2298  
Qy 741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760  
Db 2299 AGCATTTCTGACGTACACCACTGCTTGTGGCTCCAAAGGAAATGTTTCAGGTTGCACAG 2358  
Qy 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780  
Db 2359 TCAATCTCACCAAGGACCGTTCTATGAGGAAAGCTTTTGACATGGGAGGAGAACTCTG 2418  
Qy 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800  
Db 2419 TTGCTGTCTCTGCCATGTGCGAAGGACTTGGGCAAAATCTTTGTCTGTGCCAAACCTG 2478  
Qy 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGlySerSerGlySerArg 820  
Db 2479 ATCAGTCCAGCCGAGGAACCTGAATATACAACTTTTCAGGAGTGAGTCAAGTGGCTCCAGA 2538  
Qy 821 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840  
Db 2539 GGCAGCCCAAGATTTTACCCCAATGGAGGAAATCCAAATTTGTTTATAACTGATCAAGAG 2598  
Qy 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 860  
Db 2599 GTGGGTCCGAGAGACAGACACACTTTTGTATGCCGACCCGACGCTGCCAGGGAA 2658  
Qy 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerGlnSerIleCys 880  
Db 2659 GCTGCCCTTGCATCAGACTCTCTAAGGACTCGAAGTCCAGATCATCTCAGAGCAATTGT 2718  
Qy 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897  
Db 2719 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACCTGAAA 2769  
RESULT 9  
AAH43634  
ID AAH43634 standard; cDNA; 3111 BP.  
XX  
AC AAH43634;  
DT 21-JAN-2002 (first entry)  
DE Human ion-channel forming protein coding sequence.  
DE Ion-channel forming protein; voltage-gated potassium channel; fetal;  
KW brain; thymus; prostate; heart; skeletal muscle; probe; ss.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
CDS 59..2831  
FT /\*tag= a  
FT /product= "Human ion-channel forming protein"  
XX  
FN WO2001/75108-A1.  
XX  
PD 11-OCT-2001.  
XX  
PF 03-APR-2001; 2001WO-US010875.  
XX  
PR 03-APR-2000; 2000US-0194255P.  
XX  
PA (LEXI-) LEXICON GENETICS INC.  
XX  
HU Hu Y, Kieke JA, Turner AC, Nehls MC, Friedrich G, Zambrowicz B;

PI	Sands AT;	QY	161	ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla	180
XX		Db	645	AGGTTTCTCGAAGCCCTTCTGTATAGATACCATTTGTTCTTATCGCTTCAATAGCA	704
DR	WPI; 2001-656987/75.	QY	181	ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg	200
XX	P-PSDB; AAB47678.	Db	705	GTTGTTTCTGCAAAACTCAGGTAATAATTTTGGCACGCTCTGCACCTCAGAAAGTCTCCGT	764
PT	New human ion channel protein and polynucleotides encoding the protein,	QY	201	PheLeuGlnIleLeuArgMetValArgMetAspArgGlyGlyThrTrpLysLeuLeu	220
XX	useful in diagnosing or treating diseases, in drug screening, and in	Db	765	TTCTACATCTCCGCATGGTGGCATGGACCGAAGGGAGGCACTTGGAAATTTACTG	824
PT	clinical trial monitoring.	QY	221	GlySerValValTyrAlaHisSerLysGluLeuThrAlaTrpTyrIleGlyPheLeu	240
XX	Disclosure; Page 37-38; 41pp; English.	Db	825	GGTTCTAGTGGTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTG	884
CC	The sequences in AAH43633-34 encode a novel ion-channel forming protein.	QY	241	ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe	260
CC	The protein shares structural similarity with mammalian ion channel	Db	885	GTTCTTATTTTTCGTCTTCTCTATCTGGTGGAAAGGATGCCAATAAAGAGTTT	944
CC	proteins, particularly voltage-gated potassium channel proteins. The	QY	261	SerThrTyrAlaAspAlaLeuTyrTrpGlyThrIleThrLeuThrThrIleGlyTyrGly	280
CC	protein is expressed in many human cell lines including fetal brain,	Db	945	TTTACATATGCAATGCTCTCTGGTGGGCGACAAATTAATGACAACCTATTGGCTATGGA	1004
CC	brain, thymus, prostate, heart and skeletal muscle. The novel protein can	QY	281	AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly	300
CC	be used in the diagnosis or treatment of diseases, in drug screening, and	Db	1005	GACAAAACTCCCTAACTTGGCTGGGAAGATTGCTTCTGCAGGCTTTCACCTCTTGGC	1064
CC	in clinical trial monitoring. The oligonucleotides may be used as	QY	301	IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln	320
CC	hybridization probes for screening libraries, and assessing gene	Db	1065	ATTCTTTCTTTTGGACTTCTCGCGGCAATCTTGGCTCAGTTTGGCATTAAGAATACAA	1124
CC	expression patterns (particularly using a micro array or high throughput	QY	321	GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln	340
CC	chip format). The nucleic acids and novel protein can also be used in the	Db	1125	GAACAACACCCCGCAGAAACACTTTTGAGAAAGAAAGAACCCAGCTGCCAACCTCAATTCAG	1184
CC	identification, selection and validation of novel molecular targets for	QY	341	CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro	360
CC	drug discovery, to screen collections of genetic material from patients	Db	1185	TGTGTTTGGGCTAGTTACGCAGCTGATGAGAAATCTGTTTCCCATTTGCACTAAGAAGCCA	1244
CC	who have a particular medical condition, to identify mutations associated	QY	361	HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyAlaSerSer	380
CC	with a particular disease, as a diagnostic or prognostic assay, and to	Db	1245	CACTTTGAAGGCTTGCACACTGCAGCCCTTACC-----	1277
CC	screen for drugs which can be used to treat symptomatic or phenotypic	QY	381	SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle	400
CC	manifestations of perturbing the normal function of novel human protein.	Db	1278	AATCAGAAGCTTAAGTTTAAAGGAGCGAGTGCATGCTAGCCCGCAGGCGCCAGAGTATT	1337
XX	The polypeptides are further used in generating antibodies	QY	401	LysSerArgGlnAlaSerValGlyAspArgSerProSerThrAspIleThrAlaGlu	420
QY	Sequence 3111 BP; 814 A; 771 C; 789 G; 737 T; 0 U; 0 Other;	Db	1338	AAGAGCCGACAAAGCTCAGTAGGTGACAGGAGGTCCCCAGACCCGACATCACAGCCGAG	1397
Alignment Scores:		QY	421	GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro	440
Pred. No.:	0	Db	1398	GGCAGTCCCAACCAAGTGCAGAGAGCTGGAGCTTCAACGACCGAACCCGCTTCGGGCC	1457
Score:	4527.50	QY	441	SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly	460
Percent Similarity:	99.00%	Db	1458	TCGCTGCGCCCTCAAAAGTTCTCAGCCAAACCAAGTAGATGCTGACACAGCCCTTGGC	1517
Best Local Similarity:	98.89%	QY	461	ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr	480
Query Match:	98.68%	Db	1518	ACTGATGATGATATGATGATAAAGAGTCCAGCTGTGATGTATCAGTGAAGAGACCTCACC	1577
DB:	5	QY	481	ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg	500
US-09-810-796-4 (1-897) x AAH43634 (1-3111)		Db	1578	CCACCACTTAAACTGTCTATTCGAGCTATCAGAAATTTATGAAATTTTCATGTTGCAAAACGG	1637
QY	1 MetLysAspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaAlaArgGly	QY	501	LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla	520
Db	165 ATGAAGGATGTGAGTTCGGCGCGGCGAGGTGCTGCTGAACCTCGCGAGCCGACGGGC	Db	1638	AAAGTTTAAAGGAAACATTAAGTCCATCATGATGATAAAGATGTCATTTGAACATATTCGCT	1697
QY	21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu	QY	521	GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu	540
Db	225 GACGGCTGCTACTGCTGGGCACCCCGCGGCCACGCTCGGTGGCGCGCGGTGGCCTG				
QY	41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer				
Db	285 AGGAGAGCCCGCGGCGAAGCGGGCGCGGATGAGCTGCTGGGGAAGCCGCTCTCT				
QY	61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu				
Db	345 TACACGAGTAGCCAGAGCTGCCGCGCAACGCTCAAGTACCAGCGCGGTGCAGAACTACCTG				
QY	81 TyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu				
Db	405 TACAACGTGCTGAGAGACCCCGCGCTGGCGCTTCATCTACACCTTTTCGTTTCTC				
QY	101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu				
Db	465 CTGCTCTTGGTTCGTTGATTTTGTGAGTGTTCCTTACCATCTCGAGCACCAAAATTG				
QY	121 AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe				
Db	525 GCCTCAAGTTCCTCTTGAATCCCTGGAGTTCGATGATGTCGCTCTTGTGTTGGAGTTC				
QY	141 IleIleArgIleTrpSerAlaGlyCysCysCysArgTyrArgGlyTrpGlnGlyArgLeu				
Db	585 ATCATTCGAATCTGGTCTGGGGTTGCTGTGTCGATATAGAGATGGCAAGGAGACTG				

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Db 1698 GGTCAATCTGGACATCTTGTGTAGAAATTAAGCCCTTCAACACAGGTGTGATCAAAATCTT 1757
Qy GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560
Db 1758 GGAAAGGGCAAAATCACATCAGATAAGAGAGCGGAGAGAAATAACACAGACATCAG 1817
Qy 561 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 580
Db 1818 ACCACAGACGATCTCAGTATGCTCGGTGGGTGAGTCAAGGTTGAAAAACAGTACAGTCC 1877
Qy 581 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 600
Db 1878 ATAGAAATCCAGCTGAGTCTCTACTAGACATCTATCAACAGTCTCTTCGGAAGGCTCT 1937
Qy 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620
Db 1938 GCCTCAGCCCTCGCTTGGCTTCAATCCAGATCCCACTTTTGAATGTGAACAGACATCT 1997
Qy 621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640
Db 1998 GACTATCAAGCCCTGTGGATAGCAAGATCTTTTCGGGTTCGACAAAAACAGTGGCTGC 2057
Qy 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660
Db 2058 TTATCCAGATCAACTAGTGGCAACATCTCGAGAGCCTGCAGTTTCAATCTGACGCCAAT 2117
Qy 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680
Db 2118 GAGTTCAAGTCCAGACATCTTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2177
Qy 681 ValProIleSerGlnSerAspGlySerAlaValAlaIleThrAsnThrIleAlaAsnGln 700
Db 2178 GTGCCAATTAGTCAAGGCGATGGCTCAGCAGTGGCAGCCACCAACACCAATTCGCAACCA 2237
Qy 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro 720
Db 2238 ATAATACGGACCCACAGCCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2297
Qy 721 AlalIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740
Db 2298 GCCATCAAGCATCTGCCCGAGCCAGAACTCTGCACCCCTAACCCCTGCAGGCTTACAGAA 2357
Qy 741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760
Db 2358 AGCATTTCTGACGTCAACCACTGCTTGTGCTTCAAGGAAATGTTTCAGGTTGCACAG 2417
Qy 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780
Db 2418 TCAATCTCACCAGAGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG 2477
Qy 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800
Db 2478 TTGTCGTCTGCCATGTCGCGAAGGACTTGGGCAAACTCTTGTCTGTGCAAAACCTG 2537
Qy 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 820
Db 2538 ATCAGTCCGAGGAGAACTGAATATACAACTTTTCAGGAGTGTAGTCAAGTGGCTCCAGA 2597
Qy 821 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840
Db 2598 GGCAGCCCAAGATTTTTTACCCAAATGGGAGGGAATCCAAATGTTTATTAACATGATGAAG 2657
Qy 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnPProAlaArgGlu 860
Db 2658 GTGGTCCCGAAGACAGACACACACTTTTGTATGCGCACCGCACCTGCCAGGGA 2717
Qy 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 880
Db 2718 GCTGCTTTTGCATCAGACTCTCTAAGGACTTGAAGTCAAGGTCAAGTATCTCTCAGACATTTGT 2777
Qy 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897
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Db 2778 AAGCAGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAA 2828
RESULT 10
AAC64371
ID AAC64371 standard; cDNA; 3718 BP.
XX
AC AAC64371;
XX
DT 07-FEB-2001 (first entry)
XX
DE Human KCNQ5 (KCN6q) cDNA sequence SEQ ID NO:2.
XX
KW Human; KCNQ5; KCN6q; chromosome 6; voltage-gated potassium channel;
Stargardt-like macular dystrophy; cone-rod macular dystrophy;
Salla disease; ophthalmological; auditory; central nervous system;
cardioactive; anticonvulsant; gastrointestinal; muscular active;
age-related macular degeneration; macular degeneration; deafness;
epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;
gastrointestinal disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200061606-A1.
XX
PD 19-OCT-2000.
XX
PF 10-APR-2000; 2000WO-US009587.
XX
PR 14-APR-1999; 99US-0129274P.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Petrukhin K, Caskey CT, Li W, Metzker ML;
P-PSDB; AAB24241.
XX
DR WPI; 2000-647417/62.
XX
PT Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying
inhibitors and activators which can treat e.g. Stargardt-like macular
dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy.
XX
PS Claim 3; Fig 2; 99pb; English.
XX
CC The present sequence encodes the human KCNQ5 (also called KCN6q) protein,
which is a voltage-gated potassium channel protein. Human KCNQ5 has
ophthalmological, auditory, central nervous system (CNS), cardioactive,
anticonvulsant, gastrointestinal and muscular active activities.
CC Sequences and methods from the present invention are useful for
identifying activators or inhibitors of KCNQ5 protein. These activators
and inhibitors are useful for treating Stargardt-like macular dystrophy,
cone-rod dystrophy, Salla disease, age-related macular degeneration,
other forms of macular degeneration, deafness, epilepsy, and different
forms of neuropsychiatric, heart, gastrointestinal, and muscle disorders.
CC Stargardt-like macular dystrophy and cone-rod dystrophies are located at
chromosome 6q
XX
SQ Sequence 3718 BP; 1054 A; 845 C; 866 G; 953 T; 0 U; 0 Other;
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## Alignment Scores:

Pred. No.:	0	Length:	3718
Score:	4407.00	Matches:	860
Percent Similarity:	99.88%	Conservative:	0
Best Local Similarity:	99.88%	Mismatches:	1
Query Match:	96.05%	Indels:	0
DB:	3	Gaps:	0

US-09-810-796-4 (1-897) x AAC64371 (1-3718)

Qy	37	GlyGlyGlyLeuArgGluSerArgGlyLysGlnGlyAlaArgMetSerLeuLeuGly 56
Db	93	GGCGGTGCTCTGAGGAGAGCGCGGGCAAGCAGGGGGCCGCGATGAGCTGTCTGGG 152
Qy	57	LysProLeuSerTyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgVal 76

153	Db		AAGCGCTCTCTTACACGAGTAGCCGCGCAAGCTCAAGTACCGGGGGTG	212
77	Qy		GlnAsnTyrLeuTyrAsnValLeuGluArgProAcrGlyTrpAlaPheIleTyrHisAla	96
213	Db		CAGAACTACCTGTACAAACGTCGTGGAGACCCCGCGCTGGCGGTTCATCATCACCGCT	272
97	Qy		PheValPheLeuLeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGlu	116
273	Db		TTGGTTTTCTCCTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTCTACCATCCCTGAG	332
117	Qy		HisThrLysLeuAlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPhe	136
333	Db		CACACAAAATGGCGCTCAAGTGCCTCTTGATCCTGGAGTTCGTGAAGTATGCGTCTTT	392
137	Qy		GlyLeuGluPheIleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrp	156
393	Db		GGTTTGGATTTCATCATTCGAATCTGGTCGCGGTTGCTGTGTGCATATAGAGATGG	452
157	Qy		GlnGlyArgIleArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIle	176
453	Db		CAAGGAAGACTGAGGTTTGTGCGAAAGCCCTCTGTGTATATAGATACCATGTTCTTATC	512
177	Qy		AlaSerIleAlaValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeu	196
513	Db		GCTTCAATAGCAGTTGTTTCTGCAAAACTCAGGTAATATTTTGCACGCTCGACATC	572
197	Qy		ArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgGlyGlyThr	216
573	Db		AGAAAGTCTCGTTTCTTACAGATCCTCGCATGGTCGCATGGACCGCAAGGGAGGCACT	632
217	Qy		TrpLysIleLeuGlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyr	236
633	Db		TGGAAATTTACGGGTTTCAGTGGTTTATGCTCAGACAGGAATTAATCATCAGCTTGGTAC	692
237	Qy		IleGlyPheLeuValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAla	256
693	Db		ATAGGATTTTGTGTTCTTATTTTTTTCGTTCTCTTCTGTCTATCTGGTGGAAAGGATGCC	752
257	Qy		AsnLysGluPheSerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThr	276
753	Db		AATAAAGAGTTTCTACATATGCAATGCTCTCTGGTGGGGCAATATCATTTGACAACT	812
277	Qy		IleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPhe	296
813	Db		ATTGGCTATGGAGACAAACTCCCTTAACCTTGGCTGGGAAGATGCTTTCTGCAGGCTTT	872
297	Qy		AlaLeuLeuGlyIleSerPheAlaLeuProAlaGlyIleLeuGlySerGlyPheAla	316
873	Db		GCACCTCCTTGGCAVTTCTTTTGGCACTCTCTGCGCGCATCTCTGGCTCAGGTTTGCA	932
317	Qy		LeuLysValGlnGluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAla	336
933	Db		TTAAAAGTACAAAGAACACACCGCCAGAAACACTTTTGAGAAAAGAAAGAACAGGCG	992
337	Qy		AsnLeuIleGlnCysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAla	356
993	Db		AACTCTCATTTAGTGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATGCA	1052
357	Qy		ThrTrpLysProHisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGly	376
1053	Db		ACCTGGAAGCCACACTTGAGGCTTGCACACTTCGACGCTCACCAGAAAGAACAGGG	1112
377	Qy		GluAlaSerSerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArg	396
1113	Db		GAAGCATCAAGCAGTCAGAACTAAGATTTTAAAGAGCGAGTGCCTAGCTGGCTAGCC	1172
397	Qy		GlyGlnSerIleLysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAsp	416
1173	Db		GGCCAGAGTATTAAGAGCCGACAGCCTCAGTAGTACAGAGAGTCTCCACAGCACCGAC	1232
417	Qy		IleThrAlaGluGlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThr	436

1233	ATCAGCCGAGGGAGTCCCAACAAAGTGTCAGAAGCTCGAGCTTCAGAGCTTCCAACGCCGAACC	1239
437	ArgPheArgProSerLeuA:rgLeuLysSerSerGlnProLysProValIleAspAlaasp	456
1293	CGCTTCGGGCCTCGCTGGCCTCAAAGTTCTTCAGSCAAAACACAGTGTATAGATGCTGCAC	1352
457	ThrAlaLeuGlyThrAspAspValTyrAspGluLysGlyCyseGlnCyseAspValSerVal	476
1353	CACAGCCCTTGGCATGTATGTATATGATGAAGAAAGAGTAGCCAGTGTGATTAAGT	1412
477	GluAspLeuThrProProLeuLysThrValIleA:rgAlaIleA:rgIleMetLysPheHis	496
1413	GAAGACTCACCCACCACCTTAAACCTGTCAITTCGAGCTATTCAAGAAATATGAAATTCAT	1472
497	ValAlaLysA:rgLysPheLysGluThrLeuA:rgProTyrAspValIysAspValIleGlu	516
1473	GTTGCAAAACGGAAAGTTTAAAGAAACAATTACGTCCTATATGATGATAAAGATGTCAITGAA	1532
517	GlnTyrSerAlaGlyHisLeuAspMetLeuCysA:rgIleLysSerLeuGlnThrA:rgVal	536
1533	CAATATTCTGCTGGTTCATCTGGACATGTTGTGTAGAAATTAAGAAGCTTCAAACACGTTGT	1592
537	AspGlnIleLeuGlyLysGlyGlnIleThrSerAspLysPlysSerA:rgGluLysIleThr	556
1593	GATCAAAATCTTGGAAAGAGGCAAAATCACATCAGATTAAGAAGAGCGCAGAGAAATACAA	1652
557	AlaGluHisGluThrThrAspAspLeuSerMetLeuGlyA:rgValValLysValGluLys	576
1653	GCAGAACATGAGACACACAGCATCTCGATATGCTCGCTCGGGTGGTCAAGTTGNAAAA	1712
577	GlnValGlnSerIleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeu	596
1713	CAGGTACAGTCCATAGAATCCAAAGCTGCACTGCCTACTAGACATCTATTCAACAGAGTCCCT	1772
597	A:rgLysGlySerAlaSerAlaLeuAlaLeuAser:PheGlnIleProPropheGluCys	616
1773	CGAAAGGCTCTGCTCGAGCCCTCGCTTGGCTTCATTCCAGATCCCACCTTTTGAATGT	1832
617	GluGlnThrSerAspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGln	636
1833	GAACAGACATCTGACTATCAAAAGCCCTGGATAGCAAAAGATCTTTCGGGTTCCGCAAA	1892
637	AsnSerGlyCyseLeuSerA:rgSerThrSerAlaAsnIleSerA:rgGlyLeuGlnPheIle	656
1893	AACAGTGGCTGCTTATCAGATCAACTAGTAGTGCACCAATCTTCAGAGAGCCTCGAGTTCAIT	1952
657	LeuThrProAsnGluPheSerAlaGlnThr:PheTyrAlaLeuSerProThrMetHisSer	676
1953	CTGACGCCAAATGAGTTCAGTGCCACAGACTTCTTACGGCTTAGCCCTACTATGCACAGT	2012
677	GlnAlaThrGlnValProIleSerGlnSerAspGlySerAlaValAlaIleThrAsnThr	696
2013	CAAGCAACACAGGTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACC	2072
697	IleAlaAsnGlnIleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIlePro	716
2073	ATTGCAACCAATAAATACGGCACCCACGACGCCCCAACACTTTACAGATCCCA	2132
717	ProProLeuProAlaIleLysHisLeuProA:rgProGluThrLeuHisProAsnProAla	736
2133	CCTCCTCTCCACGCCATCAAGCATCTGCCAGGCGCAAAACTCTGCACCTTAACCTCGCA	2192
737	GlyLeuGlnGluSerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnVal	756
2193	GGCTTACAGAAAGCANTTCTGACGTCCACACTGCTTGTGCTTCCAAAGGAAATGTT	2252
757	GlnValAlaGlnSerAsnLeuThrLysAspA:rgSerMetA:rgLysSerPheAspMetGly	776
2253	CAGGTTGCACAGTCAAACTCTCACCAAGACCGTTCATTAGGAGAAAGCTTTTCACATGGGA	2312
777	GlyGluThrLeuLeuSerValCysProMetValIProLysAspLeuGlyLysSerLeuSer	796
2313	GGAAACACTGTGTGTGTCTGCTCCCATGGTCCGAGAGCATCTGGGCAAACTTTGTCT	2372



Qy 797 ValGlnAenLeuileArgSerThrGluGluLeuAenIleGlnLeuSerGlySerGluSer 816  
 Db 2373 GTGCAAAACCTGATCAGGTCGACCGAGAACTGAATATACAACTTTCAGGCGAGTGAGTCA 2432  
 Qy 817 SerGlySerArgGlySerGlnAspPheTyProLysTTPArgGluSerLysLeuPheile 836  
 Db 2433 AGTGCTCCAGAGGCGAGCAGAGATTTTACCCCAATGGAGGGAATCCAAATTTGTTATA 2492  
 Qy 837 ThrAspGluGluValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGln 856  
 Db 2493 ACTGATGAAGAGTGGTCCCGAGAGACAGACAGACACTTTTGTATGCGCAGCGCAG 2552  
 Qy 857 ProAlaArgGluAlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSer 876  
 Db 2553 CCGTCCAGGGAAGCTGCTTTGTCATCAGACTCTCTAAGGACTGGAAGGTCAAGTCAATCT 2612  
 Qy 877 GlnSerIleCysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeu 896  
 Db 2613 CAGACATTTGTAAGGAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTG 2672  
 Qy 897 Lys 897  
 Db 2673 AAA 2675

## RESULT 11

AAAA47618  
 ID AAA47618 standard; cDNA; 2335 BP.

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CC Mutations in 3 known genes of the KCNQ branch of the potassium channel  
 CC gene family underlie inherited cardiac arrhythmia's, neonatal epilepsy  
 CC and in some cases associated with deafness. KCNQ4 has been mapped to the,  
 CC DFNA2 locus for autosomal dominant hearing loss, and a dominant negative  
 CC KCNQ4 mutation that causes deafness in a DNA2 pedigree has been  
 CC identified. KCNQ4 is the first potassium channel gene underlying non-  
 CC syndromic deafness. KCNQ4 forms heteromeric channels with other KCNQ  
 CC channel subunits, especially KCNQ3. Nucleotides encoding the KCNQ4  
 CC protein and the protein itself may be used in the prevention, treatment  
 CC and diagnosis of diseases associated with inappropriate KCNQ4 expression.  
 CC The nucleotides may also be used as DNA probes in diagnostic assays (e.g.  
 CC polymerase chain reactions (PCR)) to detect and quantify the presence  
 CC of similar nucleic acid sequences in samples and to identify mutations  
 CC within them, and hence which patients may be in need of restorative  
 CC therapy. They may also be used to study the expression and function of  
 CC KCNQ4 polypeptides and their role in metabolism, for example through the  
 CC production of transgenic animals. The KCNQ4 polypeptides may be used as  
 CC antigens in the production of antibodies and to identify modulators  
 CC (agonists and antagonists) of KCNQ4 expression and activity. The anti-  
 CC KCNQ4 antibodies and KCNQ4 antagonists may also be used to down regulate  
 CC KCNQ4 expression and activity. They may be used in this way to treat  
 CC tinnitus, loss of hearing (especially progressive hearing loss, neonatal  
 CC deafness and presbycusis (deafness of the elderly)) and disease or  
 CC adverse conditions of the central nervous system (CNS) such as affective  
 CC disorder, Alzheimer's disease, anxiety, ataxia, CNS damage caused by  
 CC trauma, stroke or neurodegenerative illness, cognitive deficits,  
 CC compulsive behavior, dementia, depression, Huntington's disease, mania,  
 CC memory impairment, memory disorders and dysfunctions, motion disorders,  
 CC motor disorders, neurodegenerative diseases, Parkinson's disease,  
 CC Parkinson-like motor disorders, phobias, Pick's disease, psychosis,  
 CC schizophrenia, spinal cord damage, stroke and/or tremor. Conversely,  
 CC antisense nucleic acid molecules may be administered to down regulate  
 CC KCNQ4 expression by binding with the cells own KCNQ4 genes and preventing  
 CC their expression

XX SQ Sequence 2335 BP; 396 A; 812 C; 719 G; 408 T; 0 U; 0 Other;  
 SQ Alignment Scores:

Pred. No.: 7.58e-158 Length: 2335  
 Score: 2012.00 Matches: 437  
 Percent Similarity: 65.45% Conservative: 82  
 Best Local Similarity: 55.11% Mismatches: 136  
 Query Match: 43.85% Indels: 138  
 DB: 3 Gaps: 16

US-09-810-796-4 (1-897) x AAA47618 (1-2335)

Qy 8 ArgGlyArgValLeuLeuAenSerAlaAlaArgGlyAspGlyLeuLeuLeuGly 27  
 Db 127 CGGGGAGCGCCCGCGCGAGCTAGTGCGCTCAGCGC----- 165  
 Qy 28 ThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 47  
 Db 166 ---CGTCAGAGCGACAGCGCGAGCGG-----CGGGGCGG 201  
 Qy 48 GlnGlyAla-ArgMetSerLeuLeuGlyLysProLeu----- 59  
 Db 202 CTCGCCGCGCGCGCTCGCGCTCTCTGGGCGAGCCCGCGCGCGCGCGCGCGCG 261  
 Qy 60 -----SerTyrThrSerSerGlnSerCysArgArgAsnValLysTy 73  
 Db 262 GCGGGGTCCGGCTCGGGCTCCGGCGCGCGCGCTCTCTGGCGCGCGCGCGCGCTA 321  
 Qy 73 rArgArgValGlnAsnTyrLeuTyrAsnValLeuGluArgProArgGlyTTPAlaPhe11 93  
 Db 322 CCGCGCGCTGCAGAACTGGGTCTACACGTCGTGGAGCGGCCCGCGCGCTCGT 381  
 Qy 93 eTyrHisAlaPheValPheLeuLeuValPheGlyCysLeuLeuLeuSerValPheSerTh 113  
 Db 382 CTACACGCTCTCATATTTTGTGCTTTCAGCTGCTGCTGCTGCTGCTGCTCCAC 441  
 Qy 113 rIleProGluHisThrLysLeuAlaSerSerCysLeuLeuLeuGluPheValMet11 133

Nucleic acids encoding the novel KCNQ4 potassium channel subunit, useful  
 e.g. for treating tinnitus, deafness, Alzheimer's and Parkinson's  
 diseases.

Claim 1; Page 43-48; 65pp; English.

Db 442 TATCCAGAGACCCAGGAACCTTGGCAACGAGTGTCTCTCATCTTGGAAATTCGTGATGAT 501  
 Qy 133 eValValPheGlyLeuGluPheIleAArgileTriPserAlaGlyCysCysArgTy 153  
 Db 502 CGTGGTTTCGGCTTGGAGTACATCGTCCGGTCTGTGTCGGGATGCTGCTCGCGCTA 561  
 Qy 153 rArgGlyTrpGlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrI 173  
 Db 562 CCGAGATGGCAGGCTGCTTCCGCTTGGCAGAAAGCCCTCTGTGTCTATCGACTTCAT 621  
 Qy 173 eValLeuIleAlaSerIleAlaValSerAlaLysThrGlnIlyAenIlePheAlaTh 193  
 Db 622 CGTGTCTGGCTCGGTGGCGGTCATCGCCGGGTACCCAGGCGAACATCTTGGCCAC 681  
 Qy 193 rSerAlaLeuArgSerLeuPheGlnIleLeuArgMetValArgMetAspArgAr 213  
 Db 682 GTCCGCGCTCGCAGCATGCTTCTCGCATCTGCGCATGCTGCGCATGGACCGCG 741  
 Qy 213 gGlyGlyThrTrpLysLeuGlySerValValIlyAlaHisSerLysGluLeuIleTh 233  
 Db 742 CGCGCGCACCTGGAAAGCTGCTGGGCTCAGTGGTCTACGCGCATAGCAAGGAGCTGATCAC 801  
 Qy 233 rAlaTrpTrpIleGlyPheLeuValLeuIlePheSerSerPheLeuValIlyLeuValG 253  
 Db 802 CGCCTGGTACATCGGTTCTGTGCTCATCTTCCCTCTCTTCTGTGTCTACCTGGCGCA 861  
 Qy 253 uLysAspAlaAenLysGluPheSerThrTyAlaAspAlaLeuTrpTrpGlyThrIleTh 273  
 Db 862 GAAGACGCCAACTCCGACTTCTCTCTCCTACGCGACTCGTCTGTGGTGGGAGCGATTAC 921  
 Qy 273 rLeuThrThrIleGlyTyArgLysPheThrProLeuThrTrpLeuGlyArgLeuLeuSe 293  
 Db 922 ATTGACAACTATCGGTATGTGTGACAGACACCGCACATCGTGGTGGCAGGGTCTTGGC 981  
 Qy 293 rAlaGlyPheAlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySe 313  
 Db 982 TGCTGGCTTCGCTTACTGGCATCTCTTCTTCTTCTGCTGCTGCGGCATCTTAGGCTC 1041  
 Qy 313 rGlyPheAlaLeuLysValGlnGluGlnHisArgGlnLysPheGluLysArgArgAs 333  
 Db 1042 CGGCTTTCGCTTGAAGGTCAGAGACGACCGCGAGAGACCTTCGAGAGCGGAGAT 1101  
 Qy 333 nProAlaAlaAenLeuIleGlnCysValTrpArgSerTyAlaAlaAsp---GluLysSe 352  
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 Qy 352 rValSerIleAlaThrTrp----- 358  
 Db 1162 CTACCTGACAGCACCTGGTACTTACTATGACAGTATCTCTCCATCTCTTCCAGAGCTGGC 1221  
 Qy 358 ----- 358  
 Db 1222 CCTCTTTGTTGACAGCTGCAACGGCGCGCAATGGGGCCCTACGGCCCTCGAGGTGGC 1281  
 Qy 359 -----LysProHisLeuLysAlaLeuHisTh 367  
 Db 1282 GCGGGCGCGGTACCCGACGAGCACCTCCCGTTTACCGCGCGGTGGCCACCTGCGCACCG 1341  
 Qy 367 rCysSerProThrLysLysGluGlnGlyAlaSerSerSerGlnLysLeuSerPheTy 387  
 Db 1342 GCGGGCGAGCACCTCTCTGCTGCGCGTGGGAAAGCAGC-----CGGATGGGATCA 1392  
 Qy 387 sGluArgValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGln-----Al 405  
 Db 1393 AGACCGCATCCGATGGGAGCTCCAGCGCGGCGAGCGGTCTCTTCCAGCAGCAGCTGGC 1452  
 Qy 405 aSerValGlyAspArgSerProSerThrAspIleThrAlaGluGly---SerProTh 424  
 Db 1453 ACCTCCAAACATGCCACCTCCCAAGCAGCAGCAGGTGGGTGGGCCACACCGCCCCAC 1512  
 Qy 424 rLysValGlnLysSerTrpSerPheAenAspArgThrArgPheArgProSerLeuArgLe 444  
 Db 1513 CAAGGTGCAAAAGCTGGAGCTTCATGACCGCACCGCTTCGGGCATCTCTGAGACT 1572

Qy 444 uLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspAspVa 464  
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 Db 1615 AGCAGAGGAGAGAGAGTACCAGTGTGAGTCCAGGTGGACGACATCATCGCTGCTGTGAA 1674  
 Qy 484 sThrValIleArgAlaIleArgIleMetIlyPheHisValAlaLysArgLysPheLysG 504  
 Db 1675 GACAGTCACTCCCTCATCAGGATTCCTCAAGTTCCTGTGGTGGCCAAAGAAATTCAGGA 1734  
 Qy 504 uThrLeuArgProTyAspValIleGluGlnIlyTrsAlaGlyHisLeuAs 524  
 Db 1735 GACACTGCGACCGTACGAGCGTCAAGGACGTCTTTCAGCAGTACTCAGCAGGCGACCTGGA 1794  
 Qy 524 pMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGly 544  
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 Db 1853 -----CCCGGGGACAGGAGCGCGGAGGAAGCGGCACAGGGGCCCTCCGACGCGAGT 1908  
 Qy 561 rThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSerI 581  
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 Qy 581 eGluSerLysLeuAspCysLeuLeuAspIleTyGlnGlnValLeuArgLysGlySerAl 601  
 Db 1969 CGAGCAACAGCTGACCTGCTGTGGGTCTTATTCGCGCTGCTGCTGCTGCGCACCTC 2028  
 Qy 601 aSerAlaLeuAlaLeuAlaSerPheGlnIleProPheGluCysGluGlnThrSerAs 621  
 Db 2029 GGCC-----AGCTGGCGCGCTGCAAGTGGCGCTTTCGACCCCGACATCACCTCCGA 2082  
 Qy 621 pTyGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCysLe 641  
 Db 2083 CTACCAACAGCCTGTGGACCCAGGACATCTCCGTCTCGGACAGACGCTCAGC---AT 2139  
 Qy 641 uSerArgSerThrSerAlaAenIleSerArgGlyLeuGlnPheIleLeuThrProAsnG 661  
 Db 2140 CTCCCGCTCGGTGACGACCAACATGACTGAGG----- 2173  
 Qy 661 uPheSerAlaGlnThrPheTyAlaLeuSerProThrMetHisSerGlnAlaThrGlnVa 681  
 Db 2173 ----- 2173  
 Qy 681 lProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGlnI 701  
 Db 2174 -----ACTTCTCAGAGGCGGCGAGCACA----- 2197  
 Qy 701 eAsnThrAlaProLysProAlaAlaProThrThrLeu-GlnIleProProLeuProA 721  
 Db 2198 -CGGCGAGCCCGCGGCTGGCGTCCGACTGCGCTCTGAGGCTCGGAGCTCTCTCTCGT 2256  
 Qy 721 laIleLysHisLeuProArgProGluThrLeuHis 732  
 Db 2257 ACTTGAACCTCACTCCCTCAGCGGGAGAGAGACCAC 2291

RESULT 12

ADE31698 standard; DNA; 2335 BP.

ID ADE31698

XX AC ADE31698;

XX DT 29-JAN-2004 (first entry)

XX DE Human 32394 gene #SEQ ID 55.

XX KW Antiarteriosclerotic; cardiatic; vasotropic; antiinflammatory; thrombolytic; antiarrhythmic; antianginal; hypotensive; gene therapy;



QY 313 rGlyPheAlaLeuLysValGlnGlnHisArgGlnLysHisPheGluLysArgArgAs 333  
 DB 1042 CGGCTTTGCTGAGGTCCAGAGCAGCAGCCGCGAAGACACTTCAGAGAGCGAGAT 1101  
 QY 333 nProAlaAlaAsnLeuLysGlnCysValTyrArgSerTyrAlaAlaAsp---GluLysSe 352  
 DB 1102 GCCGGCAGCCAACTCATCAGGCTGCTGGCGCTGTACTCCACCGATATGACCGCGGC 1161  
 QY 352 rValSerIleAlaThrTrp----- 358  
 DB 1162 CTACTCTGACAGCCACCTGCTACTACTATGACAGATATCTCCATCTTCCAGAGAGTGGC 1221  
 QY 358 ----- 358  
 DB 1222 CCTCTTGTGAGCAGTGCACAGGGCCCGCAATGAGGGGCTTACGGCCCTCGAGGTGGC 1281  
 QY 359 -----LysProHisLeuLysAlaLeuHisTh 367  
 DB 1282 GCGGGCGCGGTACCGAGCGGACACCTCCCGTTTACCGCGCTTGCACCTGCCACCG 1341  
 QY 367 rCysSerProThrLysLysGluGlnGlyGluAlaSerSerGlnLysLeuSerPheLy 387  
 DB 1342 GCCGGCAGCACCTCTCTCTCCCTGGGGAAGCAGC-----CGGATGGGCATCAA 1392  
 QY 387 sGluArgValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGln-----Al 405  
 DB 1393 AGACCGCATCGCATGGCAGCTCCAGCGGGAGCGGTCTTCCAGCAGCAGTGGC 1452  
 QY 405 aserValGlyAspArgArgSerProSerThrAspIleThrAlaGluGly---SerProTh 424  
 DB 1453 ACCTCCAACTGCCACCTCCCAAGCAGCAGCAGGTGGTGAGGCCACAGCCGCCAC 1512  
 QY 424 rIysValGlnLysSerTyrSerPheAsnAspArgThrArgPheArgProSerLeuArgLe 444  
 DB 1513 CAAGTGCAAAAGAGCTGAGCTTCAATGACCGCAGCCGCTTCCGGGATCTCTGAGACT 1572  
 QY 444 uLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspAspVa 464  
 DB 1573 C-----AAACCCCGCACCTCTGCTGAGGATGCC---CCCTCAGAGGAAGT 1614  
 QY 464 lTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuLy 484  
 DB 1615 AGCAGAGGAGAGAGTACCTACAGTGTGAGCTCAGCGTGGACGACATCATCGCTGTGTGAA 1674  
 QY 484 sThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPheLysGl 504  
 DB 1675 GACAGTCATCCCTCATCAGATTTCTCAAGTTCTGTGTGGCCAAAGAAATCAAGGA 1734  
 QY 504 uThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAs 524  
 DB 1735 GACACTGGACCGTAGCAGCTGAAGGACGTCAATTGAGCAGTACTCAGCAGGCCACCTGGA 1794  
 QY 524 pMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGl 544  
 DB 1795 CATGTGGCGCGATCAAGAGCTGCAACTCGGTGGACCAAAATGTGGGTGGGGG-- 1852  
 QY 544 nIleThrSerAspLysLysSerArgGlu-----LysIleThrAlaGluHisGluTh 561  
 DB 1853 -----CCCGGGACAGGAGCCCGGAGAGGCGCAAGGGCCCTCCGAGCGGAGGT 1908  
 QY 561 rThrAspLeuSerMetLeuLysArgValValLysValGluLysGlnValGlnSerIl 581  
 DB 1909 GGTGATGAATCAGCATCGGACGCTGCTGCTCAAGTGGAGAGCAGGTGTCAGTCCAT 1968  
 QY 581 eGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySerAl 601  
 DB 1969 CGAGCAACAAGCTGACCTCTGTGGGCTTCTATTGCGCCTCCCTGCGCTTGGCACCTC 2028  
 QY 601 aserAlaLeuAlaLeuAlaSerPheGlnIleProPheGluCysGluGlnThrSerAs 621  
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 QY 621 pTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCysLe 641

DB 2083 CTACCACGCCCTGTGTGACCCAGGAGCATCTCCGTCCTCCGACAGACGCTCAGC---AT 2139  
 QY 641 uSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsnGl 661  
 DB 2140 CTCCCGCTCGTCAGCAGCACCAACATGGACTGAGGG----- 2173  
 QY 661 uPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGlnVa 681  
 DB 2173 ----- 2173  
 QY 681 lProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGlnIl 701  
 DB 2174 ----ACTTCTCAGAGGCGAGGCGAGCACA----- 2197  
 QY 701 eAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuProA 721  
 DB 2198 -CGGCAGGCGCGCGCTGGCGCTCCGACTGCCCTCTGAGGCTCGGACTCCTCTCGT 2256  
 QY 721 laIleLysHisLeuProArgProGluThrLeuHis 732  
 DB 2257 ACTTGAACCTCACTCCCTCAGGGGAGAGAGACCAC 2291  
 RESULT 13  
 ADS17851  
 ID ADS17851 standard; cDNA; 5595 BP.  
 XX  
 AC ADS17851;  
 XX 02-DEC-2004 (first entry)  
 DT  
 XX  
 DE Rattus norvegicus KCNQ cDNA #2.  
 XX  
 KW KCNQ; potassium channel; anxiety; insomnia; hyper-excitability disorder;  
 KW Alzheimer's disease; peripheral neuropathy; neurodegenerative disease;  
 KW neuroprotective; anticonvulsant; nootropic; tranquiliser; sedative;  
 KW norway rat; gene; ss.  
 XX  
 OS Rattus norvegicus.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1553..4111  
 FT /\*tag= a  
 FT /product= "KCNQ protein"  
 XX  
 XX US2004175691-A1.  
 XX 09-SEP-2004.  
 XX 08-APR-2004; 2004US-00820307.  
 XX 03-DEC-1998; 98US-0110804P.  
 PR 03-DEC-1999; 99US-00454868.  
 XX (BROW/) BROWN B S.  
 PA (MCKI/) MCKINNON D.  
 XX Brown BS, McKinnon D;  
 XX WPI; 2004-642119/62.  
 DR P-PSDB; ADS17852.  
 XX  
 XX Evaluating compound for utility in treating neurological disease such as  
 XX epilepsy and anxiety, involves contacting compound with cell co-  
 XX expressing KCNQ2 and KCNQ3 that form potassium channel, and measuring  
 XX activity of potassium channel.  
 PS Disclosure; SEQ ID NO 8; 38pp; English.  
 XX  
 XX The present invention relates to a method of evaluating a compound for  
 XX utility in treating neurological disease. The method involves contacting  
 XX a compound with a cell that co-expresses KCNQ2 and KCNQ3, where the KCNQ2  
 XX and KCNQ3 form a potassium channel and measuring the activity of the



617	-----GluGlnThrSerAspTyrGlnSerProValAspSerLysAspLeu	631
3479	GGGGCCAAAGGAGCCTGAGCGGACCAACACCTACCAAGCCCGAGGACACCGTGAC---	3535
632	SerGlySerAlaGlnAsnSerGlyCys-----LeuSerArgSerThrSerAlaAsn	648
3536	-----CATGCACAAAGCATGGCTGTATTATTAAAGATTGTCGCTCCACCAAGCTCT---	3586
649	IleSerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyr	668
3587	-----ACGGCCAGAGGAATAC	3604
669	AlaLeuSerProThrMethIleSerGlnAlaThrGlnValProIleSerGlnSerAspGly	688
3605	GGCGACCCCGCTCATG-----	3622
689	SerAlaValAlaIleThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAla	708
3623	-----CCCTCTGCCAGTGT	3637
709	AlaPro---ThrThrLeuGlnIleProProProLeuProAlaIleLysHisLeuProArg	727
3638	CCCCATCCACCTCGTGGCAGCA-GAGCCACCAAGCGCA-----CGGACCTCCCGCT	3690
728	ProGluThr-----LeuHisProAsn-ProAlaGlyLeuGlnGluSerIleSe	743
3691	GGGAGACCATGTGCTACTGTGTAGCATCCACACCCCTCCGACGAGCGCTCATCTGTC	3750
743	rAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGlnSerAsnLe	763
3751	TGCCTACAGTGGGGCAACAGAGCCACTACCGAGTCTTCTGAGGCTGGAGGGACCCGACG	3810
763	uThrLys-----AspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeuLe	781
3811	CTGCAGGCCCTCTCAGGACGAGCCCTCGCGGATAGC-----GACACGTCCAT	3855
781	uSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeuIle	801
3856	CTCATCTCCTTCGGTGGACACGAGGAGCTGGACGCTCTCTTTAGCCGTTTCAGTATCTC	3915
801	eArgSerThrGluGluLeuAsn	808
3916	CCAGTCCAAAGGAACTGAAT	3937

RESULT 14	
AD878687	
ID	ADB78687 standard; cDNA; 7407 BP.
XX	
AC	AD878687;
XX	
DT	04-DEC-2003 (first entry)
XX	
DE	Human potassium channel subunit mutant cDNA SEQ ID NO:58.
XX	
KW	ss; gene; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW	neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW	antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW	nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW	ion channel dysfunction; human.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
PN	WO2003008574-A1.
XX	
PD	30-JAN-2003.
XX	
PF	08-JUL-2002; 2002WO-AU000910.
XX	
PR	18-JUL-2001; 2001AU-00006452.
PR	05-MAR-2002; 2002AU-00000910.
PR	13-MAY-2002; 2002AU-00002292.
XX	
XX	

PA (BION-) BIONOMICS LTD.  
PA (WALL/) WALLACE R. W.  
XX  
XX  
XX Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;  
PI Berkovic SF, Scheffer IE;  
XX WPI; 2003-239332/23.  
XX  
XX Identifying predisposition to an ion channel dysfunction, such as  
PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,  
PT schizophrenia, anxiety and depression, by detecting encoding-gene  
PT mutation events.  
XX  
XX Claim 6; SEQ ID NO 58; 106pp; English.  
PS  
XX  
XX The invention relates to a novel method for identifying a subject  
CC predisposed to a disorder associated with ion channel dysfunction. The  
CC method comprises ascertaining if at least one of the genes encoding ion  
CC channel subunits (ICS) has undergone a mutation event so that a cDNA  
CC derived from the subject has any of 134 nucleotide sequences. The method  
CC of the invention has nontropic, neuroprotective, inotropic, antipyretic,  
CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,  
CC neuroleptic, tranquiliser, analgesic, nephrotoxic, antidiabetic, and  
CC ophthalmological activity. A polynucleotide of the invention acts as an  
CC ion channel agonist, or ion channel antagonist. The methods, isolated  
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or  
CC modulator of an ion channel, cells and genetically modified non-human  
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a  
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-  
CC kalemic periodic paralysis, myotonia, malignant hyperthermia,  
CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's  
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,  
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory  
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,  
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic  
CC fibrosis, congenital stationary night blindness and total colour  
CC blindness. The present sequence represents a mutant cDNA of the  
CC invention. The sequence data for this patent is not represented in the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at [ftp.wipo.int/pub/published/pat](http://ftp.wipo.int/pub/published/pat) sequences.

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XX      SQ      Sequence 7407 BP; 1354 A; 2330 G; 1368 T; 0 U; 0 Other;

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Score:              1820.50            Matches:             436
Percent Similarity: 56.72%             Conservative:         96
Best Local Similarity: 46.48%          Mismatches:          230
Query Match:        39.68%             Indels:               177
DB:                  10                 Gaps:                 26

US-09-810-796-4 (1-897) x ADB78687 (1-7407)

Qy      17   AlaAlaArgGlyAspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGly 36
Db      142  TCCACCGGGAGCGGGGGCTCTCATGCCGGCTCGGAGGCCCCCACAG-----CGC 192

Qy      37   GlyGlyGlyLeuArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGly 56
Db      193  GGCAGCATCCTCAGCAACCTCGCGGGGGCGGGCGGCC-----GGG 237

Qy      57   LysProLeuSerTyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgVal 76
Db      238  AAGCCC-----CCCAAGCGCAACGCCCTTCACCGCAAGCTG 273

Qy      77   GlnAsnTyrLeuTyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAla 96
Db      274  CAGAATTTCTCTACACAGTGCTGGAGCGGGCGCGGCTGGCGGTTCATCTACCACGCGC 333

Qy      97   PheValPheLeuLeuValPheGlyCysLeulleuLeuSerValPheSerThrIleProGlu 116
Db      334  TACGTGTTTCCTCTGGTTTTCTCTCGCTTCGGCTGCGTGTCTGTGTTTTCACCATCAAGGAG 393

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 3, 2005, 06:46:36 ; Search time 1202.53 Seconds  
(without alignments)  
4514.709 Million cell updates/sec

Title: US-09-810-796-4

Perfect score: 4588

Sequence: 1 MKDVESGGRVLLNSAARG.....SICKAGESTDALSPLHVKLK 897

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5607317 seqs, 3026245999 residues

Total number of hits satisfying chosen parameters: 11214634

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database :

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4: /cgn2\_6/ptodata/2/pubnpa/US06\_PUBCOMB.seq.\*  
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8: /cgn2\_6/ptodata/2/pubnpa/US08\_PUBCOMB.seq.\*  
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13: /cgn2\_6/ptodata/2/pubnpa/US10A\_PUBCOMB.seq.\*  
14: /cgn2\_6/ptodata/2/pubnpa/US10B\_PUBCOMB.seq.\*  
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19: /cgn2\_6/ptodata/2/pubnpa/US10\_NEW\_PUB.seq.\*  
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21: /cgn2\_6/ptodata/2/pubnpa/US60\_NEW\_PUB.seq.\*  
22: /cgn2\_6/ptodata/2/pubnpa/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4588	100.0	2694	9	US-09-866-020-1
2	4588	100.0	2694	9	US-09-810-796-2
3	4588	100.0	2694	19	US-10-948-493-1
4	4588	100.0	3137	18	US-10-948-493-1
5	4584	99.9	3071	9	US-09-810-796-1
6	4574	99.7	3074	9	US-09-813-148-1
7	4527.5	98.7	2667	9	US-09-810-796-3
8	4527.5	98.7	2772	9	US-09-825-147-1
9	4527.5	98.7	2772	18	US-10-803-268-1
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11	4527.5	98.7	3111	18	US-10-803-268-3
12	2012	43.9	2335	17	US-10-353-690-55
13	2012	43.9	2335	19	US-10-850-928-1
14	1832.5	39.9	5595	18	US-10-820-307-8
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16	1819.5	39.7	7411	18	US-10-295-027-281
17	1819.5	39.7	7420	18	US-10-643-795A-75
18	1819.5	39.7	7420	18	US-10-948-518-75
19	1819.5	39.7	7863	15	US-10-084-817-335
20	1813	39.5	2169	13	US-10-128-870-22
21	1813	39.5	2169	14	US-10-131-685-22
22	1806.5	39.4	3237	16	US-10-096-578-95
23	1805	39.3	3287	13	US-10-128-870-19
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44	1226.5	26.7	1425	16	US-10-116-712-662
45	1207.5	26.3	900	13	US-10-128-870-5

# ALIGNMENTS

## RESULT 1

US-09-866-020-1  
; Sequence 1, Application US/09866020  
; Publication No. US2002040000A1  
; GENERAL INFORMATION:  
; APPLICANT: DORETZKY, STEVEN I  
; APPLICANT: RAMANATHAN, CHANDRA S  
; APPLICANT: TROJNACKI, JOANNE T  
; APPLICANT: BOISSARD, CHRISTOPHER G  
; APPLICANT: GRIBKOFF, VALENTIN K  
; TITLE OF INVENTION: HUMAN KCNQ5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 3053-4091US1  
; CURRENT APPLICATION NUMBER: US/09/866,020  
; PRIORITY FILING DATE: 2001-05-24  
; PRIOR APPLICATION NUMBER: 60/207,389  
; PRIOR FILING DATE: 2000-05-26  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1



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QY 681 ValProLeuSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 700
DB 2041 GTGCCAATTAGTCAAGGAGTGGCTCAGCAGTGGCAGCACCACCAATTCGCAACCA 2100
QY 701 IleAsnThrAlaProLysProAlaAlaProThrLeuGlnIleProProProLeuPro 720
DB 2101 ATAAATACGGCACCCCAAGCAGCAGCCCAACACTTTACAGATCCCACTCTCTCCCA 2160
QY 721 AlalIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740
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QY 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 880
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## RESULT 2

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US-09-810-796-2
; Sequence 2, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jega, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: KCNQS, a No. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly-rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCNQS-1 coding sequence
; NAME/KEY: CDS
; LOCATION: (1)..(2694)
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## ; OTHER INFORMATION: KCNQS-1

US-09-810-796-2

## Alignment Scores:

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Score:	4588.00	Matches:	897
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-810-796-4 (1-897) x US-09-810-796-2 (1-2694)

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DB 61 GACGCGCTTGCTACTTGCTGGGCACCCCGCGCCGACGCTTGTGGCGCGCGGTGGCCTG 120
QY 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
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QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
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QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220
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QY 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
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Qy 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620  
Db 1801 GCTCAGCCCTCGCTTGGCTTCATTCAGATCCCACTTTTGAATGTGAACAGACATCT 1860  
Qy 621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640  
Db 1861 GACTATCAAGGCTGTGATAGCAAGATCTTTCGGGTTCGACAAACAAAGTGGCTGC 1920  
Qy 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660  
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Qy 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680

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Qy 681 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 700  
Db 2041 GTGCCAATTAGTCAAGACGATGGCTCAGCAGTGGCAGCCACCAACACCATTTGCAACCAA 2100  
Qy 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro 720  
Db 2101 ATAAATACCGCACCCCAAGCCAGCAGCCCAACCACTTTACAGATCCCACTCTCTCCCA 2160  
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Qy 741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760  
Db 2221 AGCATTTCTGACGTCACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280  
Qy 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780  
Db 2281 TCAATCTCACCAGGACCGCTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG 2340  
Qy 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800  
Db 2341 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2400  
Qy 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGlySerGlySerArg 820  
Db 2401 ATCAGTCTGACCGAGGACATGATATACAACTTTTCAGGAGTGCAGTCAAGTGCCTCAGA 2460  
Qy 821 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840  
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## RESULT 3

US-10-948-493-1  
; Sequence 1, Application US/10948493  
; Publication No. US20050064491A1  
; GENERAL INFORMATION:  
; APPLICANT: DWORETZKY, STEVEN I  
; APPLICANT: RAMANATHAN, CHANDRA S  
; APPLICANT: TROJNACKI, JOANNE T  
; APPLICANT: BOISSARD, CHRISTOPHER G  
; APPLICANT: GRIBKOFF, VALENTIN K  
; TITLE OF INVENTION: HUMAN KCNQ5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: D0023 DIV  
; CURRENT APPLICATION NUMBER: US/10/948,493  
; CURRENT FILING DATE: 2004-09-23  
; PRIOR APPLICATION NUMBER: 60/207,389  
; PRIOR FILING DATE: 2000-05-26  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 2694  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-948-493-1  
Alignment Scores:



Pred. No.: 0 Length: 2694  
Score: 4588.00 Matches: 897  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 19 Gaps: 0

US-09-810-796-4 (1-897) x US-10-948-493-1 (1-2694)

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Qy 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40  
Db 61 GACGCCCTGTACTGTGGCACC CGCGCGCCACGCTTGTGTGGCGGGGGTGGCGCTG 120

Qy 41 ArgGluSerArgAtqGlyGlyGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60  
Db 121 AGGGAGAGCCCGCGGGGCAAGCAGGGGGCCCGATGAGCCCTGTGGGAAAGCCGCTCTCT 180

Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80  
Db 181 TACACGAGTAGCCAGAGCTGCGCGCGCAACGTCAAGTACCGCGGGTGCAGAACTACCTG 240

Qy 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100  
Db 241 TACAACGTGTGGAGAGACCCCGCGCTGGCGGTTCATCTACACGCTTTCGTTTTCTC 300

Qy 101 LeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120  
Db 301 CTGTGCTTGGTGTCTGATTTGTGAGTGTTCCTACCATCCCTGAGCACACAAATTTG 360

Qy 121 AlaSerSerCysLeuLeuLeuPheValMetIleValValPheGlyLeuGluPhe 140  
Db 361 GCCTCAAGTGTGCTTGTATCTGGAGTGTGGTGTGATGTGCTTCTTTGGTGTGGAGTTC 420

Qy 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160  
Db 421 ATCATTCGAATCTGGTCTCGCGGTGTCTGTTCGATATAGAGGATGCAAGGAAGACTG 480

Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuLeuAlaSerIleAla 180  
Db 481 AGTTTGTCTGAAAGCCCTTCTGTATTATAGATACCATTTGTCTTATCGCTTCAATAGCA 540

Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200  
Db 541 GTTGTCTTGCMAAAACTCAGGGTAATATTTTGGCCACGCTGCACTCAGAACTCTCCGT 600

Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgGlyGlyThrTrpLysLeuLeu 220  
Db 601 TTCCTACAGATCCTCCGCATGTCGCGCATGGACCGAAGGGAGGCACCTTGGAAATTA 660

Qy 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240  
Db 661 GGTTCAGTGGTTTATGCTCACAGCAAGAAATTAATCACAGCTTGTGTATAGGATTTTGT 720

Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260  
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Qy 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300  
Db 841 GACAAAACCTCCCTAACTTGGCTGGGAAGATTGCTTCTGCAAGGCTTTGCACTCTCTG 900

Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320  
Db 901 ATTTCCTTCTTGGCACTTCTGCGCGGCAATCTTGGCTCAGGTTTGGCAATTAAGATACA 960

Qy 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340  
Db 961 GAAACAACCCCGCAGAAACACTTTTGAGAAAAAGAGAAACCCAGCTGCAACCTCATTCAG 1020

Qy 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360  
Db 1021 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCATTTGCAACCTGGAAAGCA 1080

Qy 361 HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyAlaSerSer 380  
Db 1081 CACTTGAAGGCTTGCACACCTGCAGCCCTACCAAGAAAGAAACAAAGGGAGCATCAAGC 1140

Qy 381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400  
Db 1141 AGTCAGAGCTAAAGTTTAAAGAGCGAGTCGCGCATGGCTAGCCCCAGGGGCGAGATATT 1200

Qy 401 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 420  
Db 1201 AAGAGCCGCAAGCCTCAGTAGGTGACAGAGGTTCCCAAGCACCAGCATCACAGCCGAG 1260

Qy 421 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 440  
Db 1261 GGCAGTCCCAACCAAGTGCAGAGAGCTGGAGCTTCAACGACCGCAACCCGCTTCCGGCCC 1320

Qy 441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460  
Db 1321 TCGCTGCGCCTCAAAAGTTCTCAGCCAAAACCAAGCTAGATAGTGTGACACAGCCCTTGC 1380

Qy 461 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480  
Db 1381 ACTGATGATGATATGATGAAGAGATGCCAGTGTGATGATCATCATGTGAAGACCTCACC 1440

Qy 481 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 500  
Db 1441 CCACCCTTAAACTGTCTATTGAGCTATCAGAAATATGAAATTTCTGTTGCAAAACGG 1500

Qy 501 LysPheLysGluThrLeuArgProTrpAspValLysAspValIleGluGlnTyrSerAla 520  
Db 1501 AAGTTTAAAGGAAACGTTTACGTCATATGATGTAAAGATGTCAATTTGAACAATTTCTGT 1560

Qy 521 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540  
Db 1561 GGTCACTCGACATGTTGTGTAGAAATTAAGCCCTTCAACACGCTGTGATCAAAATTCCT 1620

Qy 541 GlyLysGlyGlnIleThrSerAspLysSerArgGluLysIleThrAlaGluHisGlu 560  
Db 1621 GGAAGAGGCAAAATCACATCAGATAAGAGAGCGAGAGAAATAACAGCAGAACATGAG 1680

Qy 561 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 580  
Db 1681 ACCACAGACGATCTCAGTATGCTCGGTGGGTGTTCAAGGTTGAAAAACAGGTACAGTCC 1740

Qy 581 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 600  
Db 1741 ATAGAGTCCAAGCTGGACTGCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800

Qy 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620  
Db 1801 GCCTCAGCCCTCGCTTTCGCTTTCATCCAGATCCACCTTTTGAATGTGAACAGACATCT 1860

Qy 621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640  
Db 1861 GACTATCAAGCCCTGTGGATAGCAAGATCTTTTGGGTTCGCGCAAAAACAGTAGTGGCTG 1920

Qy 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660  
Db 1921 TTATCCAGATCAACTAGTGGCCAAACATCTCGAGAGGCTTCGAGTTTCATTCTTGACGCCAAT 1980

Qy 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680  
Db 1981 GAGTTCAAGTCCGACACTTTCACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040

Qy 681 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 700

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Db 2041 GTGCCAATTAGTCAAGGCGATGGCTCAGCAGTGGCAGCCACCAACCATTCGAAACCAA 2100
Qy 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro 720
Db 2101 ATAAATACGGCACCCAGCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2160
Qy 721 AlalleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740
Db 2161 GCCATCAAGCATCTGCCAGGCCAGAACTCTGACACCCCTAACCTTGCGAGGCTTACAGGAA 2220
Qy 741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760
Db 2221 AGCATTTCTGAGCTCACCACCTGCTGTTGCTCCCAAGGAATGTTTCAGTTGCACAG 2280
Qy 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780
Db 2281 TCMAATCTCACCAAGGACCGTTCTATGAGGAAAGACTTTGACATGGGAGGAGAAACTCTG 2340
Qy 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800
Db 2341 TTGCTGCTGTCTCCCATGGTCCGAGGACTTTGGGCAAACTTTTGTCTGTGCCAAACCTG 2400
Qy 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 820
Db 2401 ATCAGTTCGACCGAGGAACTGAATATACAACTTTCAGGAGTGAGTCAAGTGGCTCCAGA 2460
Qy 821 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840
Db 2461 GGCAGCCCAAGATTTTACCCCAATGGAGGGAATCCAAATTTGTTTATTAACCTGATGAAGAG 2520
Qy 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 860
Db 2521 GTGGGTCCGGAAGACAGACAGACACTTTTGTGTCGCGCACCCAGCCTGCCAGGGAA 2580
Qy 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 880
Db 2581 GCTGCTTTGTCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCATTTGT 2640
Qy 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897
Db 2641 AAGGCGAGGAGAAAGTACAGATCCCTCAGCTTGGCTCATGTCAAACTGAAA 2691

RESULT 4
US-10-661-629-1
; Sequence 1, Application US/10661629
; Publication No. US20040180405A1
; GENERAL INFORMATION:
; APPLICANT: JENTISCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNELS
; FILE REFERENCE: 2815-0236P
; CURRENT APPLICATION NUMBER: US/10/661,629
; CURRENT FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3137
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2691)
US-10-661-629-1

Alignment Scores:
Pred. No.: 0 Length: 3137
Score: 4588.00 Matches: 897
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-810-796-4 (1-897) x US-10-661-629-1 (1-3137)
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Db 1 ATGAGAGATGTGAGTCTGGGCCGGGGCAGGGTGTCTGTAACCTCGCAGCCGCGCAGGGGC 60
Qy 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeu 40
Db 61 GACGGCTGTCTACTGTCTGGGCACCCCGCGGCCACCGCTGGTGGCGCGCGCGCTGGCCTG 120
Qy 41 ArgGluSerArgArgGlyLysGlnGlyAlaAlaMetSerLeuLeuGlyLysProLeuSer 60
Db 121 AGGAGAGACCGCGCGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180
Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgValGlnAsnTyrLeu 80
Db 181 TACACGAGTAGCCAGAGCTGCCCGGCCAACAGTCAAGTACCGCGGGTGCAGAACTACCTG 240
Qy 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100
Db 241 TACAACGTGTGGAGAGACCCCGCGCTGGCGCTTCACTTACCACGCTTTTCGTTTTCTC 300
Qy 101 LeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120
Db 301 CTGTCTCTTTGGTGTCTTGATTTTGTCTAGTGTCTTCTACCAATCCCTGAGCACACAAAATTG 360
Qy 121 AlaSerSerCysLeuLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
Db 361 GCCTCAAGTTGCCCTCTTTGATCTCTGGAGTTCGTGATGATTGCTGCTTTTGGTGGAGTTC 420
Qy 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160
Db 421 ATCATTCGAATCTGCTGCTGGCGGTGCTGTGTGATATAGAGATGAGGAGGAGGAGACTG 480
Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db 481 AGTTTCTCTGAAAGCCCTCTCTGTATTAGATACCACTGTTCTTAICGCTTCAATAGCA 540
Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db 541 GTTGTCTCTGCMAAACTCAGGGGTAAATATTTTGGCCACGCTGCACCTCAGAAAGTCTCCGT 600
Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220
Db 601 TTCCTACAGATCTCCCGCATGGTGGCATGACCAAGGGGAGGACCTTGGAAATTTACTG 660
Qy 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240
Db 661 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGTGTACATAGGATTTTG 720
Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db 721 GTTCTTATTTTTCGTCTCTTCTGCTATCTGTTGAAAAGGATGCCAATAAAGAGGTTT 780
Qy 261 SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
Db 781 TCTACATATGAGATGCTCTCTGGTGGGCGCAATTAATTACATTGACAACTATTGGCTATGA 840
Qy 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db 841 GACAAAACCTCCCTTAACCTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACCTCTCTGGC 900
Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db 901 ATTTCTTTTCTTTTGCACTTCTCTGCGGCATTTCTTGCTCAGGTTTGTGCAATTAAGAGTACA 960
Qy 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
Db 961 GAACAAACCCCGCAGAAACACTTTGAGAAAAGAGGAACCCAGCTGCCAACCCTCATTCAG 1020
Qy 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
Db 1021 TGTGTTTGGCGTAGTTACGAGCTGATGAGAAATCTGTTTTCCATTGCAACCTGGAAGCCA 1080
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QY 361 HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyGluAlaSerSer 380  
Db 1081 CACTTGAAGGCCCTTGCACACCTGCGAGCCCTACCAAGAAAGAAACAGGGAAGCATCAAGC 1140  
QY 381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400  
Db 1141 AGTCAGAGCTAAGTTTAAAGGAGCGAGTGGCATGGCTAGCCCGAGGGGCGCAGAGTATT 1200  
QY 401 LysSerArgGlnAlaSerValGlyAspArgSerProSerThrAspIleThrAlaGlu 420  
Db 1201 AAGAGCCGCAAGCCCTCAGTAGTCACAGGAGTCCCAAGCACCGACATCACAGCCGAG 1260  
QY 421 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 440  
Db 1261 GCGAGTCCCAACCAAGTCAGAGAGTGGAGCTTCAACGACCGAACCCTTCGCGGCC 1320  
QY 441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460  
Db 1321 TCGCTGCCCTCAAAAGTTCTCAGCCCAAAACAGTGATAGTGTGACACAGCCCTTGGC 1380  
QY 461 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480  
Db 1381 ACTGATGATGATATGATGATCAAAAGAGTCCAGTGTGATGTATCATGTGGAAGACCTCAC 1440  
QY 481 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 500  
Db 1441 CCACCACTTAAACCTGTCAATCGAGCTATCAAGATTATGAATTTTCATGTTGCAAAACGG 1500  
QY 501 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 520  
Db 1501 AAGTTTAAAGGAACATTACGTTCCATGATGTAAAGATGTCAATTGAACATATATCTGCT 1560  
QY 521 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540  
Db 1561 GGTCACTCGACATGTTGTGTAGATTAAGAGCTTCAACACAGTGTGTGATCAAAATCTT 1620  
QY 541 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560  
Db 1621 GGAAAGGGCAAAATCACATCAGATGAAGAGAGCCGAGAGAAATTAACACAGACATGAG 1680  
QY 561 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 580  
Db 1681 ACCACAGCATCTCAGTATGCTCGTGGGTGGTCAAGTTGAAAAACAGGTACAGTCC 1740  
QY 581 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 600  
Db 1741 ATAGAATCCAAAGCTGAGCTGCTACTAGACATCTATCAACAGTCTCTCGGAAGAGCTCT 1800  
QY 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620  
Db 1801 GCCTCAGCCCTCGCTTTGGCTTCATTCAGATCCCACTTTTGAATGTGAACAGACATCT 1860  
QY 621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640  
Db 1861 GACTATCAAGCCCTGTGATAGCAAGATCTTTCGGGTTCGACACAAAACAGTGGCTGC 1920  
QY 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660  
Db 1921 TTATCCAGATCAACTAGTGCCAAACATCTCGAGAGGCTCGAGTTCATCTCGAGCCAAAT 1980  
QY 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680  
Db 1981 GAGTTCAGTGCCAGACTTTCACGCGTTTACGCTTACTATGCACAGTCAAGCAACACAG 2040  
QY 681 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 700  
Db 2041 GTGCCAATTAGTCAAAAGGATGGCTCAGCAGTGGGAGCCACCAACACCATTTGCCAAACCA 2100  
QY 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro 720  
Db 2101 ATAATACGGCACCCCAAGCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2160  
QY 721 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740

Db 2161 GCCATCAAGCATCTGCCAGGCCAGAAACTCTGCACCCCTAACCCCTGCAGGCTTTACAGAA 2220  
QY 741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760  
Db 2221 AGCATTTCTGACGTCAACACCTGCTTGTGGCTCCCAAGGAAATGTTTCAGGTTCACAG 2280  
QY 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780  
Db 2281 TCAATCTCAACCAAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAAACTCTG 2340  
QY 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800  
Db 2341 TTGTCTGTCTGCTCCATGGTCCGAGGACTTGGCAAAATCTTGTCTGTGCAAAACCTG 2400  
QY 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 820  
Db 2401 ATCAGGTCGACCGAGGAATCAATATATCAACTTTTCAGGAGTGAAGTCAAGTGGCTCCAG 2460  
QY 821 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840  
Db 2461 GGCAGCCCAAGATTTTACCCCAATGGAGGAAATCCAAATTTGTTTATAACTGATGAAGAG 2520  
QY 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 860  
Db 2521 GTGGTCCCGAAGAGACAGACAGACACTTTTGTATGCCGACCCAGCCTCCACAGGAA 2580  
QY 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 880  
Db 2581 GCTGCCITTCATCAGACTCTCTAAGGACTGGAAGTCAAGATCATCTCAGAGCATTTGT 2640  
QY 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897  
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RESULT 5  
US-09-810-796-1  
; Sequence 1, Application US/09810796  
; Patent No. US20020102677A1  
; GENERAL INFORMATION:  
; APPLICANT: Jegla, Timothy James  
; APPLICANT: ICAGEN, Inc.  
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel  
; FILE REFERENCE: 018512-005010US  
; CURRENT APPLICATION NUMBER: US/09/810,796  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 60/190,954  
; PRIOR FILING DATE: 2000-03-21  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 3071  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human outwardly rectifying, voltage-gated  
; OTHER INFORMATION: potassium channel KCNQ5-1  
; NAME/KEY: CDS  
; LOCATION: (10)..(2703)  
; OTHER INFORMATION: KCNQ5-1  
US-09-810-796-1

Alignment Scores:  
Pred. No.: 0 Length: 3071  
Score: 4584.00 Matches: 896  
Percent Similarity: 99.89% Conservative: 0  
Best Local Similarity: 99.89% Mismatches: 1  
Query Match: 99.91% Indels: 0  
DB: 9 Gaps: 0

US-09-810-796-4 (1-897) x US-09-810-796-1 (1-3071)

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Qy	21	AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeu	40	381	SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle	400
Db	70	GACGGCTGTCTACTGTGGGACCCCGCGGCCACGCTTGGTGGCGGGGGGTGGCTG	129	1150	AGTCGAAGAGCTAAGTTTAAAGGAGGAGTGGCATGGCTAGCCCCAGGGGCCAGAGTATT	1209
Qy	41	ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer	60	401	LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu	420
Db	130	AGGAGAGCGCCCGGGCAAGCAGGGGCGCGGATGAGCTGTCTGGGGAAGCGGCTCTCT	189	1210	AGAGCGGACAGCCCTCAGTAGGTGACAGGAGTCCCAAGCACCCACATCATCAGCCGAG	1269
Qy	61	TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu	80	421	GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro	440
Db	190	TACACGAGTACCGAGCTGCGGCGCAACGTCACGACCGCGGGTGGCAACTACTG	249	1270	GGCAGTCCCAACAAAGTCGAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCGGGCC	1329
Qy	81	TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu	100	441	SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly	460
Db	250	TACAACGTGTGGAGAGACCCCGCGGCTGGGGTTCATCTACCAACGCTTTCGTTTTCTC	309	1330	TCGCTCGGCTCAAAAGTTCTCAGCCAAAACCAAGTATGATGCTGACACAGCCCTTGGC	1389
Qy	101	LeuValPheGlyCysLeuLeuSerValPheSerThrIleProGluHisThrLysLeu	120	461	ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr	480
Db	310	CTTGCTTTGGTGTCTTGTATTTGTAGTGTTCATCCATCCCTGAGCACACAAATTG	369	1390	ACTGATGATGATATATGATGAAAAAGGATGCCAGTGTGATGTATCAGTGAAGACCTCAC	1449
Qy	121	AlaSerSerCysLeuLeuLeuGluPheValMetIleValPheGlyLeuGluPhe	140	481	ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg	500
Db	370	GCCTCAAGTGTGCTTGCATCTGGAGTTCGTGATGATGTGCTTGGTGGAGTTC	429	1450	CCACCACTTAAAACTGTCTTCAGCTATCAGAAATTTATGAAATTTTCATGTTCGAAAACGG	1509
Qy	141	IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu	160	501	LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla	520
Db	430	ATCATTCGAATCTGCTCGGGTGTGTTGTCATATAGAGGATGGCAAGGAGACTG	489	1510	AGTTTAAAGAAACRTTACGTCCATATGATGATAAAGATGTCTATTGAAACAATTTCTGCT	1569
Qy	161	ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla	180	521	GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu	540
Db	490	AGGTTTGTCTGAAAGCCCTTCTGTATATAGATACCATTTGTTTATCGCTTCATATGCA	549	1570	GGTCATCTCGACATGTGTGTAGAAATTAAGAGCTTCAACACAGTGTGTGATCAAAATCTTT	1629
Qy	181	ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg	200	541	GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu	560
Db	550	GTTGTTTCTGCAAAACTCAGGGTAATATTTTGGCCACTGTGCACTCAGAACTCTCGT	609	1630	GGAAAGGGCAATACATCATAGATAGAGAGCGGAGAGAAATATACAGCAGAACATGAG	1689
Qy	201	PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu	220	561	ThrThrAspAspLeuSerMetLeuGlyArgValLysValLysValGluLysGlnValGlnSer	580
Db	610	TTCTACAGATCTCCGCAATGTGGCGATGGACCGAAGGGAGGACATTGGAAATATTCTG	669	1690	ACCACACAGCATCTCAGTATGCTCGGTGGGTGGTCAAGGTTGAAACACAGGTACAGTCC	1749
Qy	221	GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrIleGlyPheLeu	240	581	IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer	600
Db	670	GGTTAGTGGTTATCTCACAGCAGGAATTAATCACAGCTTGGTACATAGGATTTTG	729	1750	ATAGAATCCAAGCTGGACTGCCCTACTAGACATCTATCAAGTCTCTTCGGAAGGCTCT	1809
Qy	241	ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe	260	601	AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProPheGluCysGluGlnThrSer	620
Db	730	GTTCTTATTTTTCGTTCTTCTTCTATCTGTTGGAAGAGATGCCAATAAAGAGTTT	789	1810	GCCTCAGCCCTCGCTTTGGCTTTCATCCAGTCCACCTTTTGAATGTGAACAGACATCT	1869
Qy	261	SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly	280	621	AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys	640
Db	790	TCTACATATGACAGATCTCTCTGGTGGGACAAATTACATTCACAACTATGGCTATGA	849	1870	GACTATCAAGCCCTGTGGATAGCAAAAGATCTTTTCGGGTTCGCGACAAAACAGTGGCTGC	1929
Qy	281	AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuGly	300	641	LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn	660
Db	850	GACAAACTCCCTTAACCTGGCTGGGAGATTGCTTTCTGCAGGCTTTGCACTCTCTGGC	909	1930	TTATCCAGATCAACTAGTGCCCAACATCTCGAGAGGCTCGCAGTTCATCTGACGCCAAT	1989
Qy	301	IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln	320	661	GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln	680
Db	910	ATTTCTTTCTTGCACCTCTCTGCGGCATTTCTGGCTCAGTTTTCATTAAGATACAA	969	1990	GAGTTTCAGTCCAGACTTTCTACGCGCTTACGCGCTTACTATGTCACAGTCAACAGCACAG	2049
Qy	321	GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln	340	681	ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln	700
Db	970	GAAACACCGCCAGAAACACTTTTGAAAGAGAGGAAACCCAGCTGCCAACCTCATTCAG	1029	2050	GTGCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGCAGCCCAACACCATTTGCAACCCA	2109
Qy	341	CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro	360	701	IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro	720
Db	1030	TGTTTGGGTAGTTACGCGAGCTGATGAGAAATCTGTTTCCATTCGCAACCTGCGAAGCA	1089	2110	ATAAATACGGCACCCCAAGCCAGCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA	2169
Qy	361	HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyGluAlaSerSer	380	721	AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu	740
				2170	GCCATCAAGCATCTGCCAGGCGCAAACTCTGCACCCCTAACCCCTGCAGGCTTACAGNA	2229

QY 741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760  
DB 2230 AGCATTTCTGAGTCCACCATCTGCTTGTGCTCCAAAGGAAATGTTTCAGGTTGCACAG 2289  
QY 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGlyThrLeu 780  
DB 2290 TCNAATCTCACCAAGACCGTCTCTATGAGGAAAGCTTTGACATGGGAGGAAACTCTG 2349  
QY 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800  
DB 2350 TTGTCTGTCTGCCATGGTCCGGAAGACCTTGGGCAAAATCTTTGTCTGTGCAAAACCTG 2409  
QY 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 820  
DB 2410 ATCAGGTCGACCGAGGAACTGAATATACAACCTTTCCAGGAGTGAGTCAAGTGGCTCCAGA 2469  
QY 821 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840  
DB 2470 GGCACCAAGATTTTACCCCAATGGAGGGAATCCAAATGTTTATTAACATGATGAGAG 2529  
QY 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 860  
DB 2530 GTGGGTCCGGAAGACAGACAGACACTTTTGTATGCGCACCGCAGCCTGCCAGGAA 2589  
QY 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 880  
DB 2590 GCTGCTTTTGATCATGACTCTCTAAAGGACTGGAAGGTCCAGCATCATCTCAGAGCATTTGT 2649  
QY 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897  
DB 2650 AAGGACAGGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAA 2700

## RESULT 6

US-09-813-148-1  
; Sequence 1, Application US/09813148  
; Patent No. US2002007680A1  
; GENERAL INFORMATION:  
; APPLICANT: STEINMEYER, Klaus  
; APPLICANT: LERCHE, Christian  
; APPLICANT: SCHERER, Constanze  
; APPLICANT: SEEBOM, Guiscard  
; APPLICANT: BUSCH, Andreas E.  
; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CEN  
; TITLE OF INVENTION: NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM  
; FILE REFERENCE: 38005-119  
; CURRENT APPLICATION NUMBER: US/09/813,148  
; PRIORITY FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: DE 100 13 732.6  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: US 60/194,041  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 3074  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-813-148-1

## Alignment Scores:

Align. No.:	0	Length:	3074
Score:	4574.00	Matches:	895
Percent Similarity:	99.78%	Conservative:	0
Best Local Similarity:	99.78%	Mismatches:	2
Query Match:	99.65%	Indels:	0
DB:	9	Gaps:	0

US-09-810-796-4 (1-897) x US-09-813-148-1 (1-3074)

QY 1 MetLysAspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaArgGly 20  
DB 215 ATGAAGGATGGAGTCGGCGCGGCGAGGGTGTCTGTAATCTGGCAGCCCGCAGGGGC 274

QY 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeu 40  
DB 275 GACGCGCTGCTACTGCTGGGCAACCGCGCGGCCACCGCTTGGTGGCGGGCGGCGCTG 334  
QY 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60  
DB 335 AGGAGAGCCCGCGGGGCAAGCAGGGGCGCCGGATGAGCCTGCTGGGAAGCCGCTCTCT 394  
QY 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80  
DB 395 TACACGAGTACCCAGAGCTGCGCGCGCAACGCTCAAGTACCGCGCGGTGCAGAACTACCTG 454  
QY 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100  
DB 455 TACAACGCTGCTGGAGAGACCCCGCGGTGGCGTTCATCTACCAACGCTTTCGTTTTCTCTC 514  
QY 101 LeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120  
DB 515 CTGTGCTTTGGTGTGCTTGTATTTTGTAGTGTTCCTACCATCCCTGACACACAAAATG 574  
QY 121 AlaSerSerCysLeuLeuLeuPheValMetIleValPheGlyLeuGluPhe 140  
DB 575 GCCTCAAGTTCGCTTGTATCTCGAGTTCGTGATGATTGTCGCTTTGGTGGAGTTC 634  
QY 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160  
DB 635 ATCATTCGAATCTGCTGCGGGTGTCTGTGATATAGAGGATGCAAGGAAGACTG 694  
QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180  
DB 695 AGGTTTGTCTGAAAGCCCTCTGTATTATATACCATGTTCTTATCGCTTCAATAGCA 754  
QY 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200  
DB 755 GTTGTCTCTGCAAAACTCAGGGTAATATTTTGCACGCTGCTGCACTCAGAAGTCTCCGT 814  
QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220  
DB 815 TTCTTACAGATCTCCGCAATGCGCATGCGATGACCGAGGAGGACCTTGGAATTTACTG 874  
QY 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240  
DB 875 GGTTCAGTGGTTTATGCTCACAGCAAGAAATTAATCACAGCTTGGTATCATGAGATTTTG 934  
QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260  
DB 935 GTTCTTATTTTTCGCTCTTCTTCTCTATCTGGTGGAAAGGATGCCAATAAGAGTTT 994  
QY 261 SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280  
DB 995 TCTACATATGCAGATGCTCTCTGGTGGGSCAAATTAATTCACAACTATTGGCTATGGA 1054  
QY 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300  
DB 1055 GACAAAACCTCCCTAACTTGGCTGGGAAGATGCTTCTGCAAGGCTTTCACCTCTTGGC 1114  
QY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320  
DB 1115 ATTTCCTTTTTCGACTTCTCTGCGGCAATCTTGGCTCAGGTTTTCGATTTAAAGTACAA 1174  
QY 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340  
DB 1175 GAACAACACCCCGAGAAACACTTTTGAGAAAAAGAGAAACCCAGCTGCGCAACCTCATTCAG 1234  
QY 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360  
DB 1235 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTTCATTGCAACCTGGAAGCCA 1294  
QY 361 HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyAlaSerSer 380  
DB 1295 CACTTGAAGGCTTGCACACCTGACGCTTACCAAGAAAGAAAGAACAGGGGAGCATCAGC 1354

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QY 381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400
Db 1355 ACTCAGAACCTAAGTTTAAAGAGCGAGTGGCATGGCTAGCCCCAGGGCCAGATATT 1414
QY 401 LysSerArgGlnAlaSerValGlyAspArgSerProSerThrAspIleThrAlaGlu 420
Db 1415 AAGAGCCGACAAAGCTCAGTAGTGGTACAGGAGGTCCCAAGCACCAGCATCACAGCCGAG 1474
QY 421 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 440
Db 1475 GGCAGTCCCAACCAAGTGCAGAAAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1534
QY 441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460
Db 1535 TCGTTCGCCCTCAAAAGTTCTCAGCCAAACAGTAGATAGTGTGACACAGCCCTTGGC 1594
QY 461 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480
Db 1595 ACTGATGATGATATGATGAAAGAGATGCCAGTGTGATGTATCAGTGGAAAGACCTCAC 1654
QY 481 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 500
Db 1655 CCACCACTTAAACCTGTCATTGAGCTATCAGAAATTATGAAATTTTCATGTTGCAAAACGG 1714
QY 501 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 520
Db 1715 AAGTTTAGGAAACATTACGTCCATCATGATGTAAAGATGTCATTGAACATATTTCTGCT 1774
QY 521 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540
Db 1775 GGTCTATCGACATGTTGTAGATTTAAAGCCCTTCAACACCGTGTGTGATCAATTTCTT 1834
QY 541 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560
Db 1835 GGAAAGGCGCAATCAGATCAGATGAAGAGCCGAGAGAAATTAACACGACAGACATGAG 1894
QY 561 ThrThrAspAspLeuSerMetLeuGlyArgValLysValGluLysGlnValGlnSer 580
Db 1895 ACCACAGACGATCTCAGTATGTCGTGGTGGTCAAGGTGAAAAACAGGTACAGTCC 1954
QY 581 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 600
Db 1955 ATAGAATCCAAAGCTGGCTGCTACTAGACATCTATCAACAGGTCTTCGGAAAGGCTCT 2014
QY 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProPheGluCysGluGlnThrSer 620
Db 2015 GCCTCAGCCCTCGCTTGGCTTCATTCAGATCCACCTTTTGATGTGAACAGACATCT 2074
QY 621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640
Db 2075 GACTATCAAGCCCTGTGGATAGCAAGATCTTTCGGGTTCGACAAAACAGTGGCTGC 2134
QY 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660
Db 2135 TTATCCAGATCAACTAGTGGCCAACTCTCAGAGGCGCTGCAGTTTCATTTGACGCCAAAT 2194
QY 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680
Db 2195 GAGTTTCAGTCCAGACTTTTCAGCGCTTAGCCCTACTATGCACATCAAGCAACACAG 2254
QY 681 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 700
Db 2255 GTGCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGCGGCCACCAACACCATTCGCAACCAA 2314
QY 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro 720
Db 2315 ATAAATACGGCCCAAGCCAGCCAGCCCAACATTTACATTCACATCCACCTCTCTCCA 2374
QY 721 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740
Db 2375 GCCATCAAGCAITCTGCCAGGCCAGAAACTCTGCACCTTAAACCTTGCAGGCTTACAGGAA 2434
QY 741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760
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Db 2435 AGCATTTCTGACGCTCACCACTTCCTTGTTCCTCCCAAGGAAATGTTCAAGTTGCACAG 2494
QY 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780
Db 2495 TCAAAATCTCACCAAGGACCGTCTTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG 2554
QY 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800
Db 2555 TTGCTGTCTGTCCATCGTGGCCGAGGACTTCGGCAAAATCTTTGCTGTGCAAAACCTG 2614
QY 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGlnSerSerGlySerArg 820
Db 2615 ATCAGGTCCGACCCGAGGAACATGAATATACACTTTTCAGGGAGTGAGTCAAGTGGCTCCAG 2674
QY 821 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840
Db 2675 GGAGGCCCAAGATTTTACCCCAATGGAGGGAATCCAAATTTGTTATTAATGATGAAGAG 2734
QY 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 860
Db 2735 GTGGTCCCGAAGAGACAGAGACAGACACTTTTGTGTCGCGCACCGCAGCCTGCCAGGAA 2794
QY 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 880
Db 2795 GCTGCCCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCAAGATCATCTCAGAGCATTTGT 2854
QY 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897
Db 2855 AAGCAGAGAGAAAGTACAGATGCCCTCAGCTTGCCCTCATGTCAAACTGAAA 2905
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## RESULT 7

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US-09-810-796-3
; Sequence 3, Application US/09810796
; Patent No. US2002010267A1
; GENERAL INFORMATION:
; APPLICANT: Jegia, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: KCNQ3, a No. US2002010267A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2667
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly rectifying, voltage-gated
; NAME/KEY: CDS
; LOCATION: (1)..(2667)
; OTHER INFORMATION: KCNQ3-2
US-09-810-796-3
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## Alignment Scores:

Pred. No.:	0	Length:	2667
Score:	4527.50	Matches:	887
Percent Similarity:	99.00%	Conservative:	1
Best Local Similarity:	98.89%	Mismatches:	0
Query Match:	98.68%	Indels:	9
DB:	9	Gaps:	1

US-09-810-796-4 (1-897) x US-09-810-796-3 (1-2667)

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Db 1 ATGAAGGATGTGGAGTCGGCGCGGCGAGGTGTGCTGAAGTGGAGCGCCGCGAGGGGC 60
QY 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
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Db 61 GACGCCCTGCTACTGCTGGGCAACCGCGGCCACGCTTGGTGGCGGCGGCTG 120  
Qy 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60  
Db 121 AGGGAGAGCGCGCGGGCAAGCAGGGGCGCGGATGAGCCTGCTGGGAAAGCGCTCT 180  
Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80  
Db 181 TACACGAGTAGCAGAGCTGCCGGCGCAACGTCAGTAGTACCGCGGGTGCAGAACTACCTG 240  
Qy 81 TyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100  
Db 241 TACACGCTGTGGAGAGACCGCGCGCTGGGGCTTCACTACCAAGCTTTCGTTTCTC 300  
Qy 101 LeuValPheGlyCysLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120  
Db 301 CTTGTCTTTGGTTGCTTGTATTTTGTAGTGTTCCTACCATCCCTGAGCACAAATG 360  
Qy 121 AlaSerSerCysLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe 140  
Db 361 GCCTCAAGTGCCTCTTGAATCCTGGAGTTCGTGATGATGTGCTCTTTGGTTGGAGTTC 420  
Qy 141 IleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu 160  
Db 421 ATCATTGAACTGTCTGCGGGTTGCTGTGATATAGAGATGGAAGAAAGCTG 480  
Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180  
Db 481 AGGTTTGTCTGAAAGCCCTTCTGTGTATAGATACCAATTTTCTTATCGCTTCAATAGCA 540  
Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200  
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Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgGlyGlyThrTyrLysLeuLeu 220  
Db 601 TTCCTACAGATCCTCCGATGCTGCGATGCGACCGAAGGAGGACCTTGGAAATACTG 660  
Qy 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTyrIleGlyPheLeu 240  
Db 661 GGTTCAGTGGTTTATGCTCACAGCAAGAAATTAATCACAGCTTGTGTACATAGGATTTTG 720  
Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260  
Db 721 GTTCTTATTTTTCGCTCTTCTCTATCTGTGTTGGAAGGATGCCAATAAAGAGTTT 780  
Qy 261 SerThrTyrAlaAspAlaLeuTyrTrpGlyThrIleThrLeuThrIleGlyTyrGly 280  
Db 781 TCTACATATGAGATGCTCTCTGGTGGGCGCAATTAATTGACAACTATTGGCTATGGA 840  
Qy 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300  
Db 841 GACAAACTCCCTTAACCTGGCTGGGAAGATGCTTCTGCGAGGCTTTGCACTCTCTGGC 900  
Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320  
Db 901 ATTTCTTTCTTGGCATCTTCTGCGGCAATCTTGTGCTCAGGTTTTTGCATTAAGATCAA 960  
Qy 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340  
Db 961 GAACAAACCGCCAGAAACACTTTGAGAAAGAAAGAACCCAGCTGCCAACCCTCAATTCAG 1020  
Qy 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360  
Db 1021 TGTGTTTGGCGTAGTACGAGCTGATGAGAAATCTGTTTCAATTGCAACCTGGAAGCCA 1080  
Qy 361 HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyAlaSerSer 380  
Db 1081 CACTTGAAGGCGCTGCACACCTGCGAGCCCTACC----- 1113  
Qy 381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400  
::: |

Db 1114 AATCAGAAGCTAAGTTTTTAAGAGCGAGTGGCGATGGCTAGCCCCAGGGGCCAGATATT 1173  
Qy 401 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 420  
Db 1174 AAGAGCCGACAAAGCCTCAGTAGTGCAGAGGAGTCCCCAAGCACGACATCAGCCGAG 1233  
Qy 421 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 440  
Db 1234 GGCAGTCCCAACAAAGTGCAGAAAGCTGGAGCTTCAACGACCGAACCCGCTTCCGGCCC 1293  
Qy 441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460  
Db 1294 TCGCTGCGCCTCAAAAGTTCTCAGCCAAACCAAGTATAGATGCTGACACAGCCCTTGGC 1353  
Qy 461 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480  
Db 1354 ACTGATGATGATATGATGAAAAAGGATGCCAGTGTGATGATATCAGTGGAGACCTCACC 1413  
Qy 481 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 500  
Db 1414 CCACCACTTAAAGCTGCTCATTTGAGCTATCAGAATTATGAAATTTTCATGTTGCAAAACGG 1473  
Qy 501 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 520  
Db 1474 AAGTTTAAAGGAACGTTACGTTCCATATGATGTAAAGATGTCATTGAAACAATATTCGT 1533  
Qy 521 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540  
Db 1534 GGTCACTCGACATGTTGTTGTAGATTTAAAGCCTTCAACACACGCTGTTGATCAAAATCTT 1593  
Qy 541 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560  
Db 1594 GGAAGAGGCGCAAAATCACATCAGATAAGAGAGCCGAGAGAAATAACACAGCAGACATGAG 1653  
Qy 561 ThrThrAspAspLeuSerMetLeuGlyValValLysValGluLysGlnValGlnSer 580  
Db 1654 ACCACAGACGATCTCAGTATGCTCGTGGGTGTCAGAGTTGAAANACAGGTACAGTCC 1713  
Qy 581 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 600  
Db 1714 ATAGAGTCCAAGCTGGACTGCTACTACACATCTATCAACAGGTCCTTCGGAAGGCTCT 1773  
Qy 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620  
Db 1774 GCCTCAGCCCTCGCTTGGCTTTCATTCAGATCCCACTTTCGAAATGTGAACAGACATCT 1833  
Qy 621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640  
Db 1834 GACTATCAAGCCCTGTGGATAGCAAGATCTTTTCGGGTTCCGCAACAAACAGTGGCTGC 1893  
Qy 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660  
Db 1894 TTATCCAGATCAACTAGTGCCCAACATCTCGAGAGGCTTCAGTTTCATTTGACGCGCAAT 1953  
Qy 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680  
Db 1954 GAGTTCAGTGCACGACTTCTACGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2013  
Qy 681 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 700  
Db 2014 GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGGCCCAACCAACCATTTGCAAAACCA 2073  
Qy 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro 720  
Db 2074 ATAAATACGGCACCAAGCCAGCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA 2133  
Qy 721 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740  
Db 2134 GCCATCAAGCATCTGCCCAGGCCGAAACTCTGCACCCCTAACCCCTGCAGGCTTACAGGAA 2193  
Qy 741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760  
Db 2194 AGCATTTCTGACGTCACCACTGCTGCTGCTCCCAAGGAAATGTTTCAGGTTGCACAG 2253



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QY 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780
DB 2254 TCAAACTCTCACAGGACCGTCTTATGAGGAAAAGCTTTGACATGGGAGGAGAAACTCTG 2313
QY 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800
DB 2314 TTGTCGTCTCCATGCTCCGAGGACTTGGGCAAAATCTTTGTCTGTGCAAAACCTG 2373
QY 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 820
DB 2374 ATCAGTTCGACCGAGGAACCTGAATATACAACTTTCAAGGAGTGAAGTCAAGTGGCTCCAGA 2433
QY 821 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840
DB 2434 GGCAGCCAAAGATTTTACCCCAATGGAGGAAATCCAAATTTGTATTAACATGATGAAGAG 2493
QY 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 860
DB 2494 GTGGTCCGAGAGACAGACAGACACTTTTGATGCCGACCGAGCTGCCAGGAA 2553
QY 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerGlnSerIleCys 880
DB 2554 GCTGCTTTTGATCAGACTCTCTAAGGACTCGAAGGTCAAGATCATCTCAGAGCATTTGT 2613
QY 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897
DB 2614 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCAITGCAAACTGAAA 2664
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## RESULT 8

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US-09-825-147-1
; Sequence 1, Application US/09825147
; Patent No. US20020042505A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020042505A1el Human Ion Channel Protein and
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; PRIOR APPLICATION NUMBER: 2001-04-03
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-1
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## Alignment Scores:

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Pred. No.: 0 Length: 2772
Score: 4527.50 Matches: 887
Percent Similarity: 99.00% Conservatives: 1
Best Local Similarity: 98.89% Mismatches: 0
Query Match: 98.68% Indels: 9
DB: 9 Gaps: 1
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US-09-810-796-4 (1-897) x US-09-825-147-1 (1-2772)

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QY 1 MetLysAspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaAlaArgGly 20
DB 106 ATGAAGGATGTGAGTTCGGCGCGGCGAGGTGCTGCTGAACTCGCAGCCCGCAGGGGC 165
QY 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
DB 166 GACGGCTGTCTACTGTGGGCACCCGCGGCGGACCACTCGGTGGCGCGGCGGTGGCTG 225
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QY 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
DB 226 AGGAGAGCGCCCGGGGCAAGAGGGGGCCCGGATGAGCTGTCTGGGGAAGCCGCTCTCT 285
QY 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
DB 286 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCACGTACCGGGGGTGCAGAACTACCTG 345
QY 81 TyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100
DB 346 TACAACGTGTGAGAGACCCCGCGGTGGCGGTTCACTTACCACCGCTTTCGTTTTCTC 405
QY 101 LeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120
DB 406 CTGTGCTTTGTTGCTTGTATTTTGTTCAGTGTCTTCTACCATCCTCGAGCACACAAAATTG 465
QY 121 AlaSerSerCysLeuLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
DB 466 GCCTCAAGTTGCCCTCTTGATCTCGAGTTCGTGATGATGATGCTCTTGTGTTGGAGTTC 525
QY 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu 160
DB 526 ATCATTCGAATCTGGTCTCGGGTGTCTGTCTCGATATAGAGATGCGCAGGAGACTG 585
QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuLeuAlaSerIleAla 180
DB 586 AGGTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTTCTTATCGCTTCAATAGCA 645
QY 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
DB 646 GTTGTCTTCTCAAAAACCTCAGGGTATATATTTTGGCCACGCTGCACACAGTCTCCGT 705
QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgGlyGlyThrTrpLysLeuLeu 220
DB 706 TTCTACAGATCTCCCATGTTGGCATGACCGAGGGGAGGACACTTGGAAATTAAGT 765
QY 221 GlySerValValTyrAlaHisSerLysGluLeuLeuThrAlaTrpTyrIleGlyPheLeu 240
DB 766 GGTTCAGTGGTTTATGCTCAGCAGAGAAATTAATCAAGCTTGGTATCATAGGATTTTG 825
QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
DB 826 GTTCTTATTTTTCGTCTTCTTCTGCTGCGGACAAATTACATTGACAACTATTGGCTATGA 885
QY 261 SerThrTyrAlaAspAlaLeuTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
DB 886 TCTACATATGACAGATGCTCTCTGCTGGGCGACAAATTACATTGACAACTATTGGCTATGA 945
QY 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
DB 946 GACAAAACCTCCCTTAACCTGGCTGGGAAGATTGCTTTCTGCGAGCTTTGCACTCCTTGGC 1005
QY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
DB 1006 ATTTCTTTCTTTGACATCTTCTGCGGCACTTCTGCTCAGGTTTTCATTATTAAGTACAA 1065
QY 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
DB 1066 GAACAACACCCCGAGAAACACTTTTGAGAAAAGAGAACCCAGCTGCCAACCTCATTTAG 1125
QY 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
DB 1126 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTTCATTGCAACTGAGAGCA 1185
QY 361 HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyAlaSerSer 380
DB 1186 CACTTGAAGGCTTGCACACCTGCAGCCCTTACC----- 1218
QY 381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400
DB 1219 AATCAGAGCTAAGTTTTTAAGGAGCGAGTGGCGCATGGCTAGCCCCCAGGGCCAGAGTATT 1278
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DB 1279 AAGACCCCAAGCCTCAGTAGTCACAGGAGGTCCCCAAGCACCGCATCACACCCGAG 1338
QY 421 GlySerProThrLysValGlnLysSerTyrPheAsnAspArgThrArgPheArgPro 440
DB 1339 GGCAGTCCCAACCAAGTCAGAGAGCTGGAGCTTCAACGACCGAACCGCTTCGGGCC 1398
QY 441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460
DB 1399 TCGCTGCGCCCTCAAAAGTTCTCAGCCAAAACCCAGTGATAGATGCTGCACACAGCCCTTGGC 1458
QY 461 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480
DB 1459 ACTGATGATGATATGATGAAAAGAGTGCCAGTGTGATGATCATCAGTGAAGACCTCACC 1518
QY 481 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 500
DB 1519 CCACCACCTTAAACCTGCTATTCGAGCTATCAGAAATATGAAATTCATGTTGCAAAACGG 1578
QY 501 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 520
DB 1579 AAGTTTAAAGGAACAATCAGTCCATGATGATGATAAAGATGTCATTGAAACAATATTCCTCT 1638
QY 521 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540
DB 1639 GGTCACTCGACATGTTGTGTAGATTAATAAGCCCTTCAAAACCGGTGTTGATCAAAATCTT 1698
QY 541 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560
DB 1699 GGAAGAAGGCAATCAGATCAGATGAAGAGCGAGGAGAAATTAACAGCAGACATGAG 1758
QY 561 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 580
DB 1759 ACCACAGACGATCTCAGTATGCTCGGTGGTGGTCAAGGTGAAAAACAGGTACAGTCC 1818
QY 581 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 600
DB 1819 ATAGAATCCAGCTGAGCTGCTACTAGACATCTATCAACAGGTCTTCGGAAGGCTCT 1878
QY 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProPheGluCysGluGlnThrSer 620
DB 1879 CCTCAGCCCTCGCTTGGCTTTCATTCAGATCCACCTTTTGAATGTAACAGACATCT 1938
QY 621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640
DB 1939 GACTATCAAGCCCTGTGATAGCAAGATCTTTCGGGTTCGCGACAAAACAGTGGCTGC 1998
QY 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660
DB 1999 TTATCCAGATCAACTAGTGCCCAACATCTCGAGAGGCTCGCATTTCAATCTGACGCCAAAT 2058
QY 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680
DB 2059 GAGTTCAAGTCCAGACATTTCTACGCGTTAGCCCTTACTATGCAGATCAAGCAACACAG 2118
QY 681 ValProIleSerGlnSerAspGlySerAlaValAlaIleThrAsnThrIleAlaAsnGln 700
DB 2119 GTGCCAATTAGTCAAAAGGATGGCTCAGCAGTGGCAGCCACCAACACCATTTGCAAAACCA 2178
QY 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro 720
DB 2179 ATAAATACGGACCAACCAAGCCAGCAGCCCAACACTTTTACAGATCCCACTCTCTCCCA 2238
QY 721 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740
DB 2239 GCCATCAAGCATCTGCCAGGCCGAAACTCTGCACCTTAACCTTGCAGGCTTACAGAA 2298
QY 741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760
DB 2299 AGCATTTCTGACGTCAACCACTGCTGTTGCTCCCAAGGAATGTTTCAGGTGTCACAG 2358
QY 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780
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QY 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 820
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QY 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaIleProGlnProAlaArgGlu 860
DB 2599 GTGGGTCCCGAAGAGACAGACAGACACTTTTGTATGCGCACCGCAGCTGCCAGGAA 2658
QY 861 AlaIlePheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 880
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RESULT 9
US-10-803-268-1
; Sequence 1, Application US/10803268
; Publication No. US20040157259A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/10/803,268
; PRIORITY FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-803-268-1

Alignment Scores:
Pred. No.: 0 Length: 2772
Score: 4527.50 Matches: 887
Percent Similarity: 99.00% Conservatives: 1
Best Local Similarity: 98.89% Mismatches: 0
Query Match: 98.68% Indels: 9
DB: 18 Gaps: 1

US-09-810-796-4 (1-897) x US-10-803-268-1 (1-2772)
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DB 106 ATGAAGATGTGGAGTCGGGCGGCGGAGGTGCTGCTGAACTCGGACGCCAGCGGCG 165
QY 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaIleThrLeuGlyGlyGlyLeu 40
DB 166 GACGCGCTGTACTGCTGGGCAACCCGCGGCCACGCTCGGTGGCGGCGGCGGCTG 225
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Qy 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60  
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Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgValGlnAsnTyrLeu 80  
Db 286 TACACGAGTACGAGAGTGC CGCGCAACGTCAGTACCGCGGGTGCAGAACTACCTG 345  
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Qy 281 AspLysThrProLeuThrTyrLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300  
Db 946 GACAAAACCTCCCTAACTTGGCTGGGAAGATTGCTTCTGCGAGCTTTGCACTCTCTGGC 1005  
Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320  
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Qy 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340  
Db 1066 GAACAACACCCCGCAAAACATTTTGAGAAAGAGAGAACCCAGCTGCGCAACCTCATTTAG 1125  
Qy 341 CysValTyrArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTyrLysPro 360  
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Qy 361 HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyGluAlaSerSer 380  
Db 1186 CACTTGAAGGCTTGCACACCTGACGCTTACC----- 1218  
Qy 381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400  
Db 1219 AATCAGAGCTAAGTTTTTAAAGAGCGAGTGGCATGGCTAGCCCCCAGGGGGCAGAGTATT 1278

Qy 401 LysSerArgGlnAlaSerValGlyAspArgSerProSerThrAspIleThrAlaGlu 420  
Db 1279 AAGAGCCGCAAGAGCTCAGTAGGTGACAGGAGGTCCCAAGCACCGACATCACAGCCGAG 1338  
Qy 421 GlySerProThrLysValGlnLysSerTyrPheAsnAspArgThrArgPheArgPro 440  
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Qy 441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460  
Db 1399 TCGCTGGCCCTCAAAAGTTCTCAGCCAAACAGTGTATGCTGACACAGCCCTTGGC 1458  
Qy 461 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480  
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Qy 481 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 500  
Db 1519 CCACCACTTAAACTGTCTCGAGCTATCAGAAATTTAATAATTTCAATTTGCAAAACGG 1578  
Qy 501 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 520  
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Qy 521 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540  
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Qy 541 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560  
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Qy 561 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 580  
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Qy 581 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 600  
Db 1819 ATAGAAATCAAGCTGGAGCTGCTACTAGACATCTATCAACAGAGTCTTCGGAAGGCTCT 1878  
Qy 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProPheGluCysGluGlnThrSer 620  
Db 1879 GCCTCAGCCCTCGCTTTGGCTTCAATCCAGATCCCTTTTGAATGTGAACACACATCT 1938  
Qy 621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640  
Db 1939 GACTATCAAGCCCTGTGGATAGCAAGATCTTTCGGGTCCGACAAAACAGTGGCTGC 1998  
Qy 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660  
Db 1999 TTATCCAGATCAACTAGTGGCCACATCTCGAGAGGCTGCAAGTTCATTTCTGACGCCAAT 2058  
Qy 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680  
Db 2059 GAGTTCAGTCCGAGACTTCTACGCGCTTAGCCCTTACTATGACACAGTCAAGACACAG 2118  
Qy 681 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 700  
Db 2119 GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCACACCATTTGCAAAACCA 2178  
Qy 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro 720  
Db 2179 ATAAATACGGCACCCCAAGCCAGCAGCCCAACAACTTTACAGATCCCCACCTCTCTCCCA 2238  
Qy 721 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740  
Db 2239 GCCATCAAGCATCTGCCAGGCCAGAACTCTGCAACCTTAACCTTGAGGCTTTACAGGA 2298  
Qy 741 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 760  
Db 2299 AGCATTTCTGACGTCACCACTGCTGCTTGTGCTCCCAAGGAAATGTTTCAGTTGACAG 2358  
Qy 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 780

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Db 2359 TCNAATCTACCAAGACCGTCTATGAGGAAAGCTTTGACATGGGAGGAAACTCTG 2418
Qy 781 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 800
Db 2419 TTGTCTGCTGTCCCATGGTCCGAGGACCTTGGGCAATCTTTGTCTGTGCAAAACCTG 2478
Qy 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGlySerGlySerArg 820
Db 2479 ATCAGTCGACCGAGGAACTGAATATACAACCTTTTCAGGAGTGAAGTCAAGTGGCTCCAGA 2538
Qy 821 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840
Db 2539 GCACCCCAAGATTTTACCCCAATGGAGGGAATCCAAATGTTTATTAACATGATGAAGAG 2598
Qy 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaLeuProGlnProAlaArgGlu 860
Db 2599 GTGGGTCCGAGAGACAGACACACTTTTGTATGCGCACCGCAGCTGCCAGGAA 2658
Qy 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerGlnSerIleCys 880
Db 2659 GCTGCTTTTGCATCAGACTCTCTAAGGACTGGAAGGTCACGATCATCTCAGAGCAATTTGT 2718
Qy 881 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 897
Db 2719 AAGCAGAGAAAGTACAGATGCCCTCAGCTTGCCTCAATGCAAACTGAAA 2769

RESULT 10
US-09-825-147-3
; Sequence 3, Application US/09825147
; Patent No.: US20020042505A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-3

Alignment Scores:
Pred. No.: 0 Length: 3111
Score: 4527.50 Matches: 887
Percent Similarity: 99.00% Conservative: 1
Best Local Similarity: 98.89% Mismatches: 0
Query Match: 98.68% Indels: 9
DB: 9 Gaps: 1

US-09-810-796-4 (1-897) x US-09-825-147-3 (1-3111)
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Db 165 ATGAGGATGTGAGTTCGGCCGGGCGAGGAGTCTGTGTAACCTGGCAGCCGCGAGGGGC 224
Qy 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
Db 225 GACGGCTGCTACTCTGGGACCCCGCGGCGACGCTCGGTGGCGGGCGGTGGCTG 284
Qy 41 ArgGluSerArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
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Db 285 AGGAGAGACCCCGGGGCAAGCAGGGGCGCCGGATGAGCCCTGCTGGGGAAGCCGCTCTCT 344
Qy 61 TyrThrSerSerGlnSerCysArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
Db 345 TACACGAGTAGCAGAGCTGCGGGCGCAACGCTCAAGTACCGCGGGTGCAGAACTACCTG 404
Qy 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100
Db 405 TACAACGCTGCTGGAGAGACCCCGGGCTGGCGGTTCATCTACCAACGCTTTCGTTTTCTC 464
Qy 101 LeuValPheGlyCysLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120
Db 465 CTGTGCTTTGGTGTGCTGATTTTGTCAAGTGTTCCTACCATCCCTGACACACAAAATG 524
Qy 121 AlaSerSerCysLeuLeuLeuGluPheValMetIleValPheGlyLeuGluPhe 140
Db 525 GCCTCAAGTTGCTCTTGATCTCGAGTTCGTGATGATTCGTCTTTGGTTGGAGTTC 584
Qy 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160
Db 585 ATCATTCGAATCTGCTGCGGGTGTGTTGTCATATAGAGGATGCAAGGAAGACTG 644
Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db 645 AGGTTGCTCGAAAGCCCTCTGTGTTATATAGATACCATTTGTTCTTATCGCTTCAATAGCA 704
Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db 705 GTTGTCTTCGCAAAACTCAGGGTAAATATTTTTCACAGCTCTGCACCTCAGAAGTCTCGT 764
Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgGlyGlyThrTrpLysLeuLeu 220
Db 765 TTCCTACAGATCTCCCGCATGTCGCGATGACGACGAGGAGGAGGACCTTGGAAATTA 824
Qy 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTrpIleGlyPheLeu 240
Db 825 GGTTCAGTGGTATTATGCTCACAGCAAGAAATTAATCACAGCTTGATCATAGGATTTT 884
Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db 885 GTTCTTATTTTTCGCTCTCTTCCTGCTATCTGCTGGGAAAGGATGCCAATAAAGAGTT 944
Qy 261 SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
Db 945 TCTACATATGAGATGCTCTCTGCTGGGCGCAATTAATACATTCACAACTATTGGCTATGA 1004
Qy 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db 1005 GACAAAACCTCCCTAACTTGGCTGGGAGATGCTTCTGCAAGCTTTGCACTCTCTTGGC 1064
Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db 1065 ATTTCTTTCTTTCGCTCTGCGGCACTTCTGCTCAGGTTTTCGCTTAAAGTACAA 1124
Qy 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
Db 1125 GAACAACACCCGAGAAACACTTTTGAGAAAAGAGAACCCAGCTGCCAACCCTCAATTCAG 1184
Qy 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
Db 1185 TGTGTTGGCGTAGTTACGACGCTGATGAGAAATCTGTTTCCATTCGAACCTGGGAAGCA 1244
Qy 361 HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyAlaSerSer 380
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Qy 381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400
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Qy 401 LysSerArgGlnAlaSerValGlyAspArgSerProSerThrAspIleThrAlaGlu 420
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Db 1338 AAGAGCCGACAAAGCTCAGTAGGTGACAGAGGTCCTCCCAAGCACCAGCATCACAGCCGAG 1397
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Db 1398 GGCAGTCCCAAGAGTGCAGAGAGTGGAGCTTCAACGACCGAACCCTTCGGGCC 1457
Qy 441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460
Db 1458 TCGTTCGCCCTCAAAAGTTCTCAGCCAAACAGTATAGTATGCTGACACAGCCCTTGGC 1517
Qy 461 ThrAspAspValTyAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 480
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Qy 481 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 500
Db 1578 CCACCACCTTAAACCTGCTATTCGAGCTATCAGAAATTATGAAATTTTCAATTTGCAAAACGG 1637
Qy 501 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 520
Db 1638 AAGTTTAAGGAAACATTAAGTCCATATGATGATAAAGATGTCATTTGAACAATATCTGCT 1697
Qy 521 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540
Db 1698 GGTCTATCTGGACATGTTGTGTAGAAATTAAGCCCTTCAACACAGCTGTGTGATCAAAATCTT 1757
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Qy 561 ThrThrAspAspLeuSerMetLeuGlyArgValLysValGluLysGlnValGlnSer 580
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Qy 581 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 600
Db 1878 ATAGAATCCAAAGCTGAGCTGCTACTAGACATCTATCAACAGCTGCTTCGGAAGGCTCT 1937
Qy 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProPheGluCysGluGlnThrSer 620
Db 1938 GCCTCAGCCCTCGCTTGGCTTCATCTCAGATCCACCTTTTGAATGGAACACAGATCT 1997
Qy 621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640
Db 1998 GACTATCAAGCCCTGTGATAGCAAGATCTTTCGGGTTCGGCACAAACAGTGGCTGC 2057
Qy 641 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 660
Db 2058 TTATCCAGATCAACTAGTGCCAAACATCTCGAGAGGCTGCGATTCATTTCTGACGCCAAT 2117
Qy 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680
Db 2118 GAGTTTCAGTGCCACACTTTCACCGCTTAGCCCTTACTATGCAAGTCAAGCAACACAG 2177
Qy 681 ValProIleSerGlnSerAspGlySerAlaValAlaIleThrAsnThrIleAlaAsnGln 700
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Db 2238 ATAAATACGGCACCCCAAGCCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2297
Qy 721 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740
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Qy 741 SerIleSerAspValThrThrCysLeuValAlaIleSerLysGluAsnValGlnValAlaGln 760
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Qy 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyLeuThrLeu 780
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Qy 801 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 820
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Qy 821 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 840
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Qy 841 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 860
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Qy 861 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerGlnSerIleCys 880
Db 2718 GCTGCCCTTTCATCAGACTCTCTAAGGACTGGAAGGTTCACGATCATCTCAGAGCATTTGT 2777
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## RESULT 11

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US-10-803-268-3
; Sequence 3, Application US/10803268
; Publication No. US20040157259A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Ion Channel Protein and
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/10/803,268
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-803-268-3
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Alignment Scores:
Pred. No.: 0 Length: 3111
Score: 4527.50 Matches: 887
Percent Similarity: 99.00% Conservative: 1
Best Local Similarity: 98.89% Mismatches: 0
Query Match: 98.68% Indels: 9
DB: 18 Gaps: 1
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US-09-810-796-4 (1-897) x US-10-803-268-3 (1-3111)

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Qy 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyLeu 40
Db 225 GACGCGCTGCTACTGCTGGGCACCCCGCGCCACGCTCGGTGGCGCGGGTGGCTG 284
Qy 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
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Db 285 AGGAGAGCCGCGGGGCAAGCAGGGGCGCGGATGAGCCCTGCTGGGAAGCCGCTCTCT 344  
Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80  
Db 345 TACACGAGTAGCCAGAGCTGCGGGCGCAACGTCAGTAGTACCGGGGGTGCAGNACTACCTG 404  
Qy 81 TyrAsnValLeuGluAurProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100  
Db 405 TACACGCTGCTGGAGAGACCCCGCGCTGGCGTTTCATCTACACGCTTTCGTTTTCCTC 464  
Qy 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu 120  
Db 465 CTGTGCTTGGTTCGTTGATTTGTGAGTGTCTTACCATCCCTGGAGCACACAAATG 524  
Qy 121 AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe 140  
Db 525 GCCTCAAGTGCCTCTGATCCTGGAGTTCGTGATGATGTCGTCCTTGGTTGGAGTTC 584  
Qy 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160  
Db 585 ATCATTTGAATCTGCTCGGGTTCGCTGTGTCATATAGAGTATGAGGATGGCAAGGAAGCTG 644  
Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180  
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Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220  
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Qy 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240  
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Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260  
Db 885 GTTCTTAATTTTCT 944  
Qy 261 SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280  
Db 945 TCTACATATGCAGATGCTCTCTGTGGGGCACAAATACATTACAACTATTGGCTATGGA 1004  
Qy 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300  
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Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320  
Db 1065 ATTTCTTTCTTGGCT 1124  
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Qy 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360  
Db 1185 TGTGTTTGGCGTAGTACGAGCTGATGAGAAATCTGTTTCATTTGCAACCTGGAAGCCA 1244  
Qy 361 HisLeuLysAlaLeuHisThrCysSerProThrLysLysGluGlnGlyGluAlaSerSer 380  
Db 1245 CACTTGAAGGCTTGCACACTGACGCTTAC----- 1277  
Qy 381 SerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 400  
Db 1278 AATCAGAAGCTAAGTTTTAAGAGCGAGTGCATGGCTAGCCCGAGGGGCCAGAGTATT 1337  
Qy 401 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 420

Db 1338 AAGAGCCGACAAGGCTCAGTAGGTGACAGGAGGTCCCCAAGACCGACATCACAGCCGAG 1397  
Qy 421 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 440  
Db 1398 GGCAGTCCCAACCAAGAGTGCAGAGAGCTGGAGCTTCAACGACCGAACCCTTCGGGCC 1457  
Qy 441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460  
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Db 1518 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1577  
Qy 481 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 500  
Db 1578 CCACCACCTTAAACTGTCATTCGAGCTATCAGAAATTTATGAAATTTATGTTGCAAAACGG 1637  
Qy 501 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 520  
Db 1638 AAGTTTAAGGAAACATTTACGTCCTCATGATGATAAAGATGTCTTTGAAACAATATTTCTGCT 1697  
Qy 521 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 540  
Db 1698 GGTCTATCTGGACATGTTGTGTAGAAATTAAGACCTTCAACACGCTTGTATCAAAATCTT 1757  
Qy 541 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 560  
Db 1758 GGAAAGGGCAAAATCACATCAGATAAGAGAGCCGAGAGAAATAAACAAGACAGACATGAG 1817  
Qy 561 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 580  
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Db 1878 ATAGAAATCAAGCTGGAGCTGCTAGTACATCTATCAACAGGCTCTTCGGAAAGGCTCT 1937  
Qy 601 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 620  
Db 1938 GCCTCAGCCCTCGCTTTGGCTTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT 1997  
Qy 621 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 640  
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Qy 661 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 680  
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Qy 681 ValProIleSerGlnSerAspGlySerAlaValAlaIleThrAsnThrIleAlaAsnGln 700  
Db 2178 GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGCAGCCACCAACACCATTTGCAAAACCAA 2237  
Qy 701 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro 720  
Db 2238 ATAAATACGGACCCCAAGCCAGAGCCCAACCACTTTACAGATCCCACTCTCTCTCCA 2297  
Qy 721 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 740  
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Qy 761 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyLeuThrLeu 780  
Db 2418 TCAATCTCAACAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAAACTCTG 2477





Qy 273 rleuThrThrIleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSe 293  
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Qy 313 rGlyPheAlaLeuLysValGlnGlnHisArgGlnLysHisPheGluLysArgArgAs 333  
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Qy 444 uLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspAspVa 464  
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Db 1615 AGCAGAGGAGAGAGCTACCACTGTGAGCTCAGGTGGAGCAGCATATGCTGCTGTGAA 1674  
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RESULT 13  
US-10-850-928-1  
; Sequence 1, Application US/10850928  
; Publication No. US20050037460A1  
; GENERAL INFORMATION:  
; APPLICANT: JENTSCH, Thomas J.  
; TITLE OF INVENTION: POTASSIUM CHANNELS AND GENES ENCODING THESE  
; FILE REFERENCE: 2815-127PUS2  
; CURRENT APPLICATION NUMBER: US/10/850,928  
; CURRENT FILING DATE: 2004-05-20  
; PRIOR APPLICATION NUMBER: 09/492,361  
; PRIOR FILING DATE: 2000-01-27  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 2335  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (1)..(2335)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (83)..(2170)  
US-10-850-928-1

Alignment Scores:  
Pred. No.: 3,89e-197 Length: 2335  
Score: 2012.00 Matches: 437  
Percent Similarity: 65.45% Conservative: 82  
Best Local Similarity: 55.11% Mismatches: 136  
Query Match: 43.85% Indels: 138  
DB: 19 Gaps: 16

US-09-810-796-4 (1-897) x US-10-850-928-1 (1-2335)

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166 Db ---CTGTGCAGCGAACAGGGCGGCGGG-----CGGGGGCGG 201  
48 Qy GlnGlyAla-ArgMetSerLeuLeuGlyLysProLeu----- 59  
202 Db CTCGGCGCGCGCTCGGCGCTCTCTGGGCGAGCCCTCTCGCGCGGGCGCGCCCTCCCTCG 261  
Qy 60 -----SerTyrThrSerGlnSerCysArgArgAsnValLysTyr 73  
262 Db GCGGGGCTCGGCTCGGGCTCGCTCGCGCCAGCGCTCTCTCGGGCGCGCACAGCGCTA 321  
Qy 73 rArgArgValGlnAsnTyrLeuTyrAsnValLeuGluArgProArgGlyTyrAlaPheIle 93  
202 Db CTCGGCGCGCGCTCGGCGCTCTCTGGGCGAGCCCTCTCGCGCGGGCGCGCCCTCCCTCG 381  
Qy 93 eTyrHisAlaPheValPheLeuLeuValPheGlyCysLeuIleLeuSerValPheSerTh 113  
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1675 GACAGTCATCCGCTCCATCAGGATTTCAAGATTCTCTGGTGGCCAAAGAGAAATTCAGGA 1734

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524 pMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyG 544

1795 CATGCTGGGCGCGATCAAGAGCCTGCAAACTCGGTGGACCAAAATGTGGGTGCGGGG-- 1852

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 3, 2005, 02:34:27 ; Search time 6898.61 Seconds  
(without alignments)  
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Title: US-09-810-796-4

Perfect score: 4588

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Ygapop 10.0	Ygapext 0.5	
Fgapop 6.0	Fgapext 7.0	
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Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gsl1:\*  
9: gb\_gsl2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4509.5	98.3	2733	9 AY407013	AY407013 Homo sapi
2	4202	91.6	2729	9 AY407015	AY407015 Mus muscu
3	3079.5	67.1	2014	9 AY407014	AY407014 Pan trogl
4	2716	59.2	2276	3 AK033079	AK033079 Mus muscu
5	1528	33.3	1571	3 AK040190	AK040190 Mus muscu
6	1260.5	27.5	997	2 BB609854	BB609854 BB609854
7	1225	26.7	797	6 CD629762	CD629762 55049367J
8	1161	25.3	732	6 CD629756	CD629756 55049343J
9	1150	25.1	742	6 CD629754	CD629754 55049327J

10	1121.5	24.4	864	7	CK772601	CK772601 961159 MA
11	1112	24.2	717	6	CD629766	CD629766 55049391J
12	1111	24.2	691	6	CD629755	CD629755 55049343H
13	1101	24.0	678	6	CD629758	CD629758 55049351J
14	1085	23.6	632	2	BB624101	BB624101 BB624101
15	1080	23.5	744	6	CB244389	CB244389 UI-M-FY0-
16	1079.5	23.5	658	2	BE158938	BE158938 MRO-HT040
17	1074	23.4	724	6	CD629752	CD629752 55049303J
18	1053.5	23.0	628	5	EX917798	EX917798 BX917798
19	1043.5	22.7	679	2	BE647997	BE647997 UI-M-BH1-
20	1038.5	22.6	1766	9	AY404832	AY404832 Homo sapi
21	1037	22.6	1742	9	AY404834	AY404834 Mus muscu
22	1035	22.6	714	6	CD629760	CD629760 55049359J
23	1031	22.5	599	6	CD629765	CD629765 55049303H
24	1013.5	22.1	624	6	CD629751	CD629751 55049303H
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26	993.5	21.7	643	6	CD629763	CD629763 55049383H
27	989	21.6	584	2	AW049888	AW049888 UI-M-BH1-
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31	966.5	21.1	737	6	CD629764	CD629764 55049383J
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36	892	19.4	914	2	BF312386	BF312386 601898926
37	864	18.8	908	2	BF240146	BF240146 601905649
38	858	18.7	659	5	BX926684	BX926684 BX926684
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44	831	18.1	506	4	BF959996	BF959996 QV2-NN004
45	827.5	18.0	1004	5	BQ219245	BQ219245 AGENCOURT

#### ALIGNMENTS

RESULT 1	AY407013	2733 bp	DNA	linear	GSS 15-DEC-2003
LOCUS	AY407013				
DEFINITION	Homo sapiens KCNQ5 gene, VIRTUAL TRANSCRIPT, partial sequence,				
ACCESSION	AY407013				
VERSION	AY407013.1	GI:39762984			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 2733) Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Inferred nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14571302				
REFERENCE	2 (bases 1 to 2733) Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
AUTHORS	Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
TITLE	This sequence was made by sequencing genomic exons and ordering them based on alignment.				
JOURNAL	Location/Qualifiers				
COMMENT	1. .2733				
FEATURES					



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## gene

## ORIGIN

## Alignment Scores:

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Score:          4509.50  Matches:      884
Percent Similarity: 98.66%  Conservative: 1
Best Local Similarity: 98.55%  Mismatches: 3
Query Match:      98.29%  Indels: 9
DB:               9      Gaps: 1

US-09-810-796-4 (1-897) x AY407013 (1-2733)

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Qy 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
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Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
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Qy 441 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 460
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 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering  
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 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
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 Adams,M.D. and Cargill,M.  
 Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering  
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 Percent Similarity: 94.53% Conservative: 14  
 Best Local Similarity: 92.97% Mismatches: 25  
 Query Match: 91.59% Indels: 25  
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AUTHORS 1 (bases 1 to 2014)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 2014)  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
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VERSION	99279253		
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus		
ORGANISM	Mus musculus		
REFERENCE	1		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE	2		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to		
	prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
REFERENCE	3		
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,		
	Kanno, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M.,		
	Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,		
	Yanamoto, R., Matsuoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,		
	Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,		
	Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,		
	Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system-384-format		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBMED	11076861		
REFERENCE	4		

## AUTHORS

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

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## JOURNAL

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## JOURNAL

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REFERENCE

The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)

6 (bases 1 to 2276)  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission  
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/

Location/Qualifiers  
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PHVLKN"

Alignment Scores:







Db 675 CTGGTGCTCATCTTTGGCTCTTCTTCTGCTTACCTGGCTGAGGAGATGCCAATCTCTGAC 734

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Db 735 TTCTCTCTCTATGCGGACTCGCTCTGTGGGGGAGCATCACACTGACGACCATTTGGCTAT 794

QY 280 GlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeu 299

Db 795 GGTGACAGACGCCACATACATGCTGGCGAGGTTCTGGCTGCGGGCTTGGCTTACTG 854

QY 300 GlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysVal 319

Db 855 GGCACTCTCTTTTGGCTGCTGCTGGCATCTGGGCTCTGGCTTTGGCCCTGAAGTC 914

QY 320 GlnGluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIle 339

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QY 340 GlnCysValTrpArgSerTyrAlaAlaAsp---GluLysSerValSerIleAlaThrTrp 358

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QY 359 ---LysProHisLeuLysAlaLeu----- 365

Db 1035 TATTACTATGACAGCATTTCCATCTTTACAGAGCTGGCCCTCTTTGAGACACATA 1094

QY 365 ----- 365

Db 1095 CAACGGGCGCAATGGGGCTTACGGCCCTGGAGGTGAGCGGGCGCCAGTACCTGAT 1154

QY 366 -----HisThrCysSerProThrLysLysGluGlnGly 376

Db 1155 GGAGCGCCTCTGCTACCGCCCTGTGCCACCTGC-----CACCGGCGCAGGC 1202

QY 377 GluAlaSer-----SerSerGlnLysLeuSerPheLysGluArgValArgMet 392

Db 1203 AGTGCTCTTCTGCTGGGAAAGCAGCGGATGGGATGAGCATCAAGACCGATCCGCATA 1262

QY 393 AlaSerProArgGlyGlnSerIleLysSerArgGln-----AlaSerValGlyAspArg 410

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QY 411 ArgSerProSerThrAspIleThrAlaGlu---GlySerProThrLysValGlnLysSer 429

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Db 1383 TGGAGCTTCAATGACCGCAGCCGCTTCGGGCGCTCTTAAGACTCAAGCCTCGCTGCTCT 1442

QY 447 SerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspValTyrAsp 466

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QY 467 GluLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuLysThrVal 486

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Db 1536 ATCCGTTCTGTGAGGATTTCTGAAGTTCTGTTAGGCC 1571

RESULT 6

BB609854

LOCUS BB609854

DEFINITION BB609854 RIKEN full-length enriched, adult male lung Mus musculus

CDNA clone 1200002P22 5', mRNA sequence.

ACCESSION BB609854

VERSION BB609854.1 GI:15390457

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 997)  
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,  
Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,  
Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,  
Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,  
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,  
Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.  
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)  
Unpublished (2001)  
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Tel: 81-45-503-9222  
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Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,  
Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,  
Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.  
and Hayashizaki, Y.

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10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,  
Sugahara, Y. and Hayashizaki, Y.  
Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A.,  
Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K.,  
Arakawa, T., Ishii, Y. and Hayashizaki, Y.

Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.  
Func. Genomics 2 pre, L72-L86 (2001)  
Please visit our web site (http://genome.gsc.riken.go.jp) for  
further details.  
e mouse tissues.

FEATURES  
source

1. 997  
/organism="Mus musculus"  
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/db\_xref="taxon:10090"  
/clone="1200002P22"  
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Genomic Sciences Center and Genome Science Laboratory in  
RIKEN. Division of Experimental Animal Research in Riken  
contributed to prepare mouse tissues. 1st strand cDNA was  
primed with a primer [5',  
GAGAGAGAGCGCGCCAACTCGAGTTTCTTTTCTTTTCTT 3'], cDNA was  
prepared by using trehalose thermo-activated reverse  
transcriptase and subsequently enriched for full-length by  
cap-trapper. Second strand cDNA was prepared with the  
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cDNA was cleaved with XhoI and SstI."

## ORIGIN

Alignment Scores: 4.6e-111 Length: 997  
Pred. No.:



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RESULT 8
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LOCUS      CD629756              732 bp      mRNA      linear      EST 12-JAN-2004
DEFINITION 55049343J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION  CD629756
VERSION     CD629756.1 GI:40278022
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE     1 (bases 1 to 732)
JOURNAL   Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
COMMENT   Circular rapid amplification of cDNA ends for high-throughput
          extension cloning of partial genes
          Genomics 84 (1), 205-210 (2004)
          Contact: Fu GK
          Incyte Genomics, Inc.
          3160 Porter Dr., Palo Alto, CA 94304, USA
          Tel: 6508454102
          Email: gfu@incyte.com.

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Query Match:    25.31%      Indels:     4
DB:             6      Gaps:     0

US-09-810-796-4 (1-897) x CD629756 (1-732)

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Qy      378 AlaSerSerGlnLyLeuSerPhelyGluArgValArgMetAlaSerProArgGly 397
Db      611 GCATCAACGACGTAGAAGCTAAGTTTAAAGAGCGAGTGGCGATGGCTAGCCCGAGGGGC 552
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Qy      458 AlaLeuGlyThrAspAspValTyrAspGluLySerGlyCysGlnCysAspValSerValGlu 477
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Qy      538 GlnIleLeuGlyLySerGlyGlnIleThrSerAspLySerArgGluLySerIleThrAla 557
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Qy      558 GluHisGlnThrThrAspAspLeuSerMetLeuGlyArgValValLySerValGluLyGln 577
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DEFINITION 55049327J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION  CD629754
VERSION     CD629754.1 GI:40278020
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE     1 (bases 1 to 742)
JOURNAL   Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.
COMMENT   Circular rapid amplification of cDNA ends for high-throughput
          extension cloning of partial genes
          Genomics 84 (1), 205-210 (2004)
          Contact: Fu GK
          Incyte Genomics, Inc.
          3160 Porter Dr., Palo Alto, CA 94304, USA
          Tel: 6508454102
          Email: gfu@incyte.com.

FEATURES             source
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Qy 289 GlyArgLeuSerAlaGlyPheAlaLeuLeuGlyIleSerPhePheAlaLeuProAla 308
Db 603 GGGAGGCTCTGGCAGCACCTTCACTCATCGGTGCTCTCTTCCGCTCTCTCTGCT 662
Qy 309 GlyIleLeuGlySerGlyPheAlaLeuLysValGlnGluGlnHisArgGlnLysHisPhe 328
Db 663 GGCATTTTGGGGTCTGGCTTTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 722
Qy 329 GluLysArgAsnProAlaAlaAsnLeuIleGlnCysValTyrArgSerTyrAlaAla 348
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RESULT 11
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DEFINITION 55049391J1 PFLP Homo sapiens cDNA, mRNA sequence.
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VERSION CD629766.1 GI:40278032
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 717)
JOURNAL Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
COMMENT Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
FEATURES
Location/Qualifiers
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Best Local Similarity: 24.24% Indels: 4
Query Match: 6 Gaps: 0
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US-09-810-796-4 (1-897) x CD629766 (1-717)

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Qy 464 alTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeu 484
Db 355 TATATGATGAAAAGGATGCCAGTGTGATGATGATGATGATGATGATGATGATGATGAT 296
Qy 484 ysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPheLysG 504
Db 295 AAACGTGTCTTCGAGCTATCAGAAATTATGAAATTTTCATGTTGCAAAACGGAAGTTAA 236
Qy 504 luThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuA 524
Db 235 AAACATTCATGCTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 176
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Db 175 ACATGTTGTGTAGAAATTTAAAGCCCTTCATAACAGCTGTGTGATCAAAATTTCTTGG 116
Qy 544 GlnIleThrSerAspLysLys-SerArgGluLysIleThrAlaGluHisGluThrThrAs 563
Db 115 CAAATCATCATGATAAGAACGAGCCGAGAGAAATAACACAGAACATGAGACACACA 56
Qy 563 pAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSerIle 581
Db 55 CGATCTCACTATGCTCGGTGGGGTCAAGTTGTTAAACAGGTACAGTACATCA 1

RESULT 12
LOCUS CD629755 691 bp mRNA linear EST 12-JAN-2004
DEFINITION 55049343H1 PFLP Homo sapiens cDNA, mRNA sequence.
ACCESSION CD629755
VERSION CD629755.1 GI:40278021
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 691)
JOURNAL Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
COMMENT Circular rapid amplification of cDNA ends for high-throughput
extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
FEATURES
Location/Qualifiers
source
1..691
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone_lib="PLP"
/note="Vector: pDrive Cloning Vector"

ORIGIN
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Pred. No.: 1111.00 Matches: 225
Score: 97.84% Conservative: 1
Percent Similarity:
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Best Local Similarity: 97.40% Mismatches: 4  
Query Match: 24.22% Indels: 3  
DB: 6 Gaps: 0

US-09-810-796-4 (1-897) x CD629755 (1-691)

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QY 286 ThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGlyIleSerPhePheAla 305
DB 61 ACTTGGCTGGGAAGATTGCTTCTGCAGGCTTTGCACCTCTTGGCAATTTCTTTCTTGA 120

QY 306 LeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGlnGlnGlnHisArgGln 325
DB 121 CTTCTGCGCGGCAATCTTGGCTTCAGGTTTTCATTAAGTACAAAGACCAACCGCCAG 180

QY 326 LysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGlnCysValTrpArgSer 345
DB 181 AAACACTTTGAGAAAGAGGAACCCAGCTGCCAACCTCATTCAGTGTGTTGGGTAGT 240

QY 346 TyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysProHisLeuLysAlaLeu 365
DB 241 TACGAGCTGATGAGAAATCTGTTTCCATTTGCACTGGAAGCCACACTTGAAGGCTTG 300

QY 366 HisThrCysSerProThrLysLysGlnGlnGlyGluAlaSerSerSerGlnLysLeuSer 385
DB 301 CACACTGCAGCCCTACCAAGAGAACAGAGGAGAGCATCAGCAGTCAGAGCTAAGT 360

QY 386 PheLysGluArgValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGlnAla 405
DB 361 TTAAAGAGCGAGTGCATGCTAGCCAGCCAG-GGCCAGAGTATTAAAGAGCCGCAAGCC 419

QY 406 SerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu-GlySerProThrLys 425
DB 420 TCAGTAGTGACAGAGGTCCCAAGCACCCAGCATCACAGCGGAGGCGAGTCCCAACAA 479

QY 425 sValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLys 445
DB 480 AGTCAGAGAGCTGGAGCTTCAAGCGCGGAACCCGCTTCGGCCCTCGCTGGCGCTCA 539

QY 445 sSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTy 465
DB 540 AAGTCTTCAGCCAAACCAAGCAGATGATGCTGACACAGCCCTTGGCACTGATGTATA 599

QY 465 rAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuLysTh 485
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QY 485 rValIleArgAlaIleArgIleMetLysPhe 495
DB 659 TGTCATTCGAGCTATCAGAAATTGAAATTC 689
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RESULT 13  
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LOCUS 55049351J1 FLP Homo sapiens cDNA, mRNA sequence. EST 12-JAN-2004

DEFINITION CD629758  
ACCESSION CD629758  
VERSION CD629758.1 GI:40278024

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 678)

AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.

TITLE Circular rapid amplification of cDNA ends for high-throughput  
extension cloning of partial genes

JOURNAL Genomics 84 (1), 205-210 (2004)

CONTACT: Fu GK

INCYTE Genomics, Inc.

3160 Porter Dr., Palo Alto, CA 94304, USA

FEATURES  
source  
Tel: 6508454102  
Email: gfu@incyte.com.  
Location/Qualifiers  
1..678  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_lib="PLP"  
/note="Vector: pDrive Cloning Vector"

## ORIGIN

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Percent Similarity: 99.12% Conservative: 1  
Best Local Similarity: 98.67% Mismatches: 1  
Query Match: 24.00% Indels: 2  
DB: 6 Gaps: 0

US-09-810-796-4 (1-897) x CD629758 (1-678)

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QY 379 rSerSerGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSe 399
DB 617 AAGCAGTCAGAGCTAAGTTTAAAGAGCGAGTGCATGCTAGCCGCCAGGCGCCAGAG 558

QY 399 rLysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAl 419
DB 557 TATTAAAGGCGCAAGCCTCAGTAGGTGACAGAGGTGCCCAAGCACCGACATCACAGC 498

QY 419 aGluGlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheAr 439
DB 497 CGAGGGCAGTCCCAAGAGTGCAGAGCTTCAACGACCGAACCCGCTTCCG 438

QY 439 gProSerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLe 459
DB 437 GCCCTCGCTGGCTCAAAAGTTCTCAGCCAAACACAGTATGATGATGATGATGATGATGAT 378

QY 459 uGlyThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLe 479
DB 377 TGGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 318

QY 479 uThrProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLy 499
DB 317 CACCCACCACTTAAACTGTTCATTCGAGCTATCAGAAATTATGAATTTCAATTTGCATA 258

QY 499 sArgLysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSe 519
DB 257 ACAGAGTTTAAAGAAACATTACGTCCATATGATGATGATGATGATGATGATGATGATGAT 198

QY 519 rAlaGlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIl 539
DB 197 TGCTGGTTCATCTGACATGTTGTGTAGAAATTTAAAGGCTTTCAAAACACGTTGTATCAAT 138

QY 539 eLeuGlyLysGlyGlnIleThrSerAspLysLysSerArgGlyLysIleThrAlaGluHi 559
DB 137 TCTTGGAAAGGGCAATTCACATCAGATAGAGAGCGGAGAGAAATTAACAGGAGAAC 78

QY 559 sGluThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGl 579
DB 77 TGAGACACACAGACGATCTCAGTATGCTCGGTGGGTGGT-AAAGTTGAAAAACAGGTACA 19

QY 579 nSerIleGluSerLys 584
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RESULT 14

LOCUS BB624101

DEFINITION BB624101 RIKEN full-length enriched, adult male cortex Mus musculus

632 bp mRNA linear EST 26-OCT-2001





## ORGANISM

## Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 744)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs@mail.nih.gov](mailto:cgapbs@mail.nih.gov)

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)

Seq primer: pYX-5.

Location/Qualifiers

1..744

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="CS7BL/6"

/db\_xref="taxon:10090"

/clone="IMAGE:6832924"

/tissue\_type="whole brain"

/dev\_stages="embryo 13.5, 14.5, 16.5, 17.5 dpc"

/lab\_host="DH10B (T1 phage resistant)"

/clone\_lib="NIH\_BMAP\_FY0"

/note="Organ: Brain; Vector: pYX-Asc; Site 1: Ecor I;

Site 2: Not I; The library was constructed according

Bonaldi, Lennon and Soares, Genome Research, 6:791-806,

1996. Denatured RNA was size fractionated on a 1% agarose

gel. First strand cDNA synthesis was primed with oligo-dT

primer containing a Not I site. Double strand cDNA was

size selected according to mRNA size fraction, ligated

with Ecor I adaptor, digested with NotI and then cloned

directionally into pYX-Asc vector. The library tag

sequence located between the Not I site and the polyA tail

is AGCGAGACAG. This library was created for the University

Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the

Developing Mouse Nervous System', supported by National

Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,

program coordinator."

## ORIGIN

## Alignment Scores:

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Percent Similarity:	91.46%	Conservative:	9
Best Local Similarity:	87.80%	Mismatches:	21
Query Match:	23.54%	Indels:	0
DB:	6	Gaps:	0

US-09-810-796-4 (1-897) x CB244389 (1-744)

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Db	7	CTGTCGGCTCAGACAAACAGCGGCTGTTTACGAGGTCAGCGAGTCCCAATCTCA	66
Qy	651	ArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyAlaLeu	670
Db	67	AGAGGCGTGCAGTTTCATCTCAACCAATGAGTTCAGTTCAGACTTTCTATGCGCTT	126
Qy	671	SerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySerAla	690
Db	127	AGCCCTACTATGACAGCAGACAGTACCAGGTACCCATGAGTCAAAATGACGGCTCTCC	186
Qy	691	ValAlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAlaPro	710
Db	187	GTGGTAGCCCAATTAACATTGCAAAACCAATAAGCGCGCAGCCAGCCAGAGCCCA	246

Qy	711	ThrThrLeuGlnIleProProProLeuProAlaIleLysHisLeuProArgProGluThr	730
Db	247	ACAACTTTACAGATCCCTCCCTCTCTCGGCCATCAGACACTTGTCCAGGCCAGAACCT	306
Qy	731	LeuHisProAsnProAlaGlyLeuGlnGluSerIleSerAspValThrThrCysLeuVal	750
Db	307	CTGCTCTCAAAACCCACCGGCTTACAAGAGAGTATTCTGATGTCAACACCTGCTGT	366
Qy	751	AlaSerLysGluAsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMetArg	770
Db	367	GCCTCCCAAGGAAGTGTTCAGTTTGCACAGTCAAAACCTGACCAAGGACCGTCCCTGAGG	426
Qy	771	LysSerPheAspMetGlyGlyLeuThrLeuSerValCysProMetValProLysAsp	790
Db	427	AAAAGTTTCGACATGGGAGGAGAACTCTGTTGTCTGTCGCCCCCATGGTGCCCAAGAT	486
Qy	791	LeuGlyLysSerLeuSerValGlnAsnLeuIleArgSerThrGluGluLeuAsnIleGln	810
Db	487	TTGGGCAAACTCTGTCTGTACAAAACCTGATCAGGTGCGACAGAGAACTGAACCTTACAG	546
Qy	811	LeuSerGlySerGluSerSerGlySerArgGlySerGlnAspPheTyrProLysTrpArg	830
Db	547	TTTTCAGCGACGAGTCAAGCGGCTCTCGAGGCGAGTCAAGATTTTATCCCAAGTGGAGA	606
Qy	831	GluSerLysLeuPheIleThrAspGluGluValGlyProGluGluThrGluThrAspThr	850
Db	607	GAATCCANATTGTTTATAACTGATGAGGAGTCTCGAGGAGTCCGAAAGACAGAAACAGATACT	666
Qy	851	PheAspAlaAlaProGlnProAlaArgGluAlaAlaPheAlaSerAspSerLeuArgThr	870
Db	667	TTTGACGGCACCCACCGCTCGCGGGGAGGCTGCTTTCTCATCAGACTCTCTNTAGGACT	726
Qy	871	GlyArgSerArgSerSer	876
Db	727	GGAAGGTCACGGTCACT	744

Search completed: April 3, 2005, 11:13:04

Job time : 6922.61 secs

GenCore version 5.1.6  
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Run on: April 3, 2005, 06:38:16 ; Search time 348.733 Seconds  
(without alignments)  
4166.553 Million cell updates/sec

Title: US-09-810-796-5

Perfect score: 4547

Sequence: 1 MKOVESGRVLLNSAARG.....SICKAGESTDLSPHVLIK 889

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Ygapop 10.0 , Ygapext 0.5  
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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database : Issued Patents NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	4547	100.0	3111	4	US-09-825-147-3
3	4527.5	99.6	3137	4	US-09-590-304-1
4	4513.5	99.3	3074	4	US-09-813-148-1
5	2007.5	44.1	2335	4	US-09-492-361-1
6	1998.5	44.0	2196	4	US-09-949-016-1823
7	1794	39.5	3237	3	US-09-177-650-95
8	1792.5	39.4	3287	3	US-09-105-058C-19
9	1790.5	39.4	2169	3	US-09-105-058C-22
10	1788	39.3	3232	3	US-09-177-650-1
11	1767	38.9	2273	3	US-09-177-650-88
12	1587.5	34.9	2565	3	US-09-105-058C-26

13	1587.5	34.9	2914	3	US-09-177-650-6
14	1550.5	34.1	2814	3	US-09-177-650-90
15	1207.5	26.6	900	3	US-09-105-058C-5
16	1201.5	26.4	900	3	US-09-105-058C-3
17	1116.5	24.6	3181	3	US-09-135-021-1
18	1116.5	24.6	3181	3	US-09-135-020-1
19	1116.5	24.6	3181	3	US-09-135-010A-1
20	1116.5	24.6	3181	3	US-09-444-871-1
21	1116.5	24.6	3181	3	US-09-597-735-1
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32	1094	24.1	2821	4	US-09-597-731-115
33	1094	24.1	2924	4	US-09-949-016-32
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45	260.5	5.7	1927	3	US-09-336-643A-3

#### ALIGNMENTS

##### RESULT 1

US-09-825-147-1  
; Sequence 1, Application US/09825147  
; Patent No. 6767736  
; GENERAL INFORMATION:  
; APPLICANT: Hu, Yi  
; APPLICANT: Kieke, James Alvin  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Nehls, Michael C.  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6767736el Human Ion Channel Protein and  
; FILE REFERENCE: Polynucleotides Encoding the Same  
; CURRENT APPLICATION NUMBER: US/09/825,147  
; CURRENT FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: US 60/194,255  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2772  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-825-147-1

Alignment Scores:  
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Score: 4547.00  
Length: 2772  
Percent Similarity: 100.00%  
Matches: 888  
Best Local Similarity: 100.00%  
Conservative: 0  
Query Match: 100.00%  
Mismatches: 0  
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DB: 4

US-09-810-796-5 (1-888) x US-09-825-147-1 (1-2772)



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## RESULT 2

US-09-825-147-3  
; Sequence 3, Application US/09825147  
; Patent No. 6767736  
; GENERAL INFORMATION:  
; APPLICANT: Hu, Yi  
; APPLICANT: Kieke, James Alvin  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Nehls, Michael C.  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6767736el Human Ion Channel Protein and  
; FILE REFERENCE: Polynucleotides Encoding the Same  
; CURRENT APPLICATION NUMBER: US/09/825,147  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: US 60/194,255  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 3111  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-825-147-3

Alignment Scores:  
Pred. No.: 0 Length: 3111  
Score: 4547.00 Matches: 888  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-09-810-796-5 (1-888) x US-09-825-147-3 (1-3111)

Qy 1 MetLysAspValGluSerGlyArgGlyValLeuLeuAsnSerAlaAlaAlaArgGly 20

Db 165 ATGAAGGATGGAGTCGGGCGGGGAGGGTGTCTGCTGAACCTCGGACGCGCCAGGGGC 224  
Qy 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeu 40  
Db 225 GACGGCTGTCTACTGTGGGCAACCGCGGGCACGCTCGGTGGCGGGGGTGGCTG 284  
Qy 41 ArgGluSerArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60  
Db 285 AGGAGAGCCCGGGGCAAGCAGGGGCGCGGATGAGCCTGCTGGGGAAGCGCTCTCT 344  
Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80  
Db 345 TACACGAGTAGCCAGAGCTGCGCGGCAACGTCAAGTACCAGCGGGGTGCAGAACTACCTG 404  
Qy 81 TyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100  
Db 405 TACAACGTGTGGAGAGACCCCGCGGTGGGGTTCATCTACACGCTTCGTGTTTCTC 464  
Qy 101 LeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120  
Db 465 CTTGTCTTGGTGTCTGATTTTGTAGTGTCTTACCATCCCTGAGCACACAAAATTG 524  
Qy 121 AlaSerSerCysLeuLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe 140  
Db 525 GCCTCAAGTTCCTTGTATCCTGGAGTTCGTGATGATGTCTGCTTTGGTTTGGAGTTC 584  
Qy 141 IleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu 160  
Db 585 ATCATTCGAATCTGTCTGGGTGTCTGTGTGATATAGAGGTGCAAGAGAGACTG 644  
Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuLeuAlaSerIleAla 180  
Db 645 AGGTTGCTCGAAAGCCCTTCTGTATTATAGATACCATTTGTTTATCGCTTCAATAGCA 704  
Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200  
Db 705 GTTGTCTCGAAAACTCAGGGTAATATTTTGCACGTCTGCACCTCAGAACTCTCGT 764  
Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTyrLysLeuLeu 220  
Db 765 TTCCTACAGATCCTCCGATGTCGCGATGACCGAGGGGAGGACACTTGGAAATTAATG 824  
Qy 221 GlySerValValTyrAlaHisSerLysGlnLeuIleThrAlaTyrTyrIleGlyPheLeu 240  
Db 825 GGTTCAGTGGTTTATGTCTACAGCAAGAAATTAATACAGCTTGTGTATAGGATTTTGT 884  
Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260  
Db 885 GTTCTTATTTTTCGTCTTCTTCTATCTGTGGGAAAGGATGCCAAATAAAGAGTTT 944  
Qy 261 SerThrTyrAlaAspAlaLeuTyrTyrGlyThrIleThrLeuThrThrIleGlyTyrGly 280  
Db 945 TCTACATATGAGATGCTCTGTGGGGGACAAATTAATGACAACTATTGGCTATGGA 1004  
Qy 281 AspLysThrProLeuThrTyrLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300  
Db 1005 GACAAAACCTCCCTAACTTGGCTGGGAAGATTTGCTTCTGCAAGGCTTTGCACCTCTTGGC 1064  
Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320  
Db 1065 ATTCTTCTTTCGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1124  
Qy 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340  
Db 1125 GAACAACACCCGACAGAAACACTTTGAGAAAGAGGAAACCCAGCTGCCCACTCATTCAG 1184  
Qy 341 CysValTyrArgSerTyrAlaAlaAspGlnLysSerValSerIleAlaThrTyrLysPro 360  
Db 1185 TGTGTTGGCGTAGTACGACGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCA 1244  
Qy 361 HisLeuLysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPheLysGluArg 380

Db 1245 CACTTGAAGGCTTGCACACCTGCAGCCCTACCAATCAGACGCTAAGTTTTAAGGAGCGA 1304  
Qy 381 ValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAsp 400  
Db 1305 GTGCGCATGGCTAGCCCCAGGGGCGAGATATTAAAGCCGACCAAGCTCTAGTAGGTGAC 1364  
Qy 401 ArgArgSerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSer 420  
Db 1365 AGGAGGTCCCAAGCAGCCGACATCACAGCCGAGGGCAGTCCACCAAGTCGACGAGAGC 1424  
Qy 421 TrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerSerGlnPro 440  
Db 1425 TGGAGCTTCAACGACCGAACCCGCTTCGGGCCCTCGCTCGCCCTCAAAAGTTCTCAGCCA 1484  
Qy 441 LysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyrAspGluLysGly 460  
Db 1485 AAACAGGTGATAGTGTGACACAGCCCTTGCGACTGATGATGATATGATGATAAAGGA 1544  
Qy 461 CysGlnCysAspValSerValGluAspLeuThrProProLeuLysThrValIleArgAla 480  
Db 1545 TGCCAGTGTGATGATCAGTGGAGAGCTCACCCACCACCTTAAACCTGTCATTCGAGCT 1604  
Qy 481 IleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThrLeuArgProTyr 500  
Db 1605 ATCAGAATTATGAATTTTCATGTTGCAAAACGGAAGTTTAAAGGAACATTAAGTCCATAT 1664  
Qy 501 AspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMetLeuCysArgIle 520  
Db 1665 GATGTAAAGATGATGATGAACAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1724  
Qy 521 LysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLys 540  
Db 1725 AAAAGCCTTCAACACAGGTTGATCAATTTCTGGAAAAGGCAAAATCACATCAGATAAG 1784  
Qy 541 LysSerArgGluLysIleThrAlaGluHisGluThrThrAspAspLeuSerMetLeuGly 560  
Db 1785 AAGAGCCGAGAGAAAATAACAGCAGAAACATGAGACCACAGACGATCTCAGTATCTCGGT 1844  
Qy 561 ArgValValLysValGluLysGlnValGlnSerIleGluSerLysLeuAspCysLeuLeu 580  
Db 1845 CGGTGGTCAAGGTTGAAAACAGTACAGTCCATAGATNATCAAGCTGGAGTGGCTACTA 1904  
Qy 581 AspletyrGlnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPhe 600  
Db 1905 GACATCTATCAACAGGCTCTTCGGAAGAGCTCTGCCTCAGCCCTCGCTTTCGCTTCATTC 1964  
Qy 601 GlnIleProProPheGluCysGluGlnThrSerAspTyrGlnSerProValAspSerLys 620  
Db 1965 CAGATCCCAACCTTTGAAATGTGAACAGACATCTGACTATCAAAAGCCCTGTGGATAGCAA 2024  
Qy 621 AspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIle 640  
Db 2025 GATCTTCGGGTTCCGCAAAACAGTGGCTGCTTATCCAGATCAACTAGTGCACACATC 2084  
Qy 641 SerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAla 660  
Db 2085 TCGAGAGCCCTGCAGTTCATTCAGGCCAAATGAGTTTCAGTGCCACGACATTTCTACGCG 2144  
Qy 661 LeuSerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySer 680  
Db 2145 CTTAGCCCTTACTATGCACAGTCAAGCAACAGAGTGCCTCAATTAGTCAAAAGCGATGGCTCA 2204  
Qy 681 AlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAla 700  
Db 2205 CGAGTGGAGCCACCAACACCATTCGAAACCAATAATATAGGCNCCCAAGCCAGCAGCC 2264  
Qy 701 ProThrThrLeuGlnIleProProLeuProAlaIleLysHisLeuProArgProGlu 720  
Db 2265 CCAACAACTTTACAGATCCACCTCTCTCCAGCCATCAAGCATCTGCCAGGCCAGAA 2324  
Qy 721 ThrLeuHisProAsnProAlaGlyLeuGlnGluSerIleSerAspValThrCysLeu 740  
Db 2325 ACTCTGCACCCCTAACCCCTGCAGGCTTACAGGAAGCATTTCTGACGTCAACACCTGCCTT 2384

Qy 741 ValAlaSerLysGluAsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMet 760  
Db 2385 GTTGCCTTCCAAGGAAATGTTAGTTTGCACAGTCAAACTCTCACCAGGACCGTTCTATG 2444  
Qy 761 ArgLysSerPheAspMetGlyGlyGluThrLeuLeuSerValCysProMetValProLys 780  
Db 2445 AGGAAAGCTTTGACATGGGAGGAGAACTCTGTTGTTCTGCTGCTCCCATGGTCCGGAAG 2504  
Qy 781 AspleuGlyLysSerLeuSerValGlnAsnLeuIleArgSerThrGluGluLeuAsnIle 800  
Db 2505 GACTTGGGCAAACTTTGTTCTGTGCAAAACCTGATCAGGTGCGACCGAGGAACCTGAATATA 2564  
Qy 801 GlnLeuSerGlySerGluSerSerGlySerArgGlySerGlnAspPheTyrProLysTyr 820  
Db 2565 CAACCTTCAGGAGTGAGTCAAGTGGCTCCAGAGGCAGCAAGATTTTATCCCAATGG 2624  
Qy 821 ArgGluSerLysLeuPheIleThrAspGluGluValGlyProGluGluThrGluThrAsp 840  
Db 2625 AGGGAATCCAAATTTGTTTATACTGATGAAGAGTGGGTCCCGAAGAGACAGACAGAC 2684  
Qy 841 ThrPheAspAlaAlaProGlnProAlaArgGluAlaAlaPheAlaSerAspSerLeuArg 860  
Db 2685 ACTTTGATCCGACCGCAGCTGCCAGGAAGCTGCCCTTTCGATCAGACTCTCTAAGG 2744  
Qy 861 ThrGlyArgSerArgSerSerGlnSerIleCysLysAlaGlyGluSerThrAspAlaLeu 880  
Db 2745 ACTGGAAGTTCAGCATCATCTCAGAGCATTTGTAAGCGAGGAGAAAGTACAGATGCCCTC 2804  
Qy 881 SerLeuProHisValLysLeuLys 888  
Db 2805 AGCTTGCTCATGTCAAACTGAAA 2828

RESULT 3  
US-09-590-304-1  
; Sequence 1, Application US/09590304  
; Patent No. 6649371  
; GENERAL INFORMATION:  
; APPLICANT: JENTISCH, Thomas  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNELS  
; FILE REFERENCE: 2815-0136P  
; CURRENT APPLICATION NUMBER: US/09/590,304  
; CURRENT FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 3137  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(2691)  
US-09-590-304-1

Alignment Scores:  
Pred. No.: 0 Length: 3137  
Score: 4527.50 Matches: 887  
Percent Similarity: 99.00% Conservative: 1  
Best Local Similarity: 98.89% Mismatches: 0  
Query Match: 99.57% Indels: 9  
DB: 4 Gaps: 1

US-09-810-796-5 (1-888) x US-09-590-304-1 (1-3137)

Qy 1 MetLysAspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaArgGly 20  
Db 1 ATGAAGGATGTGGAGTCGGGCCGGGAGGAGTGTCTGTAACCTCGGACCGCCAGGCGC 60  
Qy 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40  
Db 61 GACGCGCTGTCTGCTGGGACCCCGCGGCCACGCTCGGTGGCGGCGGCGGTGGCTG 120  
Qy 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60

Db ||||| AGGAGAGCCCGGGGCAAGCAGGGGGCCCGGATGAGCCTGCTGGGAAGCCGCTCTCT 180  
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Qy LeuValPheGlyCysLeuIleuSerValPheSerThrIleProGluHisThrIysLeu 120  
Db CTGTCCTTGGTGTCTGATTTGTGAGTGTTCATCCATCCCTGAGCACACAAAATG 360  
Qy AlaSerSerCysLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe 140  
Db GCCTCAAGTGCCTTCGATCCTGGAGTTCGTGATGATGTCGTCCTTGGTGGAGTTC 420  
Qy IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160  
Db ATCATTCGAATCTGGTCTGCGGGTTCGTTGTCGATATAGAGGATGCAAGGAAGACTG 480  
Qy ArgPheAlaArgIysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180  
Db AGGTTTGTCTGAAAGCCCTTCGTGTTATAGATACCATTTGTTTCCTTCGCTTCATAGCA 540  
Qy ValValSerAlaIysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200  
Db GTTGTTCCTGCANAACTCAGGTAATATTTTGCACGCTCGCACTCAGAACTCCGT 600  
Qy PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpIysLeuLeu 220  
Db TTCTTACAGATCCTCCGATGTCGCGCATGACCGAGGGGAGGCACCTTGAAATTTACTG 660  
Qy GlySerValValTyrAlaHisSerIysGluIleuIleThrAlaTrpTyrIleGlyPheLeu 240  
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Qy ValLeuIlePheSerSerPheLeuValTyrLeuValGluIysAspAlaAsnLysGluPhe 260  
Db GTTCTTATTTTTCGCTCTTCCTGCTCTCTGTTGGTGAAGAGGATCCATAAAGAGTTT 780  
Qy SerThrTyrAlaAspAlaLeuTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280  
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Qy AspIysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300  
Db GACAAAACCTCCCTTAACCTTGGCTGGGAAGATTTGCTTCTGCAGGCTTTGCACTCTCTGGC 900  
Qy IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320  
Db ATTTCCTTCTTTCGATCTCTGCGGCATCTTGGCTCAGGTTTGGCATTAAGTAGTACA 960  
Qy GluGlnHisArgGlnLysPheGluIysPheArgArgAsnProAlaAlaAsnLeuIleGln 340  
Db GAACAACACCGCAGAAAACATTTGAGAAAAGAGAAACCCAGCTGCGCAACTCATTCAG 1020  
Qy CysValTrpArgSerTyrAlaAlaAspGluIysSerValSerIleAlaThrTrpIysPro 360  
Db TGTGTTTGGCGTAGTTCGACAGCTGATGAGAAATCTGTTTCATTTGCAACCTGGAAGCCA 1080  
Qy HisLeuIysAlaLeuHisThrCysSerProThr----- 371  
Db CACTTGAAGGCTTGCACACCTGACGCTTACCAGAAAGAACAGGGAAGCATCAAGC 1140  
Qy AsnGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyClnSerIle 391  
Db AGTCAGAAGCTAAAGTTTTAAAGGAGGAGTGGCGATGGCTAGCCCCAGGGGCGAGAGTATT 1200  
Qy LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 411

Db 1201 AAGAGCCGACAGAGCCTCAGTAGGTGACAGGAGGTCCCCCAAGCAGCATCACAGCCGAG 1260  
Qy GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 431  
Db GGCAAGTCCCAACCAAGTGCAGAGAGCTGGAGCTTCAACGACCGAACCGCTTCGGGCC 1320  
Qy SerLeuArgLeuLysSerSerGlnProIysProValIleAspAlaAspThrAlaLeuGly 451  
Db TCGCTGGCGCTCAAAAGTCTTCAGCCAAACCAAGTGTAGATGTATCAGTGGAGAGCTCACC 1380  
Qy ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 471  
Db ACTGATGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440  
Qy ProProLeuIysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 491  
Db CCACCCTTAAACCTGTCATTTCGAGCTATCAGAAATTTATGAAATTTTCATGTTGCAAAACGG 1500  
Qy LysPheLysGluThrLeuArgProTyrAspValIysAspValIleGluGlnTyrSerAla 511  
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Qy GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 531  
Db GGTCAATCTGGACATGTTGTGTAGATTTAAAGCCCTTCAACACGCTGTGTGATCAAAATCTT 1620  
Qy GlyLysGlyGlnIleThrSerAspLysSerArgGluLysIleThrAlaGluHisGlu 551  
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Qy ThrThrAspAspLeuSerMetLeuGlyArgValLysValLysValGluLysGlnValGlnSer 571  
Db ACCACAGACGATCTCAGTATGCTCGGTGGGTGCTCAAGGTTGAAAAACAGGTACAGTCC 1740  
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Qy AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 611  
Db GCCTCAGCCCTCGCTTTGGCTTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT 1860  
Qy AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631  
Db GACTATCAAGCCCTGCTGGATAGCAAGATCTTTCCGGTTCCTCCGACAAAACAGTGGCTGC 1920  
Qy LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651  
Db TTATCCAGATCAACTAGTGCCACATCTCGAGAGGCTGCGAGTTCATTTCTGACGCCAAT 1980  
Qy GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671  
Db GAGTTTCAAGTCCGACAGCTTTCTACGCGCTTAGCCCTACTATGCAAGTCAAGCAACACAG 2040  
Qy ValProIleSerGlnSerAspGlySerAlaValAlaThrAsnThrIleAlaAsnGln 691  
Db GTGCAATATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTTGCAAAACCAA 2100  
Qy IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro 711  
Db ATAAATACGGCACCCAGCCAGCCAGCCCAACCACTTTACAGATCCCACTCTCTCTCCA 2160  
Qy AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 731  
Db GCCATCAAGCATCTGCCAGCCAGAAACTCTGCACCTTAACCTGCGAGGCTTACAGGAA 2220  
Qy SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 751  
Db AGCATTTCTGACGTCAACCATCTGCTTGTTCCTCCCAAGGAAAAATGTTCAAGTTGCAAG 2280  
Qy SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 771  
Db TCAATCTCACAAGGACCGTTCTATGAGGAAAAAGCTTTGATGGGAGGAGAAACTCTG 2340

QY 772 LeuSerValCysProMetValProlyAspLeuGlyLysSerLeuSerValGlnAsnLeu 791  
Db 2341 TTGTCTCTCTCCATGTCGCGGACCTTGGCAAACTCTTGTCTGTGCAAACTCTG 2400  
QY 792 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGlySerGlySerArg 811  
Db 2401 ATCAGTCCGACCGAGGAACCTGAATATACAACTTTTTCAGGAGTGAAGTCAAGTGGCTCCAGA 2460  
QY 812 GlySerGlnAspPheTyrProIysThrArgGluSerLysLeuPheIleThrAspGluGlu 831  
Db 2461 GCGACCCCAAGATTTTACCCCAATGGAGGAATCCAAATTTGTTTATAACTGATGAAGAG 2520  
QY 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 851  
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QY 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerGlnSerIleCys 871  
Db 2581 GCTGCTTTTGCAATCAGACTCTTAAGGACTGGAAGGTCAAGATCATCTCAGAGCATTTGT 2640  
QY 872 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 888  
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RESULT 4  
US-09-813-148-1  
; Sequence 1, Application US/09813148  
; Patent No. 6617131  
; GENERAL INFORMATION:  
; APPLICANT: STEINMEYER, Klaus  
; APPLICANT: LERCHE, Christian  
; APPLICANT: SCHERER, Constanze  
; APPLICANT: SEBOHM, Guiscard  
; APPLICANT: BUSCH, Andreas E.  
; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CEN  
; TITLE OF INVENTION: NERVOUS SYSTEM AND CARDIOVASCULAR SYSTEM  
; FILE REFERENCE: 38005-119  
; CURRENT APPLICATION NUMBER: US/09/813,148  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: DE 100 13 732.6  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: US 60/194,041  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 3074  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-813-148-1  
Alignment Scores:  
Pred. No.: 0 Length: 3074  
Score: 4513.50 Matches: 885  
Percent Similarity: 98.77% Conservative: 1  
Best Local Similarity: 98.66% Mismatches: 2  
Query Match: 99.26% Indels: 9  
DB: 4 Gaps: 1  
US-09-810-796-5 (1-888) x US-09-813-148-1 (1-3074)  
QY 1 MetLysAspValGluSerGlyArgValLeuLeuAsnSerAlaAlaAlaArgGly 20  
Db 215 ATGAAGGATGTGAGTTCGGCGCGGACAGGTGCTGCTGAACTCGCGACCGCGCGGCG 274  
QY 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40  
Db 275 GACGCGCTGCTACTGCTGGGACCCCGCGCGGACGCTTGTGTGGCGCGCGGCGGCTG 334  
QY 41 ArgGluSerArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60  
Db 335 AGGAGAGCCCGCGCGGCGGACGAGGCGGCGGCGGATGAGCTGCTGGGAGCGCGCTCTCT 394

QY 61 TyrThrSerSerGlnSerCysArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80  
Db 395 TACACGAGTAGCCAGAGTCCCGCGCAACGTCAGGTACCGCGGGTGCAGAACTACTCTG 454  
QY 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100  
Db 455 TACAACGTGCTGGAGAGACCCCGCGGTGGCGTTCATCTACCACTCTTGGTTTTCCTC 514  
QY 101 LeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120  
Db 515 CTGTCTTTTGGTTCCTTGATTTTGTCTAGTGTCTTCTACCACTCTCTGAGCAGACAAAATTG 574  
QY 121 AlaSerSerCysLeuLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe 140  
Db 575 GCCTCAAGTTTGCCTCTTGTATCTCTGGAGTTCGTGATGATTCTCTCTTGGTTTGGAGTTC 634  
QY 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160  
Db 635 ATCATTCGAATCTGGTCTCGGGTGTCTGTGTATAGATACCACTTGTCTTATCGCTTCAATAGCA 694  
QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180  
Db 695 AGTTTCTCGAAAGCCCTTCTGTGTATAGATACCACTTGTCTTATCGCTTCAATAGCA 754  
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QY 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240  
Db 875 GGTTCAGTGTGTATGTCACGACAGGAATTAATACAGCTTGTATACATAGGATTTTG 934  
QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260  
Db 935 GTTCTTATTTTCTCTTCTCTCTCTGTTGTAAGGATGCGCAATAAAGAGTTT 994  
QY 261 SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleLeuThrThrIleGlyTyrGly 280  
Db 995 TCTACATATGAGATGCTCTCTGTGGGGCAATTAATACATTTGCACTATTTGGCTATGGA 1054  
QY 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300  
Db 1055 GACAAAACCTCCCTAACTTGGCTGGGAAGATTGCTTCTGCAGGCTTTTGCACCTCTTGGC 1114  
QY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320  
Db 1115 ATTTCTTTTCTTGCATCTCTCTCGCGCATCTTGGCTCAGGTTTGTGATTAAGAGTACAA 1174  
QY 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340  
Db 1175 GAACAACACCGCCAGAAACACTTTGAGAAAAGAAAGAACCCAGCTGCAACTCATTTGAG 1234  
QY 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360  
Db 1235 TGTGTTTGGCGTAGTACGCGAGCTGATGAGAAATCTGTGTTCCATTGCAACCTGGAAGCCA 1294  
QY 361 HisLeuLysAlaLeuHisThrCysSerProThr----- 371  
Db 1295 CACTTGAAGGCTTTGCAACCTCGAGCCCTACCAAGAAAAGAACAAAGGGAAGCATCAAGC 1354  
QY 372 AsnGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 391  
Db 1355 AGTCAAGAGCTPAAGTTTTTAGAGACGAGTGGCGCATGGCTAGCCCCAGGGCCAGATATT 1414  
QY 392 LysSerArgGlnAlaSerValGlyAspArgSerProSerThrAspIleThrAlaGlu 411  
Db 1415 AAGAGCCGACAAAGCTCAGTAGGTGACAGGAGGTCCCCAAGACCCGACATCACAGCCGAG 1474



Qy 412 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 431  
Db 1475 GCGAGTCCCAAGAGTGGAGCTTCAACGACCGGACCGCTTCGGGCC 1534  
Qy 432 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 451  
Db 1535 TCGTGGCCCTCAAAAGTTCTCAGCCAAACAGGATGATGCTGCACACAGCCCTTGGC 1594  
Qy 452 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 471  
Db 1595 ACTGATGATGATATGATGATAAAGAGTGCAGTGTGATGATCATCAGTGAAGACCTCACC 1654  
Qy 472 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 491  
Db 1655 CCACCACATTAACACTGTCAATCGAGCTATCAGAAATTTATGAAATTTTCATGTTGCAAAACGG 1714  
Qy 492 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 511  
Db 1715 AAGTTTAAGGAACATTAAGTCCATATGATGTAAAGATGTCAATGAACATATCTGCT 1774  
Qy 512 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 531  
Db 1775 GGTCACTGGACATGTTGTGTAGATTAAGAGCTTCAACACAGGTGTGATCAAAATTCCT 1834  
Qy 532 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 551  
Db 1835 GGAAGAGGCAAAATCACATCAATGAAGAGCGGAGAGAAATTAACAGCAGAACATGAG 1894  
Qy 552 ThrThrAspAspLeuSerMetLeuGluValArgValLysValGluLysGlnValGlnSer 571  
Db 1895 ACCACAGACGATCTCAGTATGCTCGGTGGTGAAGTTTGAAGAACAGGTACAGTCC 1954  
Qy 572 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 591  
Db 1955 ATAGAATCCAAGCTGACTGCTACTACATCATCAACAGGTCTTCGGAAGGCTCT 2014  
Qy 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 611  
Db 2015 GCCTCAGCCCTCGCTTGGCTTCATTCAGATCCACACCTTTTGAATGTGAACAGACATCT 2074  
Qy 612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631  
Db 2075 GACTATCAAGCCCTGTGGATAGAAAGATCTTCGGGTTCGACACAAAACAGTGGCTGC 2134  
Qy 632 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651  
Db 2135 TTATCCAGATCAACTAGTGCACACATCTCGAGAGGCTGCAGTTCATTCAGCGCAAT 2194  
Qy 652 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671  
Db 2195 GAGTTTCAGTGGCCAGACTTCTACGCGCTTACGCTTACTATGCACAGTCAAGCAACACAG 2254  
Qy 672 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 691  
Db 2255 GTGCCAATTAGTCAAGCGATGGCTCAGAGTGGCAGCCACCAACCATTTGCAAAACCA 2314  
Qy 692 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro 711  
Db 2315 ATAATACGGCACCCCAAGCCAGCAGCCCAACAATTTACAGATCCCACTCTCTCCA 2374  
Qy 712 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 731  
Db 2375 GCCATCAAGCATCTGCCAGGCCAGAAACTCTGCACCCCTTAACCTTCAGGCTTACAGAA 2434  
Qy 732 SerIleSerAspValThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 751  
Db 2435 AGCATTTCTGACGTCAACCTGCTGTGTGCTCCCAAGGAAATGTTCAGGTTCACAG 2494  
Qy 752 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 771  
Db 2495 TCAATCTCAACAGACCGTCTCATGAGAAAGCTTTGACATGGGAGGAGAACTCTG 2554  
Qy 772 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 791

Db 2555 TTGCTGCTGCTCCATGGTCCGAGGACTTTGGCAAAATCTTTGCTGTGCAAAACCTG 2614  
Qy 792 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGlySerSerGlySerArg 811  
Db 2615 ATCAGGTCCGACCGAGGAACCTGAATATACAACCTTTCCAGGAGGTGAGTCAAGTGGCTCCAGA 2674  
Qy 812 GlySerGlnAspPheTyrProLysTyrArgGluSerLysLeuPheIleThrAspGluGlu 831  
Db 2675 GGCAGCCCAAGATTTTACCCCAATGGAGGAATCCAAATTTGTTTATAACTCATGAAGAG 2734  
Qy 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 851  
Db 2735 GTGGTCCCGAAGACACAGACAGACACTTTTGTATGCCGACCCGACCTTGCAGGAA 2794  
Qy 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 871  
Db 2795 GCTGCTTTGATCATCAGACTCTCTAAGGACTCGAAGGTCAAGTCAATCATCTCAGAGCATTTGT 2854  
Qy 872 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 888  
Db 2855 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAA 2905

RESULT 5  
US-09-492-361-1  
; Sequence 1, Application US/09492361  
; Patent No. 6794161  
; GENERAL INFORMATION:  
; APPLICANT: JENTSCH, Thomas J.  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE  
; TITLE OF INVENTION: POTASSIUM CHANNELS  
; FILE REFERENCE: 2815-127P  
; CURRENT APPLICATION NUMBER: US/09/492.361  
; CURRENT FILING DATE: 2000-01-27  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 2335  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (1)..(2335)  
; NAME/KEY: CDS  
; LOCATION: (83)..(2170)  
US-09-492-361-1

Alignment Scores:  
Pred. No.: 5,98e-203 Length: 2335  
Score: 2007.50 Matches: 434  
Percent Similarity: 65.32% Conservative: 82  
Best Local Similarity: 54.94% Mismatches: 133  
Query Match: 44.15% Indels: 141  
DB: 4 Gaps: 16

US-09-810-796-5 (1-888) x US-09-492-361-1 (1-2335)  
Qy 8 ArgGlyArgValLeuLeuAsnSerAlaAlaAlaArgGlyAspGlyLeuLeuLeuGly 27  
Db 127 CGGGAGCGCCCGCGGGAGCTAGTGGCGCTCAGGC----- 165  
Qy 28 ThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyGlyLeuArgGluSerArgArgGlyLys 47  
Db 166 ---CGTCAGAGCGAAACAGGGCGAGCGG-----CGGGGGCGG 201  
Qy 48 GlnGlyAla-ArgMetSerLeuLeuGlyLysProLeu----- 59  
Db 202 CTCCCGCGCGCGCTCGGCTCTCGGCGAGCCCTTCGCCCGCGGCGCGCCCTCCCTCG 261  
Qy 60 -----SerTyrThrSerSerGlnSerCysArgArgAsnValLys 73  
Db 262 GCCGGGCTCCGGCTCGGGCTCCGGCTCGGGCGAGCGCTCTCTCGCGCGCGCACAGCGCTA 321

Qy 73 rArgValGlnAsnTyrLeuTyrAsnValLeuGluArgProArgGlyTyrAlaPheI1 93  
Db 322 CGCGCGCTGCAGAACTGGGTCTACAACGTCGTGGAGCGGCCCGCGCTGGCTTGT 381  
Qy 93 eTyHisAlaPheValPheLeuValPheGlyCysLeuLeuLeuSerValPheSerTh 113  
Db 382 CTACCACGCTCTCATATTTTGTGGTCTTCAGCTGCGCTGGTGTCTGTGTCTGCAC 441  
Qy 113 rIleProGluHisThrLysLeuAlaSerSerCysLeuLeuLeuLeuLeuPheValMetI1 133  
Db 442 TATCAGAGGACACGAGAACTTGCACAGAGTGTCTCTCATCTTGGAAATTCGTGATGAT 501  
Qy 133 eValValPheGlyLeuGluPheIleAArgIleTyrPheAlaGlyCysCysArgTy 153  
Db 502 CGTGGTTTCGGCTTGGAGTACATCGTCCGGGTCTGGTCCCGGATGCTGCTGCCGCTA 561  
Qy 153 rArgGlyTyrGlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAaspThrI1 173  
Db 562 CCGAGGATGGCAGGGTCTCTCCGCTTGGCCAGAAAGCCCTTCTGTGTCTATCGACTTCAT 621  
Qy 173 eValLeuIleAlaSerIleAlaValValSerAlaLysThrGlnGlyAsnIlePheAlaTh 193  
Db 622 CGTGTTCGGCTCGGTGGCGCTCATCGCGCGGTACCCAGGGCAACATCTTCGCCAC 681  
Qy 193 rSerAlaLeuArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgAr 213  
Db 682 GTCCGCGCTGCAGCATGCGCTTCTGCAGATCTGCGCATGCTGGTGGCAGTGGACCGCG 741  
Qy 213 gGlyGlyThrTrpLysLeuLeuGlySerValValTyrAlaHisSerLysGluLeuIleTh 233  
Db 742 CGCGCGCACCTTGGAGCTGTGGGCTCAGTGGTCTACCGCATGACAAAGAGCTGATCAC 801  
Qy 233 rAlaTrpTyrIleGlyPheLeuValIlePheSerSerPheLeuValTyrLeuValG1 253  
Db 802 CGCTGTGTACATCGGTTCCTGGTCTCATCTTCGCTCTCTTCTGTCTACCTTGGCGCA 861  
Qy 253 uLysAspAlaAsnLysGluPheSerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleTh 273  
Db 862 GAAGGACGCCAACTCCGACTTCTCTCTACCGCGACTCGCTCTGGTGGGGGACGATTAC 921  
Qy 273 rLeuThrThrIleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSe 293  
Db 922 ATTGAACACCATCGCTATGTGTGACAAACACCGCACATGGCTGGCGAGGGTCTTGGC 981  
Qy 293 rAlaGlyPheAlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySe 313  
Db 982 TGCTGGCTTCGCTTACTGGGCACTCTCTTTCTTGGCTGTGCTGCGGCATCTTAGGCTC 1041  
Qy 313 rGlyPheAlaLeuLysValGlnGlnHisArgGlnLysHisPheGluLysArgArgAs 333  
Db 1042 CGGCTTTGCCCTGAAGGTCAGGAGCAGCACCGGCAGAAAGCACATTCGAGAAAGCGAGGAT 1101  
Qy 333 nProAlaAlaAsnLeuIleGlnCysValTyrArgSerTyrAlaAlaAsp---GluLysSe 352  
Db 1102 GCCGGCACCAACCTCATCCAGGTCGCTGGCGCTGTACTCCACCGATATGACCCGGGC 1161  
Qy 352 rValSerIleAlaThrTrp----- 358  
Db 1162 CTACTGACGCCACCTGGTACTACTATGACAGTATCTCCCATCTTCAGAGAGCTGGC 1221  
Qy 358 ----- 358  
Db 1222 CCTCTTTTGAGCAGCTGCAACGGGCCCAATGGGGGCTTACGGCCCTTCGAGGTGCG 1281  
Qy 359 -----LysProHisLeuLysAlaLeuHisTh 367  
Db 1282 CGGGCGCGGTACCCGAGGAGCACCTCCGCTTACCCCGCTGTGCCACTGCTGCCACCG 1341  
Qy 367 r-----CysSerProThrAsnGlnLysSerPheLysGluArgVa 381  
Db 1342 GCCGGCAGCACCTCTCTTCGCTGGGGAAGCAGCGGATGGGCATCAAGACCGCAT 1401  
Qy 381 lArgMetAlaSerProArgGlyGlnSerIleLysSerArgGln-----AlaSerValG1 399

Db 1402 CCGCATGGCAGCTCCAGCGCGCGAGGGGCTTCTCAAGCAGCAGCTGGCAGCTCCAAC 1461  
Qy 399 yAspArgSerProSerThrAspIleThrAlaGluGly---SerProThrLysValG1 418  
Db 1462 AATCCCCACCTCCCAAGCAGCAGAGGTGGGTGGAGGCCACCAAGGAGGTGCA 1521  
Qy 418 nLysSerTrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerSe 438  
Db 1522 AAAGAGCTGGAGCTTCAATGACCGCACCGCTTCGGGGCATCTCTGAGACTC----- 1573  
Qy 438 rGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyrAspG1 458  
Db 1574 -----AAACCCCGCACCTCTGCTGAGGATGCC---CCCTCAGAGGAAGTAGCAGAGGA 1623  
Qy 458 uLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuLysThrValI1 478  
Db 1624 GAAGAGCTACCAAGTGTGAGCTCACGGTGGAGCATCATGCTCTGTGAAGACAGTAT 1683  
Qy 478 eArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThrLeuAr 498  
Db 1684 CCGCTCCATCAGGATTCCTCAAGTTCCTGGTGGCCAAAGGAATTCAGAGGACACTGCG 1743  
Qy 498 gProTyrAspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMetLeuCy 518  
Db 1744 ACCGTACGAGCTGAAGACGCTCATTGAGCAGTACTCAGCAGGCCACCTGGACATGCTGG 1803  
Qy 518 sArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSe 538  
Db 1804 CCGGATCAAGAGCTGCAAACTCGGGTGGACCAAAATTTGGGTGCGGGG-----CCCGG 1857  
Qy 538 rAspLysLysSerArgGlu-----LysIleThrAlaGluHisGluThrThrAspAs 555  
Db 1858 GGACAGAGAGCCCGGAGAGGCGCGACAGGGGCCCTCCGACCGGAGGTGGTGATGA 1917  
Qy 555 pLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSerIleGluSerLy 575  
Db 1918 AATCAGCATGATGGACCGCTGGTCAAGGTGGAGAGCGGTGCGTGCATCGAGCACA 1977  
Qy 575 sLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySerAlaLe 595  
Db 1978 GCTGGACCTGTGTGGGCTTCTATCGCGTGTGCTGCTGCGACCTCGGCC----- 2032  
Qy 595 uAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSerAspTyrGlnSe 615  
Db 2033 -AGCTTGGCGCGCTGCAAGTGGCTGTTCCGCCCGACATCATCTCCGACTACCACAG 2091  
Qy 615 rProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSe 635  
Db 2092 CCCTGTGGACCAAGGACATCTCCGCTCCGCAAGACGCTCAGC---ATCTCCCGCTC 2148  
Qy 635 rThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAl 655  
Db 2149 GGTCAAGCACCAATGACTGAGGG----- 2173  
Qy 655 aGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGlnValProIleSe 675  
Db 2174 -----ACTTC 2178  
Qy 675 rGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAl 695  
Db 2179 TCAGAGCAGCGGCAGACA-----CGCCACG 2205  
Qy 695 aProLysProAlaAlaProThrThrLeu-GlnIleProProProLeuProAlaIleLysH 715  
Db 2206 CCGCGCGCTGGCGCTCGACTGCCCTCTGAGGCGCTCGGACTCTCTCTGACTTGA 2265  
Qy 715 isLeuProArgProGluThrLeuHis 723  
Db 2266 CACTCCCTCACGGGAGAGAGACCAC 2291  
RESULT 6  
US-09-949-016-1823

; Sequence 1823, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIORITY FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1823  
; LENGTH: 2196  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-1823

Alignment Scores:  
Pred. No.: 4,86e-202 Length: 2196  
Score: 1998.50 Matches: 426  
Percent Similarity: 66.14% Conservative: 78  
Best Local Similarity: 55.91% Mismatches: 124  
Query Match: 43.95% Indels: 134  
Gaps: 4

US-09-810-796-5 (1-888) x US-09-949-016-1823 (1-2196)

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Qy 35 GlyGlyGlyGlyGlyLeuArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeu 54
Db 52 GCGGGGGGCGCTCCCGCGC-----CGCTCGGCGTC 84

Qy 55 LeuGlyLysProLeu-----Ser 60
Db 85 CTGGGCGACCCCTCGCGCGCGCGCGCTCCCTCGCGCGCGCTCGGCTCGGCGTCC 144

Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgValGlnAsnTyrLeu 80
Db 145 GCCTCGCGCGCGCGCTCCCTCGCGCGCGCGCGCTCCCTCGCGCGCGCTCGGCGTCC 204

Qy 81 TyrAsnValLeuGluArgProArgGlyTyrAlaPheLeuTyrHisAlaPheValPheLeu 100
Db 205 TACAACTGCTGGAGCGCGCGCGCGCTGGCGCTCGCTACCACTTCATATTTTG 264

Qy 101 LeuValPheGlyCysLeuLeuSerValPheSerThrLeuProGluHisThrLysLeu 120
Db 265 CTGGTCTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 324

Qy 121 AlaSerSerCysLeuLeuLeuGluPheValMetLeuValPheGlyLeuGluPhe 140
Db 325 GCCAACAGTGTCTCTCTCATCTTGAATTCGTGATGATCGTGGTTTCGGCTCGAGTAC 384

Qy 141 IleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu 160
Db 385 ATCGTCGGGTCTGGTCCGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 444

Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db 445 CGCTTTGCCAAGACCCCTCTGTGTATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 504

Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db 505 GTCATCGCGCGGTGATCCACGGGCAACATCTTCGCCACGCTCGCGCTCGCGCATGCGC 564

Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTyrLysLeuLeu 220
Db 565 TTCTTCGAGATCTTCGCGATGGTGGCGATGGACCGCGCGCGCGCGCGCGCGCGCGCGCTG 624
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Qy 221 GlySerValValTyrAlaHisSerLysGluLeuLeuThrAlaTyrTyrIleGlyPheLeu 240
Db 625 GGCTCAGTGTCTACGCGCATAGCAAGAGCTGATCACCGCTCGGTATACATCGGGTCTCTG 684

Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db 685 GTGCTCATCTTCGCTCTCTCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 744

Qy 261 SerThrTyrAlaAspAlaLeuTyrTyrGlyThrIleThrLeuThrThrIleGlyTyrGly 280
Db 745 TCCTCTCTACGCGCATCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 804

Qy 281 AspLysThrProLeuThrTyrLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db 805 GACAAGACACCGCACATCGCTGCGGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 864

Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db 865 ATCTCTTTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 924

Qy 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
Db 925 GAGCAGCACCGCGAAGCACTTCGAGAAGCGGAGGATGCGCGCAGCACTCATCCAG 984

Qy 341 CysValTyrArgSerTyrAlaAlaAsp---GluLysSerValSerIleAlaThrTyr--- 358
Db 985 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1044

Qy 358 ----- 358
Db 1045 TACTATCAGATATCTCCATCTCTTCAGAGAGTGGCCCTCTTGTGTGACGACGTGCAA 1104

Qy 358 ----- 358
Db 1105 CGGSCCGCAATGGGGCGCTAGCGCCCTCGAGGTGGGGCGCGCGGTACCCGACGGA 1164

Qy 359 -----LysProHisLeuLysAlaLeuHisThr-----Cys 368
Db 1165 GCACCTCTCCGTTACCCGCGCTGTCACCTCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1224

Qy 369 SerProThrAsnGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGly 388
Db 1225 CTGGGGAAGACCGCGATGGGATCAAGACCGCATCGCATCGCATGGGCGAGTCCGAGCGG 1284

Qy 389 GlnSerIleLysSerArgGln-----AlaSerValGlyAspArgArgSerProSerThr 406
Db 1285 CGGACGGGTCTCTTCAAGCAGCATCTGCACCTCCCAACATGCCACCTCCCAAGCAGC 1344

Qy 407 AspIleThrAlaGluGly---SerProThrLysValGlnLysSerTyrSerPheAsnAsp 425
Db 1345 GAGCAGGTGGGTGAGGCGCACCGCCCAAGGTGCAAAAGAGCTGAGAGCTTCAATGAC 1404

Qy 426 ArgThrArgPheArgProSerLeuArgLysSerSerGlnProLysProValIleAsp 445
Db 1405 CGCACCGCTTCCGGGATCTCTGAGACTC-----AAACCCCGGACCTCT 1449

Qy 446 AlaAspThrAlaLeuGlyThrAspAspValTyrAspGluLysGlyCysGlnCysAspVal 465
Db 1450 GCTGAGGATGCC---CCCTCAGAGAAAGTACGACAGGAGAGAGTACCATGCTGAGCTC 1506

Qy 466 SerValGluAspLeuThrProLeuLysThrValIleArgAlaIleArgIleMetLys 485
Db 1507 ACGGTGACGACATCATGCTGCTGTGAAGACATCATCGCTCCATCCATCAGGATTTCTCA 1566

Qy 486 PheIleValAlaLysArgLysPheLysGluThrLeuArgProTyrAspValLysAspVal 505
Db 1567 TTCTGTGGCCAAAGAAATTCAGGACATCTGCGACCGCTGACGCTGAGGAGACGCTC 1626

Qy 506 IleGluGlnTyrSerAlaGlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThr 525
Db 1627 ATTGAGCAGTACTCAGCAGCGCCACCTGACATGCTGGCGCGATCAAGAGCTGCACACT 1686

Qy 526 ArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLysLysSerArgGlu--- 544
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Db 1139 GGCCTGATCAGTCGGCTGGAGATTCTACGCCACCAACCTCTCGGCACAGACTGCAC 1198  
Qy 350 -----GluysSerValSerIleAlaThrTrpLys----- 359  
Db 1199 TCCAGTGGCAGTACTACAGCGAAGCGTACCGTGGCCATGTTCGAAACTCAA 1258  
Qy 360 -----ProHisLeuLysAlaLeuHisThr----- 367  
Db 1259 ACCTACGGGGCTCCAGACTTATCCCGCTGAACACAGCTGGAGCTGCTGAGGAACCTC 1318  
Qy 367 ----- 367  
Db 1319 AAGAGTAAATCTGGACTCGCTTCAGGAAGGACCCCGCGGAGCCGCTCTCCAAGTAA 1378  
Qy 368 -----CysSerPro-----ThrAsnGlnLysLeu 375  
Db 1379 GGCAGCCCGTGCAGAGGCGCCCTGTGTGGATGCTGCCCGGAGCGCTCTAGCAGAGAAGTGC 1438  
Qy 376 SerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGln 395  
Db 1439 AGTTTGAAGATCGGTGTC---TTCACAGCCCGCGAGCGGTGCTGCCAAGGGGAAGGGG 1495  
Qy 396 AlaSerValGlyAsp-----ArgArgSerProSerThrAspIleThrAlaGluGlySer 413  
Db 1496 TCCCGCAGGCCAGACTGTGAGCGGTCAACCCAGCGCGGACAGAGCTCGAGGACAGC 1555  
Qy 414 ProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgProSerLeu 433  
Db 1556 CCCAGAGGTGCCCAAGAGCTGGAGCTTCGGGAGCCGACGCGGGCAGCCAGCGCTTTC 1615  
Qy 434 ArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAsp 453  
Db 1616 CGCATCAAGGTGGCGCGCTCAGCGGAGAACTCAGAA---GAAGCAAGCCTCCCGGAGAG 1672  
Qy 454 AspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThrProPro 473  
Db 1673 GACATTGGATGACAGAGCTGCCCTGCGAGTTGTGACCGAGGACCTGACCCCGGCG 1732  
Qy 474 LeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPhe 493  
Db 1733 CTCAAAGTCAGCATCAGAGCGGTGTGTGTCATGCGTTCTCTGGTGTCCAAGCGGAAGTTC 1792  
Qy 494 LysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAlaGlyHis 513  
Db 1793 AAGGAGACCCCTCGCGCCCTACAGCTGATGACGCTCATCGAGCATCTACGCGGCCAC 1852  
Qy 514 LeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLysGlyLys 533  
Db 1853 CTGGACATGCTGTCCCGAATTAAAGCTCTGAGTCCAGAGTGGACCATGTGTGGGGCGG 1912  
Qy 534 GlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGluThrThr 553  
Db 1913 GGCCAGCGATCAGCGAC---AAGGACCGCAACGAGGCGCCCGCGGCGGAGCTGCC 1969  
Qy 554 AspAspLeuSerMetLeuGlyArgValLysValLysValGluLysGlnValGlnSerIleGlu 573  
Db 1970 GAGGACCCCATGATGGAGCGGTCCGGAGGTGGAGAGCAGAGTCTTGTCCATGGAG 2029  
Qy 574 SerLysLeuAspCysLeuAspIleTyrGlnGlnValLeuArgLysGlySerAlaSer 593  
Db 2030 AAGAGCTGGACTTCTCGTGAATATCTACATGCG---CGATGGGC----- 2074  
Qy 594 AlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCys----- 607  
Db 2075 -----ATCCCCCGCAGACAGAGCGGCGCTACTTTGGGCGC 2110  
Qy 608 -----GluGlnThrSerAspTyrGlnSerProValAspSerLysAspLeuSerGly 624  
Db 2111 AAAGAGCGGAGCGCGCGCGGTACACAGCCCGGAAGACAGCGCGGAG----- 2161  
Qy 625 SerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIleSerArgGlyLeu 644  
Db 2162 CATGTGACAGGACGCGGTGATTTGCAAGATCGTGGCGCTCCAGCAGCTCCACGCGGC--- 2218

Qy 645 GlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAlaLeuSerProThr 664  
Db 2218 ----- 2218  
Qy 665 MethisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySerAlaValAlaAla 684  
Db 2218 ----- 2218  
Qy 685 ThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAlaProThrThrLeu 704  
Db 2219 -----CAGAAGAATCTTCTCGGCGCCCGCGCGCGCC---CCTGTC 2257  
Qy 705 GlnIleProPro-----ProLeuProAlaIleLysHis 715  
Db 2258 CAGTGTCCGCGCTCCACCTCTGCGCAGCCACAGAGCCACCGCGC---CCAGGCGCAGGCAC 2316  
Qy 716 LeuProArg-----ProGluThr-----LeuHis---ProAsnProAlaGlyLeuGlnI 731  
Db 2317 CTCCCCCGTGGGAGCACAGGCTCCTGTGGTGGCATCCCGCGCGCTGCCACGAGG 2376  
Qy 731 uSerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaG 751  
Db 2377 GTCGCTGTCCGCTACGCGGGGGCAACCGCGCCAGCATGAGTTCCTCGCGGACGAGGA 2436  
Qy 751 nSerAsnLeuThrLys-----AspArgSerMetArgLysSerPheAspMetGlyGly 769  
Db 2437 CACCCCGGCTGTCAGGCGCCCGCGGAGAACCTCGGGACAGC-----GA 2481  
Qy 769 uThrLeuLeuSerValCysProMetValProLysAspIleuGlyLysSerLeuSerVal 789  
Db 2482 CAGCTCCATCTCCATCCGCTCCGTCGAGCACCGAGGAGTGGAGCGTCTTTCAGCGGCTT 2541  
Qy 789 nAsnLeuIleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerG 809  
Db 2542 CAGCATCTCCAGTCCAGGAGAACCTGGATGCTCTCAACAGCTGCTACGCGCGCGTGGC 2601  
Qy 809 ySerArgGlySerGlnAspPheTyrProLysTyrArgGluSerLysLeuPheIleThrAs 829  
Db 2602 GCCTTGTGCCAAAGTCAGGCGCTACATTCGCGAGGAGAGTCCAGAC-----ACGA 2652  
Qy 829 pGluGluVal-----GlyPro-----GluGluThrG 838  
Db 2653 CTCCGACCTGTGTACCCGCTGCGGGCGCCCGCCACGCTCGGCCCGAGGGTCCCTT 2712  
Qy 838 uThrAspThrPheAspAlaAlaProGlnProAlaArgGluAlaAlaPheAlaSerAspSe 858  
Db 2713 TGGTGACGTGGCTGGCGCGCGCGCGGAGGAGTGGAGCGCGCTGGGC----- 2764  
Qy 858 rLeuArgThrGlyArgSerArgSerSerGlnSerIleCysLysAlaGly 874  
Db 2765 ----CAGTGGACCGCGCGCGCGCTCTCAGCAGCGTCCCTCGAGGT 2809

## RESULT 8

US-09-105-058C-19  
; Sequence 19, Application US/09105058C  
; Patent No. 6403360  
; GENERAL INFORMATION:  
; APPLICANT: Blonar, Michael A.  
; APPLICANT: Dworetzky, Steven  
; APPLICANT: Gribkoff, Valentin K.  
; APPLICANT: Levesque, Paul C.  
; APPLICANT: Little, Wayne A.  
; APPLICANT: Neubauer, Michael G.  
; APPLICANT: Yang, Wen-pin  
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME  
; FILE REFERENCE: 3053-4052  
; CURRENT APPLICATION NUMBER: US/09/105.058C  
; CURRENT FILING DATE: 1998-06-26  
; PRIOR APPLICATION NUMBER: US 60/055,599  
; PRIOR FILING DATE: 1997-08-12  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 19
; LENGTH: 3287
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-105-058C-19

Alignment Scores:
  Pred. No.:      9.4e-180      Length:      3287
  Score:         1792.50      Matches:      411
  Percent Similarity: 58.90%      Conservative: 102
  Best Local Similarity: 47.19%      Mismatches: 181
  Query Match: 39.42%      Indels: 178
  DB: 3      Gaps: 22

US-09-810-796-5 (1-888) x US-09-105-058C-19 (1-3287)

Qy 17 AlaAlaArgGlyAspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGly 36
Db 160 TCCACCCGGGAGCGGGCGCTGCTGATCGCCGGCTCCGAGGCGCCCAAG-----CGC 210
Qy 37 GlyGlyLeuLeuArgGlySerArgGlyLeuGlyLeuGlyLeuGlyLeuGlyLeuGly 56
Db 211 GGCAGCATCTCAGCAAACTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 255
Qy 57 LysProLeuSerTyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgVal 76
Db 256 AAGCCC-----CCCAAGCGCAACGCTTCTACCGCAAGCTG 291
Qy 77 GlnAsnTyrLeuTyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAla 96
Db 292 CAGAAATTCCTCTCAACAGCTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 351
Qy 97 PheValPheLeuLeuValPheGlyCysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 116
Db 352 TACGTGTTCCTCCCTGGTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 411
Qy 117 HisThrLysLeuAlaSerSerCysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuVal 136
Db 412 TATGAGAGAGCTCGGAGGGGGCGCTCTACATCTCTGGAATCGTGACTATCGTGGTGT 471
Qy 137 GlyLeuGluPheIleAlaArgIleTyrSerAlaGlyCysCysCysCysCysCysCys 156
Db 472 GCGTGGAGTACTTCGTGCGGATCTGGCCCGCGCGCGCTGCTGCTGCGGATCCGCGGTG 531
Qy 157 GlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrIleValLeu 176
Db 532 AGGGGGCGGCTCAGTTTCCCGGAAACCGTTCTGTGTGATGATCATCGTGTCTCATC 591
Qy 177 AlaSerIleAlaValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeu 196
Db 592 GCCTCCATTGCGGTGCTGCGCGCGCGCTCCCGAGGCAACGCTTTTGGCACAATCTGCG 651
Qy 197 ArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThr 216
Db 652 CGGAGCCTCGCTTCTCCTCAGATTCTGCGGATGATCCGATGAGCCGCGGGAGGCAACC 711
Qy 217 TrpLysLeuLeuGlySerValValTyrAlaHisSerLysGluLeuLeuLeuLeuLeu 236
Db 712 TGGAACTGCTGGGCTCTGTGCTATGCCACAGCAAGAGGCTGGTCACTGCTCTGTATC 771
Qy 237 IleGlyPheLeuValLeuPheSerSerPheLeuValTyrLeuValGluLysAspAla 256
Db 772 ATCGGCTTCTTGTCTCATCTGCGCTCGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 831
Qy 257 AsnLysGluPheSerThrTyrAlaAspAlaLeuTyrTyrGlyThrIleThrLeuThrThr 276
Db 832 AACGACCACTTGTACACCTAGCGGATGATCTGCTGGTGGCGGCTGATCACGCTGACACC 891
Qy 277 IleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPhe 296
Db 892 ATTGGCTACGGGACAGTACCCCGACACCTGGAAAGCGGCGCGCTCTTGGCGCAACCTTC 951
Qy 297 AlaLeuLeuGlyIleSerPheAlaLeuProAlaGlyIleLeuGlySerGlyPheAla 316
Db 952 ACCCTCATCGGTGCTCTCTTTCGGCGCTGCTGCGAGCATCTTGGGGTTCGGGTTTGGCC 1011
Qy 317 LeuLysValGlnGlnGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAla 336
Db 1012 CTGAAGTTTCAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1071
Qy 337 AsnLeuIleGlnCysValTrpArgSerTyrAlaAlaAsp----- 349
Db 1072 GGCCTGATCAGTCGGCTCGGCTCGAGATTTTACGCCCAACCACTCTCGCGCAGACCTGCAC 1131
Qy 350 -----GluLysSerValSerIleAlaThrTrpLys----- 359
Db 1132 TCCACGTGGCAGTACTACGAGCGAAGCGTACCGTCCCTATGATGATGCTGCAAACTCAA 1191
Qy 360 -----ProHisLeuLysAlaLeuHisThr----- 367
Db 1192 ACCTACGGGGCTCCAGACTTATCCCGCTGACCCAGCTGGAGCTGCTGAGAAACCTC 1251
Qy 367 ----- 367
Db 1252 AAGAGTAAATCTGAGCTCGCTTTCAGGAAGAGACCCCGCGGAGCGCTCTCCAAGTAA 1311
Qy 368 -----CysSerPro-----ThrAsnGlnLysLeu 375
Db 1312 GGCAGCCCGTCAGAGGGCGCTGTGTGGATGCTGCCCGCGAGCGCTCTAGCCAGAGGTC 1371
Qy 376 SerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGln 395
Db 1372 AGTTTGAAGATCTGTGTC-----TTCCTCAGCCCGCGAGCGTGGTGCACAGGGGAAGGG 1428
Qy 396 AlaSerValGlyAsp-----ArgArgSerProSerThrAspIleThrAlaGluGlySer 413
Db 1429 TCCCGCAGGCGCCAGACTGTGAGCGGTCTACCCAGCGCCAGCAGACCTCGAGGACAGC 1488
Qy 414 ProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgProSerLeu 433
Db 1489 CCAGCAAGTGGCCAAAGAGCTGGAGCTTCGGGACCGCGAGCGCGGACCGCGGCTTTC 1548
Qy 434 ArgLeuLysSerSerGlnProLysProValIleAspAlaAlaThrAlaLeuGlyThrAsp 453
Db 1549 CGCATCAAGGTGGCGCGCTCAGGCGAG-----AACTCAGAACCAAGCCTCCCGGAGAG 1602
Qy 454 AspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThrProPro 473
Db 1603 GACATTCTGGATGACAAGAGCTGCCCTCGAGTTTGTGACCGAGGACCTGACCCCGGCG 1662
Qy 474 LeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPhe 493
Db 1663 CTCAAGTTCAGCATCAGAGCGGTGTGTCTATGCGGTTCCTGGTGTCCAGCGGAAGTTC 1722
Qy 494 LysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAlaGlyHis 513
Db 1723 AAGAGAGCCTTCGGCGCTCAGCGCTGATGAGCGTCTATCAGAGCAGTACTCAGCGCGCAC 1782
Qy 514 LeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyLys 533
Db 1783 CTGGACATGCTGTCCCGAATTAAGAGCTGTCAGTCCAGAGTGGACCAAGTCTGTTGGGGCG 1842
Qy 534 GlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGluThrThr 553
Db 1843 GGCCCGAGCGATCAGGAC-----AAGGACCGCACCAAGGGCGCGCGGCGGAGCTGCC 1899
Qy 554 AspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSerIleGlu 573
Db 1900 GAGGACCCCGCATGATGGGACCGCTCGGAGGTGGAGAGCAGGCTTCTTCATCGAGAG 1959
Qy 574 SerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySerAlaSer 593
Db 1960 AAGAAGCTGGACTTCCTGGTGAATATCTACATGAG-----CGGATGGG----- 2004
Qy 594 AlaLeuAlaLeuAlaSerPheGlnIleProPheGluCys----- 607
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Qy 337 AsnLeuIleGlnCysValTrpArgSerTyrAlaAlaAsp----- 349
Db |||||
1012 GGTCTGATCCAGTCTGCTCGAGATTTCTACTAACCCTCTACGACCGACCTGCAC 1071
Qy |||||
350 -----GluLysSerValSerIleAlaThrTrpLys-----ProHis 361
Db |||||
1072 TCCAGTGGCAGTACTACGAGCGGACAGTCTCTCCCATGTACAGACTCATCCCACT 1131
Qy |||||
362 LeuLysAlaLeuHisThrCys----- 368
Db |||||
1132 CTGAACAGCTGGAGCTCTGAGGAATCTCAAGAGCAAAATCTGAGCTCACCTTCAGGAAG 1191
Qy |||||
369 -----SerProThrAsnGlnLysLeuSerPheLysGluArgValArg 382
Db |||||
1192 GAGCACAGCCAGAGCCATCACCA---AGTCAGAGGTCAGTTTCAAGATCGTGC--- 1245
Qy |||||
383 MetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAsp----- 400
Db |||||
1246 TTCTCCAGCCCGAGGATGCTGCCAAGGAAAGGGGTCTCCCGAGCCGACAGCGTC 1305
Qy |||||
401 ArgArgSerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSer 420
Db |||||
1306 CGGCGGTCCCCAGTGGAGTCAAGTCTTATGACAGCCCGAGCAAGTGTCCCAAGAGC 1365
Qy |||||
421 TrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerSerGlnPro 440
Db |||||
1366 TGGAGCTTTGGTACCGCGAGCGCACAGCGCTTTCGCGATCAAGGGTGTGCATCC 1425
Qy |||||
441 LysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyrAspGluLysGly 460
Db |||||
1426 CGGCAGATTCAGAAGCAAGCTCCCT---GGGGAGGACATCGTAGAGCAACAAGAGC 1482
Qy |||||
461 CysGlnCysAspValSerValGluAspLeuThrProLeuLysThrValIleArgAla 480
Db |||||
1483 TGTAACTCGAGTTGTGACTGAGATCTTACCCCTGGCCCTCAAGTTAGCATCAGAGCT 1542
Qy |||||
481 IleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThrLeuArgProTyr 500
Db |||||
1543 GTGTGTATTATCGGTTCTTGTATCTAAGCGAAGTTCAAGAGAGTCTGCGCCCATAT 1602
Qy |||||
501 AspValLysAspValIleGluGlnTrpSerAlaGlyHisLeuAspMetLeuCysArgIle 520
Db |||||
1603 GATGTGATGGAGCGTCATCGAAGCAGTACTCGCTGACACTTGGATATGTTCTCCGCGATC 1662
Qy |||||
521 LysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLys 540
Db |||||
1663 AAGAGCTTCAGTCCAGAGTGGACAGATTGTGGCGCGGGCCCAACAATAACGAT--- 1719
Qy |||||
541 LysSerArgGluLysIleThrAlaGluHisGluThrThrAspAspLeuSerMetLeuGly 560
Db |||||
1720 AAGGATCGCACCAAGGCGCCAGCGAAGCGAGCTGCCCGAAGACCCCGAGCATGATGGA 1779
Qy |||||
561 ArgValValLysValGluLysGlnValGlnSerIleGluSerLysLeuAspCysLeuLeu 580
Db |||||
1780 CGGCTTGGGAAGGTGGAGAAACAGTCTTGTCCATGGAAAAGAGCTCGACTTCTGTGTG 1839
Qy |||||
581 AspIleTyrGlnGlnValLeuArgLysGlySerAlaLeuAlaLeuAlaSerPhe 600
Db |||||
1840 AGCATCTATACAG-----AGATGGGC----- 1863
Qy |||||
601 GlnIleProProPheGluCys-----GluGlnThrSer 611
Db |||||
1864 ---ATCCACACAGACAGACAGAGCGCTATTTTGGGGCCAAAGAGCGCTGAGCCGCGACCA 1920
Qy |||||
612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
Db |||||
1921 CCTTACCACAGCCAGAGAGCAGCGGTGAC-----CATGCAGCAACAGCATGGTGTGT 1971
Qy |||||
632 -----LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeu 648
Db |||||
1972 ATCATTAGATCGTCGGTCCACAGCTCT----- 2001
Qy |||||
649 ThrProAsnGluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGln 668
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Db 2002 -----ACGGCCAGAGGAAGTACGACGACCCCGAGCCATC-----CCC 2040
Qy 669 AlaThrGlnValProIleSerGlnSer 677
Db 2041 CTTGCCAGTGTCTCTCCCTCCACCTCG 2067

RESULT 10
US-09-177-650-1
; Sequence 1, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3232
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (128)..(2743)
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (975)..(976)
; OTHER INFORMATION: There is an insertion of a GT between nucleotides
; OTHER INFORMATION: 975 and 976 in kindred KI504.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (978)
; OTHER INFORMATION: The mutation A to G occurs at this base in kindred
; OTHER INFORMATION: K3904.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1043)
; OTHER INFORMATION: The mutation G to A occurs at this base in kindred
; OTHER INFORMATION: K1705.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1691)..(1703)
; OTHER INFORMATION: The thirteen nucleotides from 1691-1703 are
; OTHER INFORMATION: deleted in kindred K3369.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1039)
; OTHER INFORMATION: This polymorphism of C to T was seen in 7.0% of
; OTHER INFORMATION: the control population.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1846)
; OTHER INFORMATION: This polymorphism of C to T was seen in 0.57% of
; OTHER INFORMATION: the control population.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1459)
; OTHER INFORMATION: The mutation C to T occurs at this base in kindred
; OTHER INFORMATION: K1525.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1094)
; OTHER INFORMATION: The mutation C to T occurs at this base in kindred
; OTHER INFORMATION: K4443.
; FEATURE:
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277 IleGlyTyrGlyAspLysThrProLeuThrTrrPLeuGlyArgLeuLeuSerAlaGlyPhe 296  
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Qy 297 AlaLeuLeuGlyIleSerPheAlaLeuProAlaGlyIleLeuGlySerGlyPheAla 316  
Db 1019 ACCTCATCGGTGTCTCTTCCTCGCGCTGCCCTGCAGGCATCTTGGGGTCTGGGTTC 1078  
Qy 317 LeuLysValGlnGluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAla 336  
Db 1079 CTGAAGGTTTCAGGAGCAGCACAGCAGAGAAGCACTTTTGAGAAGAGCGCGAACC CGGACGA 1138  
Qy 337 AsnLeuIleGlnCysValTrrArgSerTyrAlaAlaAsp 349  
Db 1139 GGCTTGATCGAGTCGGCTCGAGATTTCTACGCCACCAACCTCTCGCGCACAGACCTGCAC 1198  
Qy 350 -----GluLysSerValSerIleAlaThrTrpLys 359  
Db 1199 TCCACGTGGCAGTACTACGAGCGAAGCGGTCAACGTCGCCCATGTACAGTTTCGCAAACTCAA 1258  
Qy 360 -----ProHisLeuLysAlaAlaLeuHisThr 367  
Db 1259 ACCTACGGGCTCCAGACTTATCCCCCGCTGAACCACTGTGAGCTGTGTGAGGAACCTC 1318  
Qy 367 ----- 367  
Db 1319 AAGAGTAAATCTGGACTCGCTTTTCAGGAAGGACCCCGCGGAGCGGTCTCCAAGTAAA 1378  
Qy 368 -----CysSerPro-----ThrAsnGlnLysLeu 375  
Db 1379 GGCAGCCCGTCAGAGGGGCCCTGTGTGGATGTCGCCCGGACGCTCTACCCAGAAGGTC 1438  
Qy 376 SerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGln 395  
Db 1439 AGTTTGAAGATCGTGTC---TTCTCCAGCCCCCGAGGCGTGCTGCCAAGGGGAAGGG 1495  
Qy 396 AlaSerValGlyAsp-----ArgArgSerProSerThrAspIleThrAlaGluGlySer 413  
Db 1496 TCCCCCGCAGCCCCAGACTGTGAGCGGTCAACCAGCGCGCACAGACGCTTCGAGGACAGC 1555  
Qy 414 ProThrLysValGlnLysSerTrrSerPheAsnAspArgThrArgPheArgProSerLeu 433  
Db 1556 CCAGCAAGGTGCCAAGAGCTGGAGCTTCGGGGACCGCAGCGCGGCGACGCCAGGCTTTC 1615  
Qy 434 ArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAsp 453  
Db 1616 CGCATCAGGGTCCCGCTCACGGCAACTCAGAA---GAACCAAGCTTCCCGGAGAG 1672  
Qy 454 AspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThrProPro 473  
Db 1673 GACATTGTGGATGACAAGAGCTGCCCTCGGAGTTTGTGACCCGAGGACCTGACCCCGGGC 1732  
Qy 474 LeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPhe 493  
Db 1733 CTCAAAGTCAGCATCAGACCGGTGTGTCTATCGGTTCTGTGTGTCTCAAGCGGAAGTTC 1792  
Qy 494 LysGluThrLeuArgProTrrAspValLysAspValIleGluGlnTrrSerAlaGlyHis 513  
Db 1793 AAGGAGAGCTCGGGCCCTACAGACGTGATGGAGCTCATCGACGAGTACTCAGCCGGCCAC 1852  
Qy 514 LeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyLys 533  
Db 1853 CTGGACATGCTGTCCCGAATTAGAGCCTGCAGTCCAGAGTGGACAGAGCTCGTGGGCGG 1912  
Qy 534 GlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGluThrThr 553  
Db 1913 GGCGCCAGCATCACGAC---AAGGACCGCACCAAGGGCCCGCGGCGGAGCTGCC 1969  
Qy 554 AspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSerIleGlu 573  
Db 1970 GAGACCCACGACATGAGCGGCTCGGGAAGGTGGAGAACGAGGTCTTGTTCATGGAG 2029  
Qy 574 SerLysLeuAspCysLeuLeuAspIleTrrGlnGlnValLeuArgLysGlySerAlaSer 593



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Db 892 ACCCTCATTGCTGCTGCTTTCTTTGCTCTTCCGGCTGCAATTTGGGATCCGGCTTTGCC 951
Qy 317 LeuLysValGlnGlnHisArgGlnHisPheGluLysArgArgAsnProAlaAla 336
Db 952 CTGAAGTCCCAAGACGACATCGGCAAAACACATTTGAGAAACGGCGGAAACCTCGCGCA 1011
Qy 337 AsnLeuLeuGlnCysValTyrArgSerTyrAlaAlaAsp----- 349
Db 1012 GGTCTGATCCAGTCTGCTCGAGATCTATGCTACTAACTCTCAGCCACCGACTGCGAC 1071
Qy 350 -----GluLysSerValSerAlaAlaThrTyrLysProHisLeuLys 363
Db 1072 TCCAGTGGCAGTACTACGAGCGNACAGTCACTGTCCCATGTACAGCTCACAACTCAA 1131
Qy 364 -----AlaLeuHisThrCysSerProThrAsnGln----- 373
Db 1132 ACCTATGGGGCTCCAGACTATCCACCTCTGAACACAGCTGGAGCTGCTGAGGAATCTC 1191
Qy 374 -----LysLeuSerPheLysGluArgValArg-----MetAlaSerPro 386
Db 1192 AAGAGCAAACTGGACTCACCTTCAGGAAGAGAGCCACAGCCAGAGCCATCACCAGCCCC 1251
Qy 387 ArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAsp-----ArgArgSerPro 404
Db 1252 CGAGCGATGGCTGCCAAGGGAAGGGGTCTCCCNAGGCCAGAGCGTCCGGCGGTCCCCC 1311
Qy 405 SerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSerTyrSerPheAsn 424
Db 1312 AGTCGGATCAGAGTCTTGTGACAGCCGAGCAAGGTGCCAAGAGCTGGAGCTTTGGT 1371
Qy 425 AspArgThrArgPheArgProSerLeuArgLeuLysSerSerGlnProLysProValIle 444
Db 1372 GACCGCAGCCGACACCGCGAGCTTTCGCGATCAAGGGTGTGCATCCCGCGCAAGATTCA 1431
Qy 445 AspAlaAspThrAlaLeuGlyThrAspValTyrAspGluLysGlyCysGlnCysAsp 464
Db 1432 GAAGNAGCAAGCTCCCTGGGAGAGACATCTAGAGGACACAGAGCTGTAACTGGAG 1491
Qy 465 ValSerValGluAspLeuThrProLeuLysThrValIleArgAlaIleArgIleMet 484
Db 1492 TTTGTGACTGAAGATCTTACCCCTGGCCTCAAAGTYAGCATCAGAGCCGTGTGTATG 1551
Qy 485 LysPheHisValAlaLysArgLysPheLysGluThrLeuArgProTyrAspValLysAsp 504
Db 1552 CGGTCTCTTGGTATCTTAACGGAAGTTCAAGAGAGTCTGCGCCCATATGATGTATGAC 1611
Qy 505 ValIleGluGlnTyrSerAlaGlyHisLeuAspMetLeuCysArgIleLysSerLeuGln 524
Db 1612 GTATCGAACAGTACTCGGTGGACACATTGGATATGTTGTCGGCATCAAGAGCTGCGAG 1671
Qy 525 ThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLysLysSerArgGlu 544
Db 1672 ACCAGATGGACAGATTGTGGGGGGGGGCCCAACAATAACGGAT--AAGGATCGCACC 1728
Qy 545 LysIleThrAlaGluHisGluThrThrAspAspLeuSerMetLeuGlyArgValLys 564
Db 1729 AAAGCCCGACGGAAACGGAGCTGCCGGAAGACCCAGCATGATGGGACGGCTGGGAAG 1788
Qy 565 ValGluLysGlnValGlnSerIleGluSerLysLysLeuAspCysLeuLeuAspIleTyrGln 584
Db 1789 GTGGAGAAACAGGTTCTGTCAATGAAAAGAGCTCGACTTCTTGGTGAGCATCTATACA 1848
Qy 585 GlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPheGlnIlePro 604
Db 1849 CAG-----AGAATGGCATCCACACGACGAGACAGAGCGCTATTTTGGGGCCCAAG--- 1899
Qy 605 PheGluCysGlnThrSerAspTyrGlnSerProValAspSerLysAspLeuSerGly 624
Db 1900 ---GAGCCTGAGCCCGCCACCCCTTACCACAGCCCGAGAGGACAGCGGTGAC----- 1947
Qy 625 SerAlaGlnAsnSerGlyCys-----LeuSerArgSerThrSerAlaAsnIleSer 641
Db 1948 CATGCAGACAAGCATGGCTGTATCATTAAGATCTGTCCTCCGCTCCACCAGCTCTACGG--GCC 2005
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Qy 642 ArgGly-----LeuGlnPheIleLeuThrProAsnGlu 652
Db 2006 AGAGGAAGTACGACGACACCCACCATCCCTCCCTGCGCAGTGTCTCTCCCTCCACCTCGT 2065
Qy 653 PheSerAlaGlnThr-----PheTyr 659
Db 2066 GGCGGCGAGACCAACGAGCGCATGCGACCTCCCTGTGGGAGACCATGGCTCACTGGTATC 2125
Qy 660 AlaLeuSerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGly 679
Db 2126 GCATCCCACTCCCTGTCACACGAGCGGTGCTGTCTGCT----- 2167
Qy 680 SerAlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsn---ThrAlaProLysPro 698
Db 2168 ---ACGGTGGGGGCAACAGAGCCAGTACCGAGTTCTTGAAGCTGGAGGCGACCCAGCCT 2224
Qy 699 AlaAlaProThrThrLeu 704
Db 2225 GCAGGCCCTCTGAGGCTG 2242
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## RESULT 12

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US-09-105-058C-26
; Sequence 26, Application US/09105058C
; Patent No. 6403360
; GENERAL INFORMATION:
; APPLICANT: Blonar, Michael A.
; APPLICANT: Dworetzky, Steven
; APPLICANT: Gribkoff, Valentin K.
; APPLICANT: Levesque, Paul C.
; APPLICANT: Little, Wayne A.
; APPLICANT: Neubauer, Michael G.
; APPLICANT: Yang, Wen-Pin
; TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
; CURRENT APPLICATION NUMBER: US/09/105,058C
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 60/055,599
; PRIOR FILING DATE: 1997-08-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 2565
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-105-058C-26
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Alignment Scores:
Pred. No.: 4,24e-158 Length: 2565
Score: 1587.50 Matches: 386
Percent Similarity: 54.61% Conservative: 106
Best Local Similarity: 42.84% Mismatches: 244
Query Match: 34.91% Indels: 165
DB: Gaps: 3
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US-09-810-796-5 (1-888) x US-09-105-058C-26 (1-2565)

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Qy 3 AspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaArgGlyAspGly 22
Db 91 GACGTGGAGCAA-----GTCACCTTGGCGCTCGGGCGCGGAGCCGCAAGACGGG 141
Qy 23 LeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeuArgGlu 42
Db 142 ACCCTGTGCTGTG-----GAGGGCGGGCGCGCGACGAGGGG 177
Qy 43 SerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLys---ProLeuSerTyr 61
Db 178 CAGCGGAGGACCCCGCAGGGC-----ATCGGGTCTCTGGCCAGACCCCGCTGAGCGCG 231
Qy 62 ThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeuTyr 81
Db 232 CCAGTCAAG-----AGAAACAACGCCAAGTACCGCGCGCATCCAACTTTGATCTAC 282
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Db 2263 CGAATCTCCCCCGCAG-----AGACGTAGCATCAGC 2295
Qy 766 MetGlyGluThrLeuLeuSerValCysProMetValProLysAspLeuGlyLysSer 785
Db 2296 CGAGACAGTGACACACCTCTGTCCCTG----- 2322
Qy 786 LeuSerValGlnAsnLeuLeuArgSerThrGluGluLeuAsnLeuGlnLeuSerGlySer 805
Db 2323 ATGTCGGTCAACCAC-----GAGGAGCTGGAGAGTCTCCAAGTGGCTTC 2367
Qy 806 GluSerSerGlySerArgGlySerGlnAspPheTyrPro-----LysTyrArg 821
Db 2368 AGCATCTCCAGGACAGAGATGATGTGTGCGCCCAATGGGGGTGCGAGCTGGATG 2427
Qy 822 GluSerLysLeuPheIleThrAspGluGluValGluProGluGluThrGluThrAspThr 841
Db 2428 AGGGAGAAGCGGTACTCTGCCGAG-----GGTGAGACGGACACAGACGACGCC 2478
Qy 842 Phe 842
Db 2479 TTC 2481

RESULT 13
; Sequence 6, Application US/09177650
; Patent No. 6413719
; GENERAL INFORMATION:
; APPLICANT: Leppert, Mark F.
; APPLICANT: Singh, Nanda
; APPLICANT: Charlier, Carole
; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)
; FILE OF INVENTION: AND OTHER EPILEPSIES
; FILE REFERENCE: 2323-134
; CURRENT APPLICATION NUMBER: US/09/177,650
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/063,147
; EARLIER FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 2914
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)..(2634)
; FEATURE:
; NAME/KEY: allele
; LOCATION: (840)
; OTHER INFORMATION: The polymorphism of a T to a C at this position
; OTHER INFORMATION: has appeared in one individual.
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (947)
; OTHER INFORMATION: The missense mutation from a G to a T occurs at
; OTHER INFORMATION: this position in a BFNC family.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (678)
; OTHER INFORMATION: This position is polymorphic for C or T.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (750)
; OTHER INFORMATION: This position is polymorphic for T or C.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (1089)
; OTHER INFORMATION: This position is polymorphic for G or C.
; FEATURE:
; NAME/KEY: allele
; LOCATION: (2598)
; OTHER INFORMATION: This position is polymorphic for T or C.
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US-09-177-650-6

Alignment Scores:

Pred. No.:	5,37e-158	Length:	2914
Score:	1587.50	Matches:	386
Percent Similarity:	54.61%	Conservative:	106
Best Local Similarity:	42.84%	Mismatches:	244
Query Match:	34.91%	Indels:	165
DB:	3	Gaps:	28

US-09-810-796-5 (1-888) x US-09-177-650-6 (1-2914)

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Qy 3 AspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaAalaArgGlyAspGly 22
Db 163 GACCTGGAGCAA-----GTCACCTTGGCGTCGGGGCCGAGCGACAAAGACGGG 213
Qy 23 LeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeuArgGlu 42
Db 214 ACCCTGTGCTG-----GAGGGCGGCGCGCGCAGCAGGGG 249
Qy 43 SerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLys---ProLeuSerTyr 61
Db 250 CAGCGGAGGACCCCGCAGGGC-----ATCGGGCTCTGTGGCCAAAGACCCCGTGAGCGCG 303
Qy 62 ThrSerSerGlnSerCysArgAsnValLysTyrArgArgValGlnAsnTyrLeuTyr 81
Db 304 CCAGTCAAG-----AGAAACACACGCCCAAGTACCGCGCATCCAAACATTTGTATCTAC 354
Qy 82 AsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeuLeu 101
Db 355 GACCCCTGGAGAGACCGCGGGCTGGCGCTGTTTACCACGCGTGGTGTCTCTGAT 414
Qy 102 ValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeuAla 121
Db 415 GTCTCGGGGTGCTTGTATCTGCTGCTCCTGACCACATTCAGAGGAGTATGAGACTCTCTCG 474
Qy 122 SerSerCysLeuLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPheIle 141
Db 475 GGAGACTGGCTTCTGTACTGGAGACATTTCTATTTTCTTTTGGAGCGAGTTTGTCT 534
Qy 142 IleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeuArg 161
Db 535 TTGAGGATCTGGGCTGCTGGATGTTGTCGCATACAAAGCTGGCGGGCGGAGCTGAAG 594
Qy 162 PheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAlaVal 181
Db 595 TTTGCCAGGAAGCCCTGTGCTGCTGTCATCTTTGTGCTGATTTGCTCTGTGTCAGCTG 654
Qy 182 ValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArgPhe 201
Db 655 GTTCTGTGGGAAACCAAGGCAATGTTCTGCGCCACCTCC---CTGCGAAGCCTGCGCTTC 711
Qy 202 LeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTyrLysLeuGly 221
Db 712 CTGAGATCTCTGCCCATGCTCGGATGGACCGAGAGGTGGACCTGGAAGCTTCTGGGC 771
Qy 222 SerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTyrIleGlyPheLeuVal 241
Db 772 TCAGCCATCTGTGCCACAGCAAGAACTCATCAGGCTGTGTACATCGGTTTCTCTGACA 831
Qy 242 LeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAla----- 256
Db 832 CTCATCTCTTCTCTTCTTCTGTCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 891
Qy 257 -----AsnLysGluPheSerThrTyrAlaAspAlaLeuTyrIleGlyThr 271
Db 892 CAAGGAGAGGAGTGAAGAGAGTTTGAGACCTATGCAGATGCCCTGTGTGTGTGTGTGTGT 951
Qy 272 IleThrLeuThrThrIleGlyTyrGlyAspLysThrProLeuThrTyrLeuGlyArgLeu 291
Db 952 ATCACACTGGCCACCATTTGGCTATGGAGACAAAGACCCCAAAACGTTGGGAAGCGCTGTG 1011
Qy 292 LeuSerAlaGlyPheAlaLeuLeuGlyLysSerPheAlaLeuProAlaGlyIleLeu 311
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Db 1012 ATTCCGCCACCTTTCTTAATGGCGTCTCTCTTTTGGCCCTTCCAGCGGCATCTCG 1071  
Qy 312 GlySerGlyPheAlaLeuLeuValGlnGlnHisArgGlnLysHisPheGluLysArg 331  
Db 1072 GGGTCGGGGCTGGCCCTCAAGGTGAGGAGCAACACCGTCAAGACACTTTTGAAGAAAGG 1131  
Qy 332 ArgAsnProAlaAlaAsnLeuIleGlnCysValTyrArgSerTyrAlaAlaAspGluLys 351  
Db 1132 AGGAAGCCAGCTGTGAGCTCATTCAGGCTCCCTGGAGGTATATGTCTACCAACCCCAAC 1191  
Qy 352 SerValSer---IleAlaThrTriPlys-----ProHisLeu 362  
Db 1192 AGGATTGCGTGGTGGCAGCATGAGATTATGAATCAGTCGTCTCTTTTCTTCTTC 1251  
Qy 363 LysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPheLysGluArgValArg 382  
Db 1252 AGGAAGAACAGCTGGAGGAGCAGCATCCAGCCAGCAAGCTGTCTTGGATCGGGTTGCG 1311  
Qy 383 MetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAspArgArg 402  
Db 1312 CTTTCTAATCTCTGTGTAGCAATACTAAA-----GGAAAGCTATTT 1353  
Qy 403 SerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSerTriPser 422  
Db 1354 ACCCTCTGAATGTAGATGCCATAGAGAAAGTCTTCTAAGAAACCAAGCCTGTGTGC 1413  
Qy 423 PheAsnAspArgThrArgPheArgProSerLeuArgLeuLys----- 436  
Db 1414 TTAACAATAAAGAGCGTTCCGACGCGCTTCGCGATGAAGCGTACGCTTTCTGGCAG 1473  
Qy 437 SerSerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspValTyr 456  
Db 1474 AGTTCTGAA-----GATGCCGGGACAGT-----GACCCCATGGCG 1509  
Qy 457 AspGluLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuLysThr 476  
Db 1510 GAAGACAGGGCTATGGGAATGACTTCCCATCGAAGACATGATCCCCACCTGAAAGGCC 1569  
Qy 477 ValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThr 496  
Db 1570 GCCATCCGAGCGGTGAGAAATTTCTACAATTCGCTCTCTATAAAAAAATTAAGAGACT 1629  
Qy 497 LeuArgProTyrAspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMet 516  
Db 1630 TTGAGGCTTTACGATGAAGAGTGTATTGAGCAGATTCTTGGCGGCATCTCGACATG 1689  
Qy 517 LeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIle 536  
Db 1690 CTTTCCAGGATAAAGTACCTTCAGACGAGATAGATATGATTTTCAACCCCTGGACCTCCC 1749  
Qy 537 ThrSerAspLysLysSerArg----- 543  
Db 1750 TCCAGCCAAACACAAAGAGTCTCAGAAAGGTGACGATTCACCTTCCCATCCAGCAA 1809  
Qy 544 -----GluLysIleThrAlaGluHisGluThr-----AspAspLeuSer 557  
Db 1810 TCTCCAGGATGAACCATATGTAGCCAGACCATCCACATCAGAAATCGAAGACCAAGC 1869  
Qy 558 MetLeuGlyArgValValLysValGluLysGlnValGlnSerIleGluSerLysLeuAsp 577  
Db 1870 ATGATGGGAAGTTGTAAAAAGTTGAAAGACAGGTTCAAGACATGGGGAAGAGCTGGAC 1929  
Qy 578 CysLeuLeuAspIleTyrGlnGluValLeuArg----- 588  
Db 1930 TTTCTCTGGGATATGCAATGCAACATGAAAGCGTTGCGAGGTGCGAGTCACGAGTAT 1989  
Qy 589 -----LysGlySerAlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPhe 605  
Db 1990 TACCAACCAAGGACCTCTCG-----CCAGCT 2019  
Qy 606 GluCysGluGlnThrSerAspTyrGlnSerProValAspSerLysAspLeuSerGlySer 625

Db 2020 GAAGCAGAGAGAGAGGAGGACAAACAGGTATTTC---GATTGAAACCATCATCTGCAAC 2076  
Qy 626 AlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGln 645  
Db 2077 TATTCTGAGACAGGCCCCCGGAACCACTTACAGCTTCCAC----- 2118  
Qy 646 PheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMet 665  
Db 2119 ---CAGGTGACCATTTGACAAAGTCAGCCCTATGGTGTGTTTGGCACATGACCTT- 2169  
Qy 666 HisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySerAlaValAlaAlaThr 685  
Db 2170 -----GTGAACCTGCCCGAGGGGAGCCAGTCTCTGGAAGGTTTCAGGCACT 2217  
Qy 686 AsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAlaProThrLeuGln 705  
Db 2218 -----CCTCTTCTTCAGCAACACATATGTGGAG 2247  
Qy 706 IleProProProLeuProAlaIleLysHisLeuProArgProGluThrLeuHisProAsn 725  
Db 2248 AGGCCACAGGTCTGCTCTTCTTCTGACTCTTCTGACTCCCGAGTGCCTGCCAC---TCC 2304  
Qy 726 ProIleGlyLeuGlnGluSerIleSerAspValThrThrCysLeuValAlaSerLysGlu 745  
Db 2305 CAGGCTGACCTGCGAGGCCCTTACTCGGAC----- 2334  
Qy 746 AsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMetArgLysSerPheAsp 765  
Db 2335 CGAATCTCCCCCGGAG-----AGACGTAGCATCAGC 2367  
Qy 766 MetGlyGlyGluThrLeuLeuSerValCysProMetValProLysAspLeuGlyLysSer 785  
Db 2368 CGAGACAGTGACACACCTCTGTCTCTG----- 2394  
Qy 786 LeuSerValGlnAsnLeuIleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySer 805  
Db 2395 ATGTCGGTCAACCA-----GAGAGCTGGAGAGGTCTCCAAAGTGGCTTC 2439  
Qy 806 GluSerSerGlySerArgGlySerGlnAspPheTyrPro-----LysTriPArg 821  
Db 2440 AGCATCTCCAGGACAGACATGATTATGTGTGGCCCCCAATGGGGGTGAGCTGGATG 2499  
Qy 822 GluSerLysLeuPheIleThrAspGluGluValGlyProGluGluThrGluThrAspThr 841  
Db 2500 AGGAGAAGCGGTACTCTCGCGAG-----GGTGAGACGGACACAGACGACGCC 2550  
Qy 842 Phe 842  
Db 2551 TTC 2553  
RESULT 14  
US-09-177-650-90  
; Sequence 90, Application US/09177650  
; Patent No. 6413719  
; GENERAL INFORMATION:  
; APPLICANT: Leppert, Mark F.  
; APPLICANT: Singh, Nanda  
; APPLICANT: Charlier, Carole  
; TITLE OF INVENTION: KCNQ2 AND KCNQ3 - POTASSIUM CHANNEL GENES WHICH ARE  
; TITLE OF INVENTION: MUTATED IN BENIGN FAMILIAL NEONATAL CONVULSIONS (BFNC)  
; TITLE OF INVENTION: AND OTHER EPILEPSIES  
; FILE REFERENCE: 2323-134  
; CURRENT APPLICATION NUMBER: US/09/177,650  
; CURRENT FILING DATE: 1998-10-23  
; EARLIER APPLICATION NUMBER: 60/063,147  
; NUMBER OF SEQ ID NOS: 129  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 90  
; LENGTH: 2814  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:



; NAME/KEY: CDS  
; LOCATION: (202)..(2811)  
US-09-177-650-90

## Alignment Scores:

Pred. No.: 4, 43e-154 Length: 2814  
Score: 1550.50 Matches: 382  
Percent Similarity: 54.43% Conservative: 109  
Best Local Similarity: 42.35% Mismatches: 245  
Query Match: 34.10% Indels: 167  
DB: 3 Gaps: 27

US-09-810-796-5 (1-888) x US-09-177-650-90 (1-2814)

Qy 3 AspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaAaArgGlyAspGly 22  
Db 340 GACGTGGAGCAA-----GTACCTTGGCGCTAGGCGCGGAGCGGACCAAGACGGG 390  
Qy 23 LeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeuArgGlu 42  
Db 391 ACCCTGTGCTGTG-----GAGGCGGTGGCGCGGAGAGAGGGG 426  
Qy 43 SerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLys---ProLeuSerTyr 61  
Db 427 CAGAGGAGACCCCGCAGGCG-----ATCGGGCTCTGGCAAGACCCCTGAGCGCG 480  
Qy 62 ThrSerSerGlnSerCysArgAsnValLysTyrArgArgValGlnAsnTyrLeuTyr 81  
Db 481 CCAGTCAAG-----AGNAACAACGCCAAGTACAGCGCGCATCAAACTTTGATCTAT 531  
Qy 82 AsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeuLeu 101  
Db 532 GACGCCCTGGAGAGACCGCGGCTGGCGCTCTACCAAGCGCTTGTCTCTGAT 591  
Qy 102 ValPheGlyCysLeuLeuSerValPheSerThrIleProGluHisThrLysLeuAla 121  
Db 592 GTCTGGAGATGCTTGATTCGCGCTGCTCACCACCTTCAAGGAATATGACACTGTGTCT 651  
Qy 122 SerSerCysLeuLeuLeuGluPheValMetIleValPheGlyLeuGluPheIle 141  
Db 652 GGAGACTGGCTTGTCTGCGAACATTTGCTATTCTTTTGGAGCTGAGTTTGTCT 711  
Qy 142 IleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeuArg 161  
Db 712 TTGAGGATCTGGCTGCGAGATGTTGCTGCGATACAAAGGCTGCGTGGCGGCTAAAG 771  
Qy 162 PheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAlaVal 181  
Db 772 TTGCGCAGAGACCCCTGTGATGTGACATCTTCGTACTGATTCCTCTGTGCCAGTG 831  
Qy 182 ValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArgPhe 201  
Db 832 GTTGGCGTGGGAAACACAGGCAATGCTTGTGGCCACCTCC---CTGCGAAGCTTTCGCTTC 888  
Qy 202 LeuGlnIleLeuArgMetValArgMetAspArgArgGlyThrTrpLysLeuLeuGly 221  
Db 889 CTGCAGATCTCGCATGCTTCTGATGATGATGAGGAGGCTGCGACCTGCGAAGCTTCTGCGGC 948  
Qy 222 SerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeuVal 241  
Db 949 TCGGCTATCTGTGCCCCACAGAAAGACTATCACTGCTGCTGATCATAGGCTTCTCTGACA 1008  
Qy 242 LeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAla----- 256  
Db 1009 CTCATCTTTTCTTCACTTTCTGTCTACCTGTGGTGGAGAGGATGTGCCAGAAATGGATGCC 1068  
Qy 257 -----AsnLysGluPheSerThrTyrAlaAspAlaLeuTrpTrpGlyThr 271  
Db 1069 CAAGGAGAGGAGATGAAGGAGGATTTGAGACCTATGACAGATGCTCTGTGTGGGGCGCTG 1128  
Qy 272 IleThrLeuThrThrIleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeu 291  
Db 1129 ATCACATGGCCACCATTTGGTTATGGAGACRAGACACCTAAACCTGGGAAGGAGCTGTG 1188

Qy 292 LeuSerAlaGlyPheAlaLeuLeuGlyLysSerPhePheAlaLeuProAlaGlyIleLeu 311  
Db 1189 ATTGCTGCCACCTTTTCTTAATGGCGCTCTCTCTTTTGGCCTTCCGCGCAGCATCTT 1248  
Qy 312 GlySerGlyPheAlaLeuLysValGlnGlnHisArgGlnLysHisPheGlyLysArg 331  
Db 1249 GGTCTCAGACTGGCAGCTGAAGTTTCAGAGCAGACCGCTCAGAACGACTTTTGAAGAAGA 1308  
Qy 332 ArgAsnProAlaAlaAsnLeuIleGlnCysValTrpArgSerTyrAlaAlaAspGluLys 351  
Db 1309 AGGAAGCCAGCTGCGGAACCTCATCCAGCTCGCTGGAGATATTATGCTACCAACCCCAAC 1368  
Qy 352 SerValSer---IleAlaThrTrpLys-----ProHisLeu 362  
Db 1369 AGGTGGATCTGTGGCAACCTGGAGATCTTATGAATCAGTTGTCTTTTCCCATCTTTC 1428  
Qy 363 LysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPheLysGluArgValArg 382  
Db 1429 AGGAAGAACAACTGGGAAGCAGCAGCCAGCAAGCTGGGTCTCTTGGATCGGGTTCGC 1488  
Qy 383 MetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAspArgArg 402  
Db 1489 CTTTCTAATCTCTGTGTAGCAATACTAAA-----GGAAAGCTATT 1530  
Qy 403 SerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSerTrpSer 422  
Db 1531 ACCCTCTGTAATGTAGATGCCATAGAAAGACCTTCCAAAGAGACCAAGCTTGTGGC 1590  
Qy 423 PheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSer----- 437  
Db 1591 TTAACAATAAAGACGGTTTCCGCAACCGCTTCCGCAAGGAAAGCTACGCTTCTGGCAG 1650  
Qy 438 ---SerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyr 456  
Db 1651 AGWTCTGAA-----GATCTGGGACAGCG-----GACCCCATGGCA 1686  
Qy 457 AspGluLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuLysThr 476  
Db 1687 GAACACAGGGCTATGGAAATGACWTCTCATTTGAGACATGATCCCTTCCTTAAAGCT 1746  
Qy 477 ValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThr 496  
Db 1747 GCCATCGAGCTGCAGAAATTTCTACAGTTCGCTCTATATAAAGAAAGTTCAAGAGACG 1806  
Qy 497 LeuArgProTyrAspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMet 516  
Db 1807 TTGAGGCTTATGATGTGAAGATGTGATTGAGCAGTATTTCGCGGACATCTTGACATG 1866  
Qy 517 LeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIle 536  
Db 1867 CTTTCCAGGATAAAGTACCTACAGACAAAGATAGATATGATTTTCAACCCCTGGACCTCCA 1926  
Qy 537 ThrSerAspLys---LysSerArgGluLysIleThr----- 547  
Db 1927 TCCACTCCAAACATAAAGAGTCTCAGAAAGGAGCAGCATTTACTACCCATCCACGAG 1986  
Qy 548 -----AlaGluHisGluThrThrAspAspLeuSer 557  
Db 1987 TCTCCAAGGAATGAACCATATGTAGCCAGGCGCCACCATCAGAACTGAAGACCAAGC 2046  
Qy 558 MetLeuGlyArgValValLysValGluLysGlnValGlnSerIleGluSerLysLeuAsp 577  
Db 2047 ATGATGGGAAGTTTGAAGATTGAAGACAGAGTTCATGATGATGGGGAAGAAATCGGAC 2106  
Qy 578 CysLeuLeuAspIleTyrGlnGlnValLeuArg----- 588  
Db 2107 TYCTCGTGGACATGCATATGCACATATGGAACGCTTACAGGTACATGTCTCAGTAC 2166  
Qy 589 -----LysGlySerAlaSerAlaLeuAlaLeuAlaSerPheGlnIleProPhe 605  
Db 2167 TACCAACTAARGGGGCTCTCTCC-----CCAGCC 2196

Qy	606	GluCysGluGlnThrSerAspTyrGlnSerProValaspSerLysAspLeu-SerGlyse	625
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Qy	645	nPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMe	665
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Qy	785	rLeuSerValGlnAsnLeuIleArgSerThrGluLeuAsnIleGlnLeuSerGlyse	805
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Qy	805	rGluSerSerGlySerArgGlySerGlnAspPheTyrPro-----LysTrpAr	821
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Qy	841	rPhe	842
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## RESULT 15

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/ RESULT 15
/ US-09-105--058C-5
/ Sequence 5, Application US/09105058C
/ Patent No. 6403360
/ GENERAL INFORMATION:
/ APPLICANT: Blumar, Michael A.
/ APPLICANT: Dworetzky, Steven
/ APPLICANT: Gribkoff, Valentin K.
/ APPLICANT: Levesque, Paul C.
/ APPLICANT: Little, Wayne A.
/ APPLICANT: Neubauer, Michael G.
/ APPLICANT: Yang, Wen-pin
/ TITLE OF INVENTION: KCNQ POTASSIUM CHANNELS AND METHODS OF MODULATING SAME
/ FILE REFERENCE: 3053-4052
/ CURRENT APPLICATION NUMBER: US/09/105,058C
/ CURRENT FILING DATE: 1998-06-26
/ PRIOR APPLICATION NUMBER: US 60/055,599
/ PRIOR FILING DATE: 1997-08-12
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 5

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

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Run on: April 3, 2005, 06:10:16 ; Search time 9606.32 Seconds  
(without alignments)  
4479.159 Million cell updates/sec

Title: US-09-810-796-5

Perfect score: 4547

Sequence: 1 MKDVESGRVLLNSAARG.....SICKAGESTDLSLPHVKLK 888

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Searched: 4708223 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database :

GenEmbl.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	4547	100.0	2772	6	AR565635 Sequence
2	4547	100.0	2772	6	AX268474 Sequence
3	4547	100.0	3111	6	AR565636 Sequence
4	4547	100.0	3111	6	AX268476 Sequence

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VERSION	9	4513.5	99.3	3074	6	AR393778
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REFERENCE	13	4346.5	95.6	3718	6	BD275572
AUTHORS	14	4328.5	95.2	2832	9	AF263835
TITLE	15	4227.5	93.0	3108	10	AF263836
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#### ALIGNMENTS

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LOCUS AR565635  
DEFINITION Sequence 1 from patent US 6767736.  
ACCESSION AR565635  
VERSION AR565635.1 GI:53981668  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2772)  
AUTHORS Hu,Y., Kieke,J.A., Turner,C.A. Jr., Nehls,M.C., Friedrich,G.,  
Zambrowicz,B. and Sands,A.T.  
TITLE Human ion channel protein and polynucleotides encoding the same  
JOURNAL Patent: US 6767736-A 1 27-JUL-2004;  
FEATURES Location/Qualifiers  
source 1..2772  
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Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0



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QY 741 ValAlaSerLysGluAsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMet 760
Db 2326 GTTGCTCTCAAGGAAATGTTTCTGAGTGTGACAGTCAAAATCTCACCAGGACCGTTCTATG 2385
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QY 781 AspLeuGlyLysSerLeuSerValGlnAsnLeuLeuArgSerThrGluGluLeuAsnLeu 800
Db 2446 GACTTGGGCAATCTTTCTGTCTGTGTCGAAACCTGATCAGGTCGACCGAGGAACCTGAATATA 2505
QY 801 GlnLeuSerGlySerGluSerSerGlySerArgGlySerGlnAspPheTyrProLysTyr 820
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Db 2566 AGGGAATCCAAATGTTTATTAACATCATGAGAGGTGGTCCCGAAGACAGACAGACAGAC 2625
QY 841 ThrPheAspAlaAlaProGlnProAlaArgGluAlaAlaPheAlaSerAspSerLeuArg 860
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QY 861 ThrGlyArgSerArgSerSerGlnSerIleCysLysAlaGlyGluSerThrAspAlaLeu 880
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QY 881 SerLeuProHisValLysLeuLys 888
Db 2746 AGCTTGCTCATGTCAAACTGAAA 2769

RESULT 2
AX268474 LOCUS AX268474 2772 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 1 from Patent WO0175108.
ACCESSION AX268474
VERSION AX268474.1 GI:16541652
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Hu.Y., Kieke,J.A., Turner,A.C., Nehls,M.C., Friedrich,G.B.,
AUTHORS Zambrowicz,B. and Sands,A.T.
TITLE Human ion channel protein and polynucleotides encoding the same
JOURNAL Patent: WO 0175108-A 1 11-OCT-2001;
Lexicon Genetics Incorporated (US)
FEATURES
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/organism="Homo sapiens"
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Alignment Scores:
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US-09-810-796-5 (1-888) x AX268474 (1-2772)

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QY 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
Db 286 TACACGAGTACCCAGAGCTGCGGCGCDACTCAAGTACCGCGGGTGCAACATACCTG 345
QY 81 TyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100
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QY 101 LeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120
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QY 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTyrIleGlyPheLeu 240
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QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db 826 GTTCTTATTTTTCGTCCTTCTCTATCTGGTGGAAAGGATGCCAATAAAGAGTTT 885
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QY 281 AspLysThrProLeuThrTyrLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuGly 300
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Qy	861	ThrGlyArgSerArgSerGlnSerIleCysIySsAlaGlyGluSerThrAspAlaLeu	880
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VERSION	AR565636.1	GI:53981669	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 3111)		
AUTHORS	Hu, Y., Kieke, J.A., Turner, C.A. Jr., Nehls, M.C., Friedrich, G., Zambrowicz, B., and Sands, A.T.		
TITLE	Human ion channel protein and polynucleotides encoding the same		
JOURNAL	Patent: US 6767736-A 3 27-JUL-2004;		
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US-09-810-796-5 (1-888) x AR565636 (1-3111)			
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Db	225	GACGCGCTGTACTGCTGGGCACCCCGCGGCCACGCTCGGTGGCGGGCGGTGGCGCTG	284
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VERSION AX268476.1 GI:16541653  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Hu, Y., Kieke, J. A., Turner, A. C., Nehls, M. C., Friedrich, G. B.,  
Zambrowicz, B. and Sands, A. T.  
TITLE Human ion channel protein and polynucleotides encoding the same  
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REFERENCE 1
AUTHORS Dworetzky,S.I., Ramanathan,C.S., Trojnecki,J.T., Boissard,C.G. and
Gribkoff,V.K.
TITLE Human kcnq5 potassium channel, methods and compositions thereof
JOURNAL Patent: WO 0192526-A 1 06-DEC-2001;
Bristol-Myers Squibb Company (US)
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## RESULT 6

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 ACCESSION AR430568  
 VERSION AR430568.1 GI:40191384  
 KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 3137)  
 AUTHORS Jentsch, T.J.  
 TITLE Potassium channel KCNQ5 and sequences encoding the same  
 JOURNAL Patent: US 6649371-A 18-NOV-2003;  
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 Percent Similarity: 99.00% Conservative: 1  
 Best Local Similarity: 98.89% Mismatches: 0  
 Query Match: 99.57% Indels: 9  
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 Qy 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40  
 Db 61 GACGGCTGTCTACTGCTGGGCACCGCGCGCCACGCTCGGTGGCGGGCGGTGGCGCTG 120  
 Qy 41 ArgGluSerArgGlyGlyGlyGlyGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60  
 Db 121 AGGGAGACCGCGGGGCGAGCAGGGGCGCGGATGAGCTGCTGGGGAAGCGCGTCTCT 180  
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DEFINITION AX056817  
ACCESSION AX056817  
VERSION AX056817.1 GI:12309758  
KEYWORDS  
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ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
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Alignment Scores:  
Pred. No.: 2,91e-304 Length: 3137  
Score: 4527.50 Matches: 887  
Percent Similarity: 99.00% Conservative: 1  
Best Local Similarity: 98.89% Mismatches: 0  
Query Match: 99.57% Indels: 9  
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US-09-810-796-5 (1-888) x AX056817 (1-3137)

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REFERENCE 1 (bases 1 to 3137)  
AUTHORS Schroeder,B.C., Hechenberger,M., Weinreich,F., Kubisch,C. and Jentsch,T.J.  
TITLE KCNO5, a novel potassium channel broadly expressed in brain, mediates M-type currents  
J. Biol. Chem. 275 (31), 24089-24095 (2000)  
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TITLE Direct Submission  
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
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JOURNAL	Lerche, C., Scherer, C., Seeborn, G., Busch, A. and Steinmeyer, K.		
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ACCESSION AX456864
VERSION AX456864.1 GI:21715731
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Argentieri, T. M. and Sheldon, J. H.
TITLE Methods of selecting compounds for modulation of bladder function
JOURNAL Patent: WO 0232960-A 5 25-APR-2002;
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DEFINITION AF263835.1 GI:8132996
ACCESSION AF263835
VERSION AF263835.1
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE  
AUTHORS  
TITLE  
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JOURNAL  
FEATURES  
source

1 (bases 1 to 2832)  
Kniazeva,M. and Han,M.  
A new gene of the voltage-gated potassium channel KCNQ family,  
KCNQ5, is a candidate gene for retinal disorders  
Unpublished  
2 (bases 1 to 2832)  
Kniazeva,M. and Han,M.  
Direct Submission  
Submitted (04-MAY-2000) MCDB, University of Colorado at Boulder,  
Porter Biosciences Bldg., Boulder, CO 80309, USA  
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ORIGIN

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US-09-810-796-5 (1-888) x AF263835 (1-2832)

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 DEFINITION partial cds.  
 ACCESSION AF263836  
 VERSION AF263836.1 GI:8132998  
 KEYWORDS  
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 ORGANISM Mus musculus  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 3108)  
 Kniazeva,M. and Han,M.  
 A new gene of the voltage-gated potassium channel KCNQ family,  
 KCNQ5, is a candidate gene for retinal disorders  
 Unpublished  
 2 (bases 1 to 3108)  
 Kniazeva,M. and Han,M.  
 Direct Submission  
 Submitted (04-MAY-2000) MCDB, University of Colorado at Boulder,  
 Porter Biosciences Bldg., Boulder, CO 80309, USA  
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ORIGIN

1.89e-283 Length: 3108

Alignment Scores:

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Db 1382 ACCCCACACATTAAACCGTCATCCGACATCAGAAATATGAAGTTTCATGTTGCAAG 1441
Qy 491 ArgLysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSer 510
Db 1442 CGGAAGTTTAGGAAACATTACGCCCATATGATGTAAAGATGTCATTGAACATACTCT 1501
Qy 511 AlaGlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIle 530
Db 1502 GCTGTCACTCGACATGCTTTGTAGATAATAAAGCCTTCAGACACGCGTTGATCAAAAT 1561
Qy 531 LeuGlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHis 550
Db 1562 CTTGGAAGAAGACAAATACGCTCAGATNAGAGAGCCGAGAGAAATNACAGCAGAACAC 1621
Qy 551 GluThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGln 570
Db 1622 GAGACACAGATGACCCAGCATGCTCGCCCGGTTGTGAAGTTGAGAAACAGGTCCAG 1681
Qy 571 SerIleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGly 590
Db 1682 TCCATCGAATCAAGCTGGACTGCTGCTGATATCTATCAACAGGTCCTCCGGAAGGC 1741
Qy 591 SerAlaSerAlaLeuAlaLeuAlaSerPheGlnIleProPheGluCysGluGlnThr 610
Db 1742 TCTGCTCCGCCCTCACTCTGGCATCTTTTCAGATCCCGCCTTTTGAATGTGAACAGACC 1801
Qy 611 SerAspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGly 630
Db 1802 TCTGACTATCAAGTCTCTGTGATAGCAAGACCTGTCTGGCTCAGCACAAAAACAGCGGC 1861
Qy 631 CysLeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrPro 650
Db 1862 TGTTTAAACGAGGTTCAGCCAGTCCCAACATCTCAAGAGGCTGCGAGTTCATCTTAACACCA 1921
Qy 651 AsnGluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThr 670
Db 1922 AATGAGTTCAGTGTCTCAGACTTCTATGCGGTAGCCCTACTATGCACAGCAAGCTACC 1981
Qy 671 GlnValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsn 690
Db 1982 CAGGTACCCATGAGTCAAAATGACGGCTCCTCCGTGGTAGCCACCAATAACATTGCAAAAC 2041
Qy 691 GlnIleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeu 710
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Db 2042 CAAATAAGCCGCGCACCCAGCCAGCCAGCCCAACAACTTTTACAGATCCCTCCTCCTC 2101
Qy 711 ProAlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGln 730
Db 2102 TCGGCCATCAAGCACTTGTCCAGGCCAGAACCTCTGCTCTCAAAACCCACCGGTTACAA 2161
Qy 731 GluSerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAla 750
Db 2162 GAGAGTATTTCTGATGTCACCCACCTGCTTGTGCTCCAAAGAAAGTGTTCAGTTTGCA 2221
Qy 751 GlnSerSerLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThr 770
Db 2222 CAGTCAAAACCTGACCAAGGACCGTTCCTGAGGAAAAAGTTTCGACATGGGAGGAGAACT 2281
Qy 771 LeuLeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsn 790
Db 2282 CTGTTGTCTGTCGCCCCCATGGTGGCCCAAGATTTGGCAAAATCTCTGTCTGTACAAAAC 2341
Qy 791 LeuIleArgSerThrGluGluLeuLeuAsnIleGlnLeuSerGlySerGluSerSerGlySer 810
Db 2342 CTGATCAGGTTCGACAGAAAGAACTGAACTTACAGTTTTCAGGCAGCAGTCAAGCGGCTCT 2401
Qy 811 ArgGlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGlu 830
Db 2402 CGAGGCGAGTCAAGATTTTATCCCAAGTGGAGAGATCCAAATTTGTATTAACCTGATGAG 2461
Qy 831 GluValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArg 850
Db 2462 GAGTTCGGTCCGAGAGACAGAAACAGATATCTTTGACGGCACCCACCCCTCGCGGG 2521
Qy 851 GluAlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIle 870
Db 2522 GAGGCTGCTTCTCATCAGACTCTCTAAGGACTGGAAGTCAACGCTCATCTCAGAACATT 2581
Qy 871 CysLysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeu 887
Db 2582 TGTAAGACAGAGACAGTACAGACGCGCTCAGTTTGCCTCAGCTCAAACTG 2632
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Search completed: April 3, 2005, 16:36:47

Job time : 9670.32 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model  
Run on: April 2, 2005, 23:56:51 ; Search time 1110.87 Seconds  
(without alignments)  
4732.082 Million cell updates/sec

Title: US-09-810-796-5  
Perfect score: 4547  
Sequence: 1 MOVESGRVLLNSAARG.....SICKAGESTDALSPHVKLK 888

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues  
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/cgn2\_1/usPFO spool/US09810796/runat 31032005 141120 18189/app query.fasta\_1.2126  
-DB=N\_Geneseq\_16Dec04 -QWTF=fastap -SUPFIX=ring -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=DIOSUM62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFWT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09810796 @CGN 1 1 1128 @runat 31032005 141120 18189 -NCPU=6 -ICPU=3  
-NO.MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_16Dec04:.\*  
1: geneseqn1980s:.\*  
2: geneseqn1990s:.\*  
3: geneseqn2000s:.\*  
4: geneseqn2001as:.\*  
5: geneseqn2001bs:.\*  
6: geneseqn2002as:.\*  
7: geneseqn2002bs:.\*  
8: geneseqn2003as:.\*  
9: geneseqn2003bs:.\*  
10: geneseqn2003cs:.\*  
11: geneseqn2003ds:.\*  
12: geneseqn2004as:.\*  
13: geneseqn2004bs:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4547	100.0	2667	AAS14653	Aas14653 Human cDN
2	4547	100.0	2772	Aah43633	Aah43633 Human ion
3	4547	100.0	3111	Aah43634	Aah43634 Human ion
4	4527.5	99.6	2694	AAS14652	Aas14652 Human cDN
5	4527.5	99.6	2694	AAD27192	Aad27192 Human pot

6	4527.5	99.6	3137	4	AAC85414	Human KCN
7	4523.5	99.5	3071	4	AAS14651	Human cDN
8	4513.5	99.3	3074	4	AAH49499	Human KCN
9	4513.5	99.3	3074	10	ADB78684	Human pot
10	4346.5	95.6	3718	3	AAC64371	Human KCN
11	2007.5	44.1	2335	3	AAA47618	Pot
12	2007.5	44.1	2335	10	AD831698	Human 323
13	1810	39.8	5595	13	ADSI17851	Rattus no
14	1798	39.5	7407	10	ADB78687	Human pot
15	1797	39.5	7407	10	ADB78685	Human pot
16	1797	39.5	7407	10	ADB78688	Human pot
17	1797	39.5	7407	10	ADB78686	Human pot
18	1797	39.5	7407	10	ADB78683	Human pot
19	1797	39.5	7411	10	ADD29557	Human tum
20	1797	39.5	7420	11	ADN38963	Cancer/an
21	1797	39.5	7420	11	ADP65810	Human mRN
22	1797	39.5	7420	11	ADP65731	Human pot
23	1797	39.5	7420	12	ADL06495	Human tum
24	1797	39.5	7863	10	ADJ56529	Human cDN
25	1794	39.5	3237	2	AAJ57145	Human mut
26	1792.5	39.4	3287	2	AAJ26587	Nucleotid
27	1790.5	39.4	2169	2	AAJ26588	Nucleotid
28	1790	39.4	2565	2	AAJ81548	Human bra
29	1790	39.4	3195	5	AAJ574831	DNA encod
30	1788	39.3	3232	2	AAJ57057	Human KCN
31	1788	39.3	3232	10	AAJ58489	Human pot
32	1788	39.3	3232	13	ADSI17844	Human KCN
33	1780	39.1	3232	5	AAJ574830	DNA encod
34	1775	39.0	7413	5	AAJ574832	DNA encod
35	1767	38.9	2273	2	AAJ57140	Mouse KCN
36	1762	38.8	3029	2	AAJ81547	Human bra
37	1750	38.5	4512	10	ADJ56528	Rat cDNA
38	1667.5	36.7	125910	3	AAJ64370	Human KCN
39	1611	35.4	1848	12	ADH51119	Potassium
40	1611	35.4	1848	12	ADM77995	KCNQ2-15b
41	1604	35.3	1878	12	ADH51117	Potassium
42	1604	35.3	1878	12	ADM77993	KCNQ2-15b
43	1602	35.2	1932	12	ADH51115	Potassium
44	1602	35.2	1932	12	ADM77991	KCNQ2-15b
45	1587.5	34.9	2565	2	AAJ26596	Nucleotid

ALIGNMENTS

RESULT 1  
AAS14653  
ID AAS14653 standard; cDNA; 2667 BP.  
AC AAS14653;  
XX  
DT 18-DEC-2001 (first entry)  
XX  
DE Human cDNA encoding a voltage gated potassium channel hKCNQ5-2.  
XX  
KW Human; ss; voltage-gated potassium channel; KCNQ5-2; nontropic; cerebroprotective; neurotropic; analgesic; vision disorder; central nervous system disorder; epilepsy; migraine; hearing disorder; psychotic disorder; seizure; learning disorder; memory disorder; stroke; pain; gene therapy; splice variant.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
CDS 1..2967  
FT /\*tag=a  
FT /product= "hKCNQ5-2"  
XX  
PN WO200170759-A1.  
XX  
PD 27-SEP-2001.  
XX  
PF 20-MAR-2001; 2001WO-US009328.  
XX



Qy 481 IleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThrLeuArgProTyr 500  
Db 1441 ATCAGATTATGAAATTTTCATGTTGCAAAACGGAGTTTAAGGAACCTTTACGTCCATAT 1500  
Qy 501 AspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMetLeuCysArgIle 520  
Db 1501 GATGTAAAGATGTCATTGAACAATATCTGCTGGTCATCTGGACATCTTGTGTAGAAAT 1560  
Qy 521 LysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLys 540  
Db 1561 AAAAGCCTTCAACACAGCTGTTGATCAAAATCTTGGAAAAGGCGCAATCACATCATGATAAG 1620  
Qy 541 LysSerArgGluLysIleThrAlaGluHisGluThrThrAspAspLeuSerMetLeuGly 560  
Db 1621 AAGAGCCGAGAGAAAATAACAGCAGAACATGAGACCACAGACGATCTCAGTATGTCGGT 1680  
Qy 561 ArgValValLysValGluLysGlnValGlnSerIleGluSerLysLeuAspCysLeuLeu 580  
Db 1681 CGGGTGGTCAAGTTGAAAACAGGTACAGTCCATAGAGTCCAGCTGGACTGCTACTA 1740  
Qy 581 AspleTyrGlnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPhe 600  
Db 1741 GACATCTATCAACAGCTCTTCGGAAGGCTCTGCCTCAGCCCTCGCTTTGGCTTCATTC 1800  
Qy 601 GlnIleProProPheGluCysGluGlnThrSerAspTyrGlnSerProValAspSerLys 620  
Db 1801 CAGATCCACCTTTGAATGTGAACAGACATCTGACTATCAAAAGCCCTGTGGATAGCAAA 1860  
Qy 621 AspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIle 640  
Db 1861 GATCTTCGGGTTCCGACAAAACAGTGGCTGCTTATCCAGATCACTAGTGCACATC 1920  
Qy 641 SerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAla 660  
Db 1921 TCGAGAGCCTGCAGTTCATCTCAGCCAAATAGTTCAGTGCCAGACTTTCTACGCG 1980  
Qy 661 LeuSerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySer 680  
Db 1981 CTTAGCCCTACTATGCACAGTCAAGACACACAGGTGCCAATTAGTCAAAAGCGATGGCTCA 2040  
Qy 681 AlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAla 700  
Db 2041 CGAGTGGAGCCACCAACACCATTTGCAAAACCAATTAATAGCGACCCACCCAGCAGCC 2100  
Qy 701 ProThrThrLeuGlnIleProProLeuProAlaIleLysHisLeuProArgProGlu 720  
Db 2101 CCAACAACTTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCAGGCCAGAA 2160  
Qy 721 ThrLeuHisProAsnProAlaGlyLeuGlnGluSerIleSerAspValThrThrCysLeu 740  
Db 2161 ACTCTGCACCTTAACCTTGCAGGCTTACAGGAAAAGCATTTCTGACGTCCACCCTGCCCT 2220  
Qy 741 ValAlaSerLysGluAsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMet 760  
Db 2221 GTTGCTTCCAGGAAAATGTTTCAGGTTGCACAGTCAATCTCACCAAGGACCGTTCATG 2280  
Qy 761 ArgLysSerPheAspMetGlyGlyGluThrLeuLeuSerValCysProMetValProLys 780  
Db 2281 AGSAAAAGCTTTGACATCGGAGGAGAACTCTGTGTCTGTCTGCCATGTGTCGCGAAG 2340  
Qy 781 AspLeuGlyLysSerLeuSerValGlnAsnLeulleArgSerThrGluGluLeuAsnIle 800  
Db 2341 GACTTGGCAAAATCTTTGCTGTGCAAAACCTGATCAGTGCAGCGAGGAACTGAATATA 2400  
Qy 801 GlnLeuSerGlySerGluSerSerGlySerArgGlySerGlnAspPheTyrProLysTrp 820  
Db 2401 CACTTTCCGGAGTGTGAGTCAAGTGGCTTCCAGAGCCAGCAAGATTTTATCCCAATGG 2460  
Qy 821 ArgGluSerLysLeuPheIleThrAspGluGluValGlyProGluGluThrGluThrAsp 840  
Db 2461 AGSAAATCCAAATGTTTATTAACATGATCAAGAGGTGGTCCCGAAGACAGACAGACAGAC 2520  
Qy 841 ThrPheAspAlaAlaProGlnProAlaArgGluAlaAlaPheAlaSerAspSerLeuArg 860

Db 2521 ACTTTTGATCCGACCGACCTGCCAGGAAGCTGCTTTGCATCAGACTCTCTAAGG 2580  
Qy 861 ThrGlyArgSerArgSerSerGlnSerIleCysLysAlaGlyGluSerThrAspAlaLeu 880  
Db 2581 ACTGGAAGGTCAACATCATCTCAGACGATTTGTAAGGCAGGAGAAAGTACAGATGCCCTC 2640  
Qy 881 SerLeuProHisValLysLeuLys 888  
Db 2641 AGCTTGCTCATGTCAAACTGAAA 2664  
RESULT 2  
AAH43633  
ID AAH43633 standard; cDNA; 2772 BP.  
XX  
AC AAH43633;  
XX  
DT 21-JAN-2002 (first entry)  
XX  
DE Human ion-channel forming protein ORF.  
XX  
XX Ion-channel forming protein; voltage-gated potassium channel; fetal;  
KW brain; thymus; prostate; heart; skeletal muscle; probe; ss.  
XX  
OS Homo sapiens.  
XX  
FN WO200175108-A1.  
XX  
PD 11-OCT-2001.  
XX  
PF 03-APR-2001; 2001WO-US010875.  
XX  
PR 03-APR-2000; 2000US-0194255P.  
XX  
PA (LEXI-) LEXICON GENETICS INC.  
XX  
PI Hu Y, Kleke JA, Turner AC, Nehls MC, Friedrich G, Zambrowicz B;  
PI Sands AT;  
XX  
DR WPI; 2001-656987/75.  
XX  
PT P-PSDB; AAB47678.  
XX  
XX New human ion channel protein and polynucleotides encoding the protein,  
XX useful in diagnosing or treating diseases, in drug screening, and in  
XX clinical trial monitoring.  
PS Claim 1; Page 34-35; 41pp; English.  
XX  
CC The sequences in AAH43633-34 encode a novel ion-channel forming protein.  
CC The protein shares structural similarity with mammalian ion channel  
CC proteins, particularly voltage-gated potassium channel proteins. The  
CC protein is expressed in many human cell lines including fetal brain,  
CC brain, thymus, prostate, heart and skeletal muscle. The novel protein can  
CC be used in the diagnosis or treatment of diseases, in drug screening, and  
CC in clinical trial monitoring. The oligonucleotides may be used as  
CC hybridization probes for screening libraries, and assessing gene  
CC expression patterns (particularly using a micro array or high throughput  
CC chip format). The nucleic acids and novel protein can also be used in the  
CC identification, selection and validation of novel molecular targets for  
CC drug discovery, to screen collections of genetic material from patients  
CC who have a particular medical condition, to identify mutations associated  
CC with a particular disease, as a diagnostic or prognostic assay, and to  
CC screen for drugs which can be used to treat symptomatic or phenotypic  
CC manifestations of perturbing the normal function of novel human protein.  
CC The polypeptides are further used in generating antibodies  
XX  
SQ Sequence 2772 BP; 715 A; 700 C; 713 G; 644 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 0 Length: 2772  
Score: 4547.00 Matches: 888  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.0% Indels: 0  
DB: 5 Gaps: 0  
US-09-810-796-5 (1-888) x AAH43633 (1-2772)

Qy 1 MetLysAspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaAArgGly 20  
Db 106 ATGAAGATGTGGAGTCGGCGCGGAGGAGGTCGTGCTGAACTCGGACGCGCGAGGGGC 165

Qy 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40  
Db 166 GACGCGCTGCTACTGCTGGGACCGCGCGGCCACGCTCGGTGGCGGCGGTGGCGCTG 225

Qy 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuLeuLysProLeuSer 60  
Db 226 AGGAGAGCCCGCGGGGACAGGGGCGCGGATGAGCTGCTGGGAGACCGCTCTCT 285

Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgValGlnAsnTyrLeu 80  
Db 286 TACACGAGTCCAGAGCTGCGCGCGCAACGTCAGTACCGCGGGTGCAGAACTACCTG 345

Qy 81 TyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100  
Db 346 TACAACTGCTGGAGAGACCGCGCGGCTGGCGGTTCATCTACACGCTTTCGTTTCTC 405

Qy 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu 120  
Db 406 CTGCTCTTGGTGTGCTGATTTGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 465

Qy 121 AlaSerSerCysLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe 140  
Db 466 GCCTCAAGTTCCTCTGATCTCGAGTTCGTGATGATGCTGCTGCTGCTGCTGCTGCTG 525

Qy 141 IleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu 160  
Db 526 ATCACTTCAAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 585

Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180  
Db 586 AGGTTTGTCTCGAAGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 645

Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200  
Db 646 GTTGTCTTCTGCAAACTCAGGTAATATTTTTCACGCTGCTGCTGCTGCTGCTGCTGCTG 705

Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220  
Db 706 TTCTTACAGATCCTCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 765

Qy 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTyrIleGlyPheLeu 240  
Db 766 GGTTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTG 825

Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260  
Db 826 GTTCTTATTTTTTTCGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 885

Qy 261 SerThrTyrAlaAspAlaLeuTyrTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280  
Db 886 TCTACATATGAGATGCTCTCTGTTGGGGGCAATATACATTTGCACTTTTGGCTATGGA 945

Qy 281 AsplysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300  
Db 946 GACAAAACCTCCCTAACTTGGCTGGGAAGATTGCTTTCTGCGGCTTTTTCGCTGCTGCTG 1005

Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320  
Db 1006 ATTTCTTTTCTTGGCATCTTCTGCGGCAATCTTGGCTCAGGTTTGGCAATTAAGATACAA 1065

Qy 321 GluGlnHisArgGlnLysHisPheGlyLysArgArgAsnProAlaAlaAsnLeuIleGln 340  
Db 1066 GAAACACACCGCCAGAAACACTTTGAGAAAAGAGAACCCAGCTGCGCAACTCATTCAG 1125

Qy 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360  
Db 1126 TGTGTTTGGCGTAGTTACGCGAGCTGATGAGAAATCTGTTTCCATTGCAACTGGAAGCCA 1185

Qy 361 HisLeuLysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPheLysGluArg 380  
Db 1186 CACTTGAAGGCTTTGCACACCTGCGAGCCCTACCAATCAGAAGCTTAAGTTTTTAAGAGCGA 1245

Qy 381 ValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAsp 400  
Db 1246 GTGCGCATGGCTAGCCCCAGGGCCAGAGTATTAAAGCCGACAAAGCTCTAGTAGGTGAC 1305

Qy 401 ArgArgSerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSer 420  
Db 1306 AGGAGGTCCCCAAGCACCGACATCACAGCCGAGGGCAGTCCCAACAAAGTGCAGAGAGC 1365

Qy 421 TrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerSerGlnPro 440  
Db 1366 TGGAGCTTCAACGACCGAACCCGCTTCGGCCCTCGCTGCGCTCAAAAGTTCTTCAGCCA 1425

Qy 441 LysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyrAspGluLysGly 460  
Db 1426 AACCACTGATGATGCTGACACAGCCCTTGGCACTGATGATGATGATGATGATGATGATG 1485

Qy 461 CysGlnCysAspValSerValGluAspLeuThrProLeuLysThrValIleArgAla 480  
Db 1486 TGCCAGTGTGATGTATCAGTGGAAAGACCTCACCCCAACCTTAAACCTGTCTTCAGACT 1545

Qy 481 IleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThrLeuArgProTyr 500  
Db 1546 ATCAGAAATTATGAATTTTCATGTTGCAAAACGGAAGTTTAAAGAAACATTACGTCCAT 1605

Qy 501 AspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMetLeuCysArgIle 520  
Db 1606 GATGTAAGAATGTCATTTGCAACATATTTCTGCTGCTCATCTGGACATGTTGTGTAGATT 1665

Qy 521 LysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLys 540  
Db 1666 AAAAGCCTTCAACACACGTGTTGATCAAAATCTTGAAAAGGGCAATCACATCAGATAAG 1725

Qy 541 LysSerArgGluLysIleThrAlaGluHisGluThrThrAspAspLeuSerMetLeuGly 560  
Db 1726 AAGAGCCGAGAGAAAATAACAGCAACATGAGACCAACAGATCTCAGTATCTCGGT 1785

Qy 561 ArgValLysLysValGluLysGlnValGlnSerIleGluSerLysLeuAspCysLeuLeu 580  
Db 1786 CGGTGCTCAAGTTTGAATAACAGTACAGTCCATAGATCCCAAGCTGGAGTCCCTACTA 1845

Qy 581 AsplleTyrGlnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAspPhe 600  
Db 1846 GACATCTATCAACAGGTCTCTCGAAAGGCTCTGCTCAGCCCTCGCTTTGGCTTCATTC 1905

Qy 601 GlnIleProPheGluCysGluGlnThrSerAspTyrGlnSerProValAspSerLys 620  
Db 1906 CAGATCCACCTTTTGAATGTGAACAGACATCTGACTATCAAGCCCTGTGGATAGACAA 1965

Qy 621 AspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIle 640  
Db 1966 GATCTTTTCGGGTTCCGCAACAAACAGTGGCTGCTTATCCAGATCACTAGTGCACATC 2025

Qy 641 SerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAla 660  
Db 2026 TCGAGAGCCCTGCGAGTTTCATTTCTGACGCCAAATAGTTTCAGTGGCCAGACTTTCTAC 2085

Qy 661 LeuSerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySer 680  
Db 2086 CTTAGCCCTTACTATGCAAGTCAAGCAACAGAGTGGCAATTAGTCAAGCATGGCTCA 2145

Qy 681 AlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAla 700  
Db 2146 GCAGTGGCAGCCCAACCACTTTCGAAACCAATAAATACGGCACCCAGCCAGCAGCC 2205

Qy 701 ProThrThrLeuGlnIleProProProLeuProIleLysHisLeuProArgProGlu 720

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Db 2206 CCAACAACTTTACAGATCCCACTCTCTCTCCAGCCATCAAGCATCTGCCAGGCCAGAA 2265
Qy 721 ThrLeuHisProAsnProAlaGlyLeuGlnGluSerIleSerAspValThrThrCysLeu 740
Db 2266 ACTCTGCACCTTACCTCTGAGGCTTACAGGAAGCATTTCTGAGGTCAACACCTGCTT 2325
Qy 741 VallalaSerLysGluAsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMet 760
Db 2326 GTTGCTCCAAAGGAAATGTTTCAGGTTGCAGATCAAAATCTCACCAGGACCGTTCTATG 2385
Qy 761 ArgLysSerPheAspMetGlyGlyGluThrLeuLeuSerValCysProMetValProLys 780
Db 2386 AGGAAAGCTTTGACATGGAGGAGAACTCTGTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 2445
Qy 781 AspLeuGlyLysSerLeuSerValGlnAsnLeuIleArgSerThrGluGluLeuAsnIle 800
Db 2446 GACTTGGGCAAACTCTTCTCTGTGCAAACTGATCAGTCCAGCGAGAACTGAATATA 2505
Qy 801 GlnLeuSerGlySerGluSerSerGlySerArgGlySerGlnAspPheTyProLysTrp 820
Db 2506 CAACCTTTCAGGAGTGAAGTCAAGTGGCTCCAGAGGAGCAAGATTTTATCCCAAAATGG 2565
Qy 821 ArgGluSerLysLeuPheIleThrAspGluGluValGlyProGluGluThrGluThrAsp 840
Db 2566 AGGGAATCCAAATGTTTATTAACCTGATGAAGAGGTGGTCCGGAAGACAGACAGAC 2625
Qy 841 ThrPheAspAlaAlaProGlnProAlaArgGluAlaAlaPheAlaSerAspSerLeuArg 860
Db 2626 ACTTTTGATGCGCACCGCAGCTGCCAGGAGCTGCTTGGCATCAGATCTCTAAGG 2685
Qy 861 ThrGlyArgSerArgSerGlnSerIleCysLysAlaGlyGluSerThrAspAlaLeu 880
Db 2686 ACTGGAAGTCAAGATCATCTCAGAGCATTTGTAAAGCAGGAGAAAGTACAGATGCCCTC 2745
Qy 881 SerLeuProHisValLysLeuLys 888
Db 2746 AGCTTGCTCATGTCAAACTGAAA 2769

RESULT 3
AAH43634
ID AAH43634 standard; cDNA; 3111 BP.
AC AAH43634;
XX
XX
DT 21-JAN-2002 (first entry)
XX
DE Human ion-channel forming protein coding sequence.
XX
KW Ion-channel forming protein; voltage-gated potassium channel; fetal;
KW brain; thymus; prostate; heart; skeletal muscle; probe; ss.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 59..2831
FT FT /*tag= a
FT FT /product= "Human ion-channel forming protein"
XX
XX WO200175108-A1.
XX
XX 11-OCT-2001.
XX
XX 03-APR-2001; 2001WO-US010875.
XX
XX 03-APR-2000; 2000US-0194255P.
XX
XX (LEXI-) LEXICON GENETICS INC.
XX
XX Hu Y, Kieke JA, Turner AC, Nehls MC, Friedrich G, Zambrowicz B;
XX Sands AT;
XX
XX WPI; 2001-656987/75.
```

DR P-PSDB; AAB47678.

XX New human ion channel protein and polynucleotides encoding the protein,  
PT useful in diagnosing or treating diseases, in drug screening, and in  
PT clinical trial monitoring.

XX Disclosure; Page 37-38; 41pp; English.

XX The sequences in AAH43633-34 encode a novel ion-channel forming protein.  
CC The protein shares structural similarity with mammalian ion channel  
CC proteins, particularly voltage-gated potassium channel proteins. The  
CC protein is expressed in many human cell lines including fetal brain,  
CC brain, thymus, prostate, heart and skeletal muscle. The novel protein can  
CC be used in the diagnosis or treatment of diseases, in drug screening, and  
CC in clinical trial monitoring. The oligonucleotides may be used as  
CC hybridization probes for screening libraries, and assessing gene  
CC expression patterns (particularly using a micro array or high throughput  
CC chip format). The nucleic acids and novel protein can also be used in the  
CC identification, selection and validation of novel molecular targets for  
CC drug discovery, to screen collections of genetic material from patients  
CC who have a particular medical condition, to identify mutations associated  
CC with a particular disease, as a diagnostic or prognostic assay, and to  
CC screen for drugs which can be used to treat symptomatic or phenotypic  
CC manifestations of perturbing the normal function of novel human protein.  
CC The polypeptides are further used in generating antibodies

XX Sequence 3111 BP; 814 A; 771 C; 789 G; 737 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 0 Length: 3111  
Score: 4547.00 Matches: 888  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 5 Gaps: 0

US-09-810-796-5 (1-888) x AAH43634 (1-3111)

Qy 1 MetLysAspValGluSerGlyArgGlyValLeuLeuAsnSerAlaAlaAArgGly 20  
Db 165 ATGAAGGATGTGGAGTCGGCGCGGCGAGGTGCTGTAACTCGGCAGCGCCAGGGGC 224  
Qy 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40  
Db 225 GACGGCTGTCTACTGTGGGCACCGCGCGCCACGCTCGGTGGCGGGGGGCGCTG 284  
Qy 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60  
Db 285 AGGAGAGCGCCCGGGGCGAGCAGCGGGCCCGGATGAGCTGCTGGGGAAGCCGCTCT 344  
Qy 61 TyrThrSerSerGlnSerCysArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80  
Db 345 TACACGAGTAGCAGAGCTGCGCGCGCAACGTCAGTACCGCGGGTGCAGAACTACCTG 404  
Qy 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100  
Db 405 TACAACGTGTGTGGAGAGACCCCGCGCTGGCGGTTCATCTACCAACGCTTCGTTTTCTC 464  
Qy 101 LeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120  
Db 465 CTGTCTTTGGTGTCTGATTTGTTCAGTGTTTCTACCATCCCTGAGCACACAAATTTG 524  
Qy 121 AlaSerSerCysLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe 140  
Db 525 GCCTCAAGTTGCTTGTGATCTCTGAGTTCTGATGATTGTCTTTGGTTTGGAGTTT 584  
Qy 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu 160  
Db 585 ATCATTCGAATCTGGTCTGCGGGTGTCTGTGTGTATAGAGGATGTCAGAGGAGACGTG 644  
Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180  
Db 645 AGGTTTGTCTGAAAGCCCTTCTGTGTATATAGATACCATTTGTTCTTATCGCTTCAATAGCA 704

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Qy 181 ValValSerAlaLysThrGlnGlyValAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db 705 GTTGTTTCTGCMNAACCTCAGGGTAATATTTTGGCCACGCTGCACTCAGAACTCCGT 764
Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220
Db 765 TTCTCTACAGATCCTCCGCGATGTCGCGATGGACCGAGGGAGGCACTTGGAAATTAATCTG 824
Qy 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240
Db 825 GGTTCAGTGGTTATGCTCACAGCAAGGAATTAATCACAGCTGTGTATACATAGGAATTTTG 884
Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db 885 GTTCTTAATTTTTCGTCCTTCCTGCTATCTGCTGTAATGGAAGATGCCAATAAAGAGTTT 944
Qy 261 SerThrTyrAlaAspAlaLeuTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
Db 945 TCTACATATGCAGATGCTCTCTGCTGGGCGACAATTAATTGCAACTATTGGCTATGGA 1004
Qy 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
Db 1005 GACAAACCTCCCTAACTTGGCTGGGAAGATTGCTTCTGCAGGCTTTGCACCTCCTTGGC 1064
Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db 1065 ATTCTTCTTCTGCACTTCTGCGCGCAATCTTGCTCAGGTTTGGCAATTAAGATGACA 1124
Qy 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
Db 1125 GAACAACACCGCCAGAAACACTTTGAGAAAGAGAAAGAACCCAGCTGCCAACCCTCATTCAG 1184
Qy 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
Db 1185 TGTGTTTGGCGTAGTACGCACTGATGAGAAATCTGTTCCATTGGCAACCTGGAAGCCA 1244
Qy 361 HisLeuLysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPheLysGluArg 380
Db 1245 CACTTGAAGGCTTGCACACCTGCAAGCTTACCATCAGAGCTAAGTTTAAAGAGCGCA 1304
Qy 381 ValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAsp 400
Db 1305 GTGCGCATGGGTAGCCCGCCAGGGGCGAGAGTATTAAAGCCGACAGCCCTCAGTAGGTGAC 1364
Qy 401 ArgArgSerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSer 420
Db 1365 AGGAGTCCCCAAGCACCAGCATCACAGCGGGGCGAGTCCACCCAAAGTGCAGAAAGAGC 1424
Qy 421 TrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerSerGlnPro 440
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Qy 441 LysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyrAspGluLysGly 460
Db 1485 AAACAGTGATAGATGCTGCACACAGCCCTTGGCACTGATGATATATATGATGATCAAAAGGA 1544
Qy 461 CysGlnCysAspValSerValGluAspLeuThrProProLeuLysThrValIleArgAla 480
Db 1545 TGCCAGTGTGATGATATAGTGAAGACCTCACCCGCCCTTAAACACTGTATTTCGAGCT 1604
Qy 481 IleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThrLeuArgProTyr 500
Db 1605 ATCAGAAATATGAATTTTCATGTTGCAAAACGGAAGTTTAAAGGAACATTAAGTCCATAT 1664
Qy 501 AspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMetLeuCysArgIle 520
Db 1665 GATGTAAAGATGTCAITTAAGCAATATTTCTGTGTGTCATCTGCGACATGTTGTGTAGATT 1724
Qy 521 LysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLys 540
Db 1725 AARAGCCTTCAACACAGTGTGATCAAAATTTCTTGGAAAGGGCAATCACATCAGATGAG 1784
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Qy 541 LysSerArgGluLysIleThrAlaGluHisGluThrThrAspAspLeuSerMetLeuGly 560
Db 1785 AAGAGCCGAGAGAAAATAACAGCAGAAACATGAGAACACAGACGATCTCAGTATGCTCGGT 1844
Qy 561 ArgValValLysValGluLysGlnValGlnSerIleGluSerLysLeuAspCysLeuLeu 580
Db 1845 CGGGTGGTCAAGGTTGAAAACACAGTACAGTCCATAGAAATCCAAGCTGGAGTGCCTACTA 1904
Qy 581 AspIleTyrGlnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAspPhe 600
Db 1905 GACATCTATCAACAGGCTCTTCGAAAAGGCTCTCCCTCAGCCCTCGCTTTGGCTTCATT 1964
Qy 601 GlnIleProProPheGluCysGluGlnThrSerAspTyrGlnSerProValAspSerLys 620
Db 1965 CAGATCCACCTTTTGAATGTGAACACACATCTGACTATCAAGCCCTGTGGATAGCAAA 2024
Qy 621 AspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIle 640
Db 2025 GATCTTTGGGTTCCGCACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGCACAATC 2084
Qy 641 SerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAla 660
Db 2085 TCGAGAGCCCTGCACTTCAATCTGACGCCAAATCAGATTCAAGTGCACAGACTTTCTACGC 2144
Qy 661 LeuSerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySer 680
Db 2145 CTTAGCCCTACTATGCACAGCTCAAGCAACACAGGTGCCAATTAGTCAAGCGATGGCTCA 2204
Qy 681 AlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAla 700
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Qy 701 ProThrThrLeuGlnIleProProProLeuProAlaIleLysHisLeuProArgProGlu 720
Db 2265 CCAACAACATTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCCAGGCCAGAA 2324
Qy 721 ThrLeuHisProAsnProAlaGlyLeuGlnGluSerIleSerAspValThrThrCysLeu 740
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Qy 741 ValAlaSerLysGluAsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMet 760
Db 2385 GTTGCCTCCAAAGGAAAATGTTCAAGTTGCACAGTCAAATCTCACCAGGACCGTTCTATG 2444
Qy 761 ArgLysSerPheAspMetGlyGlyGluThrLeuLeuSerValCysProMetValProLys 780
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Db 2505 GACTTTGGGCAAACTTTTGTCTGTGCAAAACCTGATCAGGTCCGACCGAGGAACCTGAATATA 2564
Qy 801 GlnLeuSerGlySerGluSerSerGlySerArgGlySerGlnAspPheTyrProLysTyr 820
Db 2565 CAATTTTCAGGGAGTGAAGTCAAGTGGCTCCAGAGGACGCCAAGATTTTATCCCAAAATGG 2624
Qy 821 ArgGluSerLysLeuPheIleThrAspGluGluValGlyProGluGluThrGluThrAsp 840
Db 2625 AGGGAATCCAAATTTGTTTAACTGATGAAGAGTGGTCCCGAAGAGACAGACAGACAGAC 2684
Qy 841 ThrPheAspAlaAlaProGlnProAlaArgGluAlaAlaPheAlaSerAspSerLeuArg 860
Db 2685 ACTTTTGTATGCGCACCGCAGCTGCCAGGGAAGCTGCCCTTTTGCATCAGACTCTCTAAGG 2744
Qy 861 ThrGlyArgSerArgSerSerGlnSerIleCysLysAlaGlyGluSerThrAspAlaLeu 880
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Qy 881 SerLeuProHisValLysLeuLys 888
Db 2805 AGCTTGGCTCATGTCAAACTGAAA 2828
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RESULT 4





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QY 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
Db 1021 TGTGTTTGGCGTAGTTACGAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080
QY 361 HisLeuLysAlaLeuHisThrCysSerProThr----- 371
Db 1081 CACTTTGAAGGCGCTTCACACCTCGAGCCCTACCAAGAAAGAACCAAGGGGAAGCATCAAGC 1140
QY 372 AsnGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 391
Db 1141 AGTCAGAAGCTAAGTTTTAGGAGCGAGTGGCATGGCTAGCCCGAGGGGCGAGAGTAAT 1200
QY 392 LysSerArgGlnAlaSerValGlyAspArgSerProSerThrAspIleThrAlaGlu 411
Db 1201 AAGAGCCGACAAAGCCTCAGTAGTGCACAGGAGTCCCAAGCACCAGCATCACAGCCGAG 1260
QY 412 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 431
Db 1261 GGCAAGTCCCAACCAAGTGCAGAAGAGCTGGAGCTTCAACGACCGAACCCGCTTCGGGCC 1320
QY 432 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 451
Db 1321 TCGCTGCCCTCCAAAGTTCTCAGCCAAACACGATGATAGTGTGACACAGCCCTTGGC 1380
QY 452 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 471
Db 1381 ACTGATGATGATATGATGAAAGAGATGCCAGTGTGATGTATCAGTGGAAAGACCTCAC 1440
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QY 612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
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QY 632 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651
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QY 652 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671
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Db 2161 GCCATCAAGCATCTGCCAGCCAGCAAACTCTGCACCCCTAACCCCTGAGGCTTACAGAA 2220
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QY 872 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 888
Db 2641 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAA 2691
RESULT 5
RAD27192
ID AAD27192 standard; cDNA; 2694 BP.
XX
AC AAD27192;
DT
DT 09-APR-2002 (first entry)
XX
DE Human potassium channel polypeptide, KCNQ5 cDNA.
XX
KW Human; potassium channel polypeptide; KCNQ5; pain; migraine; stroke;
KW dementia; trauma; epilepsy; seizure; amyotrophic lateral sclerosis; ALS;
KW multiple sclerosis; MS; Parkinson's disease; ataxia; depression;
KW anxiety disorder; bipolar disorder; sleep disorder; eating disorder;
KW addiction; myokymia; Alzheimer's disease; age-associated memory loss;
KW learning deficiency; cognitive disorder; motor disease; neuron disease;
KW neurophysiological disorder; neuropsychological disorder; asthma;
KW neuron cell death; brain tumour; gene therapy; antitense therapy;
KW synaptic transmission; electrical excitability; ss.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
CDS 1..2694
/*tag= a
/product= "Human KCNQ5 protein"
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W0200192526-Al.

06-DEC-2001.

24-MAY-2001; 2001WO-US017314.

26-MAY-2000; 2000US-0207389P.

XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX Doretzky SI, Ramanathan CS, Trojnecki JT, Boiesard CG;  
 PI Gribkoff VK;  
 XX  
 DR WPI: 2002-122069/16.  
 DR P-PSDB; AAE16599.  
 XX  
 PT Novel potassium channel polypeptide, KCNQ5 and polynucleotide encoding  
 PT it, for diagnosing, treating and identifying modulators useful in  
 PT treating neurological, neuropsychological and neuropsychological  
 PT diseases.  
 XX  
 PS Claim 3; Fig 1; 128pp; English.  
 XX  
 CC The invention relates to potassium channel polypeptides referred to as  
 CC KCNQ5 and nucleic acid molecules encoding such polypeptides. KCNQ5  
 CC polypeptides are useful for identifying compounds that modulate their  
 CC biological activity. The compounds identified and KCNQ5 polynucleotides  
 CC are useful for treating acute and chronic pain, migraine, acute stroke,  
 CC dementia, trauma, epilepsy, seizure, amyotrophic lateral sclerosis (ALS),  
 CC multiple sclerosis (MS), Parkinson's disease, ataxia, anxiety disorders,  
 CC depression, bipolar disorders, sleep disorders, eating disorders,  
 CC addiction, myokymia, Alzheimer's disease, age-associated memory loss,  
 CC learning deficiencies, cognitive disorders and motor neuron diseases. The  
 CC nucleic acid molecules of the invention are further useful for treating  
 CC neuropsychological, neuropsychological disorders, asthma, neuron cell  
 CC death and brain tumours. They are also used in gene therapy and antisense  
 CC therapy. KCNQ5 polypeptides modulate synaptic transmission and electrical  
 CC excitability in the brain and are useful for generating antibodies. They  
 CC are also useful to affinity purify biological effectors from biological  
 CC materials e.g. disease tissues or cells. The present sequence is human  
 CC KCNQ5 cDNA  
 XX  
 SQ Sequence 2694 BP; 714 A; 671 C; 669 G; 640 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 0 Length: 2694  
 Score: 4527.50 Matches: 887  
 Percent Similarity: 99.00% Conservative: 1  
 Best Local Similarity: 98.89% Mismatches: 0  
 Query Match: 99.57% Indels: 9  
 DB: 6 Gaps: 1

US-09-810-796-5 (1-888) x AAD27192 (1-2694)

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Qy	141	IleIleArgIleTrpSerAlaGlyCysCysCysArgTyrArgGlyTrpGlnGlyArgLeu	160
Db	421	ATCATTCGAATCTGCTGTCGGGTTGCTGTGTGATATAGAGGATGCAAGGAAGACTG	480
Qy	161	ArgPheAlaArgLysProPheCysValIleAspThrIleValIleAlaSerIleAla	180
Db	481	AGGTTTGCCTGAAAGCCCTCTCTGTTATATAGATACCATTTGTTTATCGCTTCAATAGCA	540
Qy	181	ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg	200
Db	541	GTTGTTTCTGCAAAAACCTCAGGGTAATATATTTTCCACGCTCTGCACCTCAGAACTCCGT	600
Qy	201	PheLeuGlnIleLeuArgMetValArgMetAspArgGlyGlyThrTrpLysLeuLeu	220
Db	601	TTCTACAGATCTCCGTCATGTCGATGACCGAAGGGGAGGCATTTGAAATTAATCTG	660
Qy	221	GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu	240
Db	661	GGTTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCAGCTTGGTACATAGGATTTTG	720
Qy	241	ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe	260
Db	721	GTTCTTATTTTTCGTTCTTCTTCTGCTATCTGTTGGTGAAGGATGCCAATAAAGATTT	780
Qy	261	SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly	280
Db	781	TCTACATATGAGATGCTCTCTGCTGGGGCAACATTAATGACAACTATTGGCTATGGA	840
Qy	281	AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly	300
Db	841	GACAAAACTCCCTTAACCTGGCTGGGAAGATTTGCTTCTGCAGGCTTTGCACTCCTTGGC	900
Qy	301	IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln	320
Db	901	ATTTCTTTCTTTCGACTTCTCGCGGCATCTTGGCTCAGGTTTTCATTAAGTACAA	960
Qy	321	GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln	340
Db	961	GAACAACACCCAGAACACTTTTGAGAAAAGAGAACCCAGCTGCCAACCCTCATTCAG	1020
Qy	341	CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro	360
Db	1021	TGTGTTGGCGTAGTTAGCGAGCTGATGAGAAATCTGTTCCATTTGCAACCTGGAAGCCA	1080
Qy	361	HisLeuLysAlaLeuHisThrCysSerProThr	371
Db	1081	CACTTGAAGGCTTTCACACCTCGAGCCCTACCAAGAAAGAACAGGGAAGCATCAAGC	1140
Qy	372	AsnGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle	391
Db	1141	AGTCAGAAGCTTAAGTTTAAAGAGCGAGTGGCATGGCTAGCCCGGAGGCGCAGAGTATT	1200
Qy	392	LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu	411
Db	1201	AAGAGCCGACAAAGCTCAGTAGGTGACAGGAGGTCCCAAGCACCGACATCACAGCCGAG	1260
Qy	412	GlySerProThrLysValGlnLysSerTyrSerPheAsnAspArgThrArgPheArgPro	431
Db	1261	GGCAGTCCCAACCAAGTGCAGAAAGCTGGAGCTTCAACGACCGNACCCGCTTCGGGCC	1320
Qy	432	SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly	451
Db	1321	TCGCTGGCGCTCAAAAGTTCTCAGCCAAAACCAAGTATAGATGCTGACACAGCCCTTGGC	1380
Qy	452	ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr	471
Db	1381	ACTGATGATGATATGATGAAAAAGGATGCCAGTGTGATGATGATGATGATGATGATGATG	1440
Qy	472	ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg	491
Db	1441	CCACCATTAACCTGTCATTCGAGGCTATCAGAAATTTCAATTTTCATTTGCAAAACGG	1500

Qy 492 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 511  
Db 1501 AAGTTTAAGGAAACGTTACGTCATATGATGTAAAGATGTCATTGAACATATTCGCT 1560  
Qy 512 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 531  
Db 1561 GGTCACTCGGACATGTTGTGTAGAAATTAAGAGCCCTCAACACACGCTGTTGATCAAAATCTT 1620  
Qy 532 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 551  
Db 1621 GGAAGAGGCAATCACATCAGATAGAGAGCGAGAGAAATAACACAGACATGAG 1680  
Qy 552 ThrThrAspAspLeuSerMetLeuGlyArgValLysValGluLysGlnValGlnSer 571  
Db 1681 ACCACAGACGATCTCAGTATGTCGGTGGGTGCTCAAGGTTGAAACACGATACAGTCC 1740  
Qy 572 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 591  
Db 1741 ATAGAGTCCAAAGCTGGACTGCTACTAGACATCTATCAACAGGTCCTTCGGAAGGCTCT 1800  
Qy 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 611  
Db 1801 CCTCAGCCCTCGCTTGGCTTCATCTCCAGATCCACCTTTTGATGTGAACACACATCT 1860  
Qy 612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631  
Db 1861 GACTATCAAGCCCTGTGTAGTAAAGATCTTTCCGGTTCGACACAAACAGTGGCTGC 1920  
Qy 632 LeuSerArgSerThrSerAlaAsnIleSerArgLysLeuGlnPheIleLeuThrProAsn 651  
Db 1921 TTATCCAGATCACTAGTGCACCAATCTCGAGAGCCCTGCAAGTTTCATTCTGACGCCAAAT 1980  
Qy 652 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671  
Db 1981 CAGTTCAAGTCCAGACCTTTCTACGGCTTAGCCCTACTATGCAGTCAAGCAACACAG 2040  
Qy 672 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 691  
Db 2041 GTGCCAATTAGTCAAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTTGCAACCAA 2100  
Qy 692 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro 711  
Db 2101 ATAATACGGCACCCCAAGCCAGACGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2160  
Qy 712 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 731  
Db 2161 GCCATCAGCATCTGCCAGCCGCAAACTCTGCACCTTAACCTGCAGGCTTACAGGAA 2220  
Qy 732 SerLeSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 751  
Db 2221 AGCATTTCTGACGTCACCACTGCTTGTGCTTCCAAAGGAAATGTTTCAGGTTGCACAG 2280  
Qy 752 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 771  
Db 2281 TCAATCTCACAGGACCGTTCTATAGGAAAAGCTTTGACATGGGAGGAGAACTCTG 2340  
Qy 772 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 791  
Db 2341 TTGTCGTCTGCTCCATGTCGCGAGGACCTTGGGCAATCTTTGCTGTGTCGCAAACTCTG 2400  
Qy 792 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGlySerGlySerArg 811  
Db 2401 ATCAGTCCGACCGAGAACTGAATATACAACTTTTCCAGGAGTGAGTCAAGTGGGTCCAGA 2460  
Qy 812 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 831  
Db 2461 GGCAGCCCAAGATTTTACCCCAATGGAGGGAATCCAAATTTGTTATTAACATGATGAAGAG 2520  
Qy 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 851  
Db 2521 GTGGTCCCGAAGACAGACAGACACACTTTTGATGCCGACCCGACCTGCCAGGAA 2580

Qy 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerGlnSerIleCys 871  
Db 2581 GCTGCTTTGCATCAGACTCTCTAAGGACTGGAAGTCAAGTCAATCATCTCAGAGCATTTGT 2640  
Qy 872 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 888  
Db 2641 AAGCAGAGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAA 2691  
RESULT 6  
AAC85414  
ID AAC85414 standard; cDNA; 3137 BP.  
XX  
AC AAC85414;  
XX  
DT 20-APR-2001 (first entry)  
XX  
DE Human KCNQ5 potassium channel subunit coding sequence.  
XX  
KW Human; KCNQ5; heteromeric channel; chromosome 6; Parkinson's disease;  
central nervous system; CNS; Alzheimer's disease; anxiety; ataxia;  
CNS damage; trauma; stroke; neurodegenerative illness; schizophrenia;  
compulsive behaviour; dementia; depression; Huntington's disease; mania;  
memory impairment; memory dysfunction; spinal cord damage; phobia;  
pick's disease; psychosis; stroke; tremor; seizure; convulsion; epilepsy;  
ds.  
KW  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..2694  
FT /\*tag= a  
FT /product= "KCNQ5 subunit"  
XX  
PN WO200077035-A2.  
XX  
DD 21-DEC-2000.  
XX  
PF 29-MAY-2000; 2000WO-DK000289.  
XX  
PR 11-JUN-1999; 99DK-00000828.  
XX  
PA (NEUR-) NEUROSEARCH AS.  
XX  
PI Jentsch TJ;  
XX  
DR WPI; 2001-080678/09.  
XX  
DR P-PSDB; AAB47046.  
XX  
PT Novel genes encoding KCNQ5 potassium channel subunits, useful for  
treating Alzheimer's disease, anxiety, ataxia, stroke, dementia,  
depression, Huntington's disease, schizophrenia and Parkinson's disease.  
XX  
PS Claim 2; Page 44-48; 50pp; English.  
XX  
CC This sequence encodes the human KCNQ5 protein. The KCNQ5 protein forms  
heteromeric channels with other KCNQ channel subunits, in particular  
KCNQ3 and KCNQ4. The KCNQ5 gene has been localised to the long arm of  
chromosome 6 (6q14). Chemicals which have the ability to bind to KCNQ5  
are useful for diagnosis, treatment, prevention or alleviation of  
diseases related to diseases or adverse conditions of the central nervous  
system (CNS), including affective disorders, Alzheimer's disease,  
anxiety, ataxia, CNS damage caused by trauma, stroke or neurodegenerative  
illness, cognitive deficits, compulsive behavior, dementia, depression,  
Huntington's disease, mania, memory impairment, memory disorders, memory  
dysfunction, motion disorders, motor disorders, neurodegenerative  
diseases, Parkinson's disease and Parkinson-like motor disorders,  
phobias, pick's disease, psychosis, schizophrenia, spinal cord damage,  
stroke, tremor, seizures, convulsions and epilepsy  
XX  
SQ Sequence 3137 BP; 865 A; 749 C; 745 G; 778 T; 0 U; 0 Other;  
Alignment Scores: 0 Length: 3137  
Pred. No.: 0

Score: 4527.50 Matches: 887  
Percent Similarity: 99.00% Conservative: 1  
Best Local Similarity: 98.89% Mismatches: 0  
Query Match: 99.57% Indels: 9  
DB: 4 Gaps: 1

US-09-810-796-5 (1-888) x AAC85414 (1-3137)

Qy 1 MetLysAspValGluSerGlyArgGlyValLeuLeuAsnSerAlaAlaAargGly 20  
Db 1 ATGAAGAGATGTGGAGTCGGCGCGGAGGAGTGTCTGTAACCTCGGAGCGCGGAGGCG 60

Qy 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40  
Db 61 GACGCGCTGCTACTGCTGGGACCGCGCGCGGCGGAGTGTCTGCGGCGGCGGCGGCTG 120

Qy 41 ArgGluSerArgGlyGlyGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60  
Db 121 AGGGAGACCGCGGCGGAGGAGGCGGCGGAGGAGGCGGAGGAGGCGGAGGAGGCGG 180

Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgValGlnAsnTyrLeu 80  
Db 181 TACACGAGTAGCAGAGTCGCGCGCGCAACGTCAAGTACCGCGCGGTCGCAAGACTAC 240

Qy 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100  
Db 241 TACACGCTGCTGGAGAGACCGCGCGGCTGGGCGTTTCATCTACCGAGCTTCGTTTTCTC 300

Qy 101 LeuValPheGlyCysLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120  
Db 301 CTGTGCTTTGGTGTCTGATTTGTGCTGTTTCTACCATCCCTGAGCAGCACAAATG 360

Qy 121 AlaSerSerCysLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe 140  
Db 361 GCCTCAAGTGTCTCTGATCTCGAGTTCGTGATGATGTCTCTCTTTGGAGTTC 420

Qy 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160  
Db 421 ATCATTCGAATCTGCTGCGGGTGTCTGTGTCGATATAGAGGATGCAAGGAGACTG 480

Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuLeuAlaSerIleAla 180  
Db 481 AGTTTGTCTGAAAGCCCTTCGTGTTATAGATACCATTTGTTATTCGCTTCAATAGCA 540

Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200  
Db 541 GTTGTCTGCAAAACTCAGGTAATATTTTGGCCAGTCTGCACTCAGAACTCTCGT 600

Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220  
Db 601 TTCCTACAGATCCTCCGATGTCGCGATGAGCCGAGGAGGAGGAGGAGGAGGAGGAG 660

Qy 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240  
Db 661 GGTTCAGTGGTTTATGCTCACAGCAAGAAATTAATCACAGCTTGTGTATAGGATTTTG 720

Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260  
Db 721 GTTCTATTTTTCGTTCT 780

Qy 261 SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280  
Db 781 TCTACATATGAGATGCTCTCTGTTGGGCGCAATTAATTAATTAATTAATTAATTAAT 840

Qy 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300  
Db 841 GACAAACTCCCTTAACCTGGGAGAGATGCTTCTCTGAGGCTTTCGACTCTCTCTGCG 900

Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320  
Db 901 ATTTCTTTCTTGCACTTCTCTGCGGATCTTCTGCTCAGGTTTTCATTAATAAGTACA 960

Qy 321 GluGlnHisArgGlnLysPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340

Db 961 GAACAACACCGCCAGAAACACTTTTGAGAAAAGAGAACCCAGCTGCCAACCTCATTTAG 1020

Qy 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360

Db 1021 TGTGTTTGGCGTAGTTACGACGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCCA 1080

Qy 361 HisLeuLysAlaLeuHisThrCysSerProThr----- 371

Db 1081 CACTTGAAGGCTTTGCACACCTGCAGCCCTACCAAGAAAGAACCAAGGGAAGCATCAAGC 1140

Qy 372 AsnGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 391

Db 1141 AGTCAGAGCTTAAGTTTTTAAGGAGCGAGTGGCGCATGCTAGCCCCAGGGGCGCAGATAT 1200

Qy 392 LysSerArgGlnAlaSerValGlyAspArgSerProSerThrAspIleThrAlaGlu 411

Db 1201 AAGAGCGCACAAAGCTCAGTAGGTGACAGGAGGTCCCCACAGCACCGACATCACAGCGAG 1260

Qy 412 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 431

Db 1261 GGCAGTCCCAAGTGCAGAGAGCTGGAGCTTCAACGACCGAACCCGCTTCGGGCCC 1320

Qy 432 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 451

Db 1321 TCGCTGCGCTCAAAAGTCTCAGCCAAACCCAGTAGATGCTGACACAGCCCTTGGC 1380

Qy 452 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 471

Db 1381 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440

Qy 472 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 491

Db 1441 CCACCCTTAAACTGTCAATTCGAGCTATCAGAAATTTATGAAATTTTCATGTTGCAAAACGG 1500

Qy 492 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 511

Db 1501 AAGTTAAGGAAACATTCAGTCCATATGATGATGATGATGATGATGATGATGATGATGAT 1560

Qy 512 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 531

Db 1561 GGTCACTCGACATGTTGTGTAGAAATTAAGCCCTTCAACACAGCTGTGTGATCAAAATCTT 1620

Qy 532 GlyLysGlyGlnIleThrSerAspLysSerArgGluLysIleThrAlaGluHisGlu 551

Db 1621 GGAAAAGGCGCAATCACATCAGATAAGAGAGCGGAGAGAAATAACACAGACAGACATGAG 1680

Qy 552 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 571

Db 1681 ACCACAGACGATCTCAGTATGCTCGGTGGGTGCTCAAGGTTGAAAGAACAGGTACAGTCC 1740

Qy 572 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 591

Db 1741 ATAGATCCAGCTGGAGTGCCTACTAGACATCTATCAACAGGTCCTTCGGAAAGGCTCT 1800

Qy 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 611

Db 1801 GCCTCAGCCCTCGCTTGGCTTCATTCAGATCCACCTTTTGAATGTGAACAGACATCT 1860

Qy 612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631

Db 1861 GACTATCAAGCCCTGTGGATAGCAAGATCTTTCGGGTCCGACAAACAGAGTGGCTGC 1920

Qy 632 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651

Db 1921 TTATCCAGATCAACTAGTGCCAACTCTCGAGAGGCTGCAGTTCATCTTCAGCGCAAT 1980

Qy 652 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671

Db 1981 GAGTTTCAGTCCGACACTTTCAGCGCTTACGCTTACTATGACAGTCAAGCAACACAG 2040

Qy 672 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 691

Db 2041 GTGCCAATTAGTCAAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCAATTCGCAACCAA 2100  
Qy IleAenThrAlaProLysProAlaAlaProThrThrThrLeuGlnIleProProLeuPro 711  
Db 2101 ATAAATACGGACCCACAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2160  
Qy AlaIleLysHisLeuProArgProGluThrLeuHisProAenProAlaGlyLeuGlnGlu 731  
Db 2161 GCCATCAAGCATCTGCCAGGCCAGAAACTCTGCACCCCTAACCTCTGCAGGCTTACAGGAA 2220  
Qy SerIleSerAspValThrThrCysLeuValAlaSerLysGluAenValGlnValAlaGln 751  
Db 2221 AGCATTTCTGACGTCAACACTGCTTCTGCTCCAAAGGAAATGTTCAAGTTGCAAG 2280  
Qy SerAenLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 771  
Db 2281 TCNAATCTCACAGGACCGTTCTATGAGGAAGCTTTGACATGGGAGGAGAACTCTG 2340  
Qy LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAenLeu 791  
Db 2341 TTGCTGTCTCTCCCATGTCGCGAAGGACTTGGCAAAATCTTTGCTGTGCAAAACCTG 2400  
Qy IleArgSerThrGluGluLeuAenIleGlnLeuSerGlySerGluSerSerGlySerArg 811  
Db 2401 ATCAGGTCGACCGAGGAAGCTGAATATACAACTTTTCAGGAGTGAAGTCAAGTGGCTCCAGA 2460  
Qy GlySerGlnAspPheTyrProLysTyrArgGluSerLysLeuPheIleThrAspGluGlu 831  
Db 2461 GGCAGCCAAATTTTACCCCAATGAGGAGAAATCCAAATGTTTATTAACATGATGAAG 2520  
Qy ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 851  
Db 2521 GTGGTCCCGAAGACAGACAGACACACTTTTGATGCCGACCGAGCCCTGCCAGGAA 2580  
Qy AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 871  
Db 2581 GCTGCTTTGATCAGACTCTCTAAGGACTGGAAGGTCAAGATCATCTCAGAGCATTTGT 2640  
Qy LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 888  
Db 2641 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAA 2691

## RESULT 7

AAS14651  
ID AAS14651 standard; cDNA; 3071 BP.  
XX  
AC AAS14651;  
XX  
DT 18-DEC-2001 (first entry)  
XX  
DE Human cDNA for voltage gated potassium channel hKCNQ5.  
XX  
KW Human; ss; voltage-gated potassium channel; hKCNQ5; nontropic;  
KW cerebroprotective; neurotropic; analgesic; vision disorder;  
KW central nervous system disorder; epilepsy; migraine; hearing disorder;  
KW psychotic disorder; seizure; learning disorder; memory disorder; stroke;  
KW pain; gene therapy.  
XX  
OS Homo sapiens.  
XX  
FN WO200170759-A1.  
XX  
PD 27-SEP-2001.  
XX  
PF 20-MAR-2001; 2001WO-US009328.  
XX  
PR 21-MAR-2000; 2000US-0190954P.  
XX  
PA (ICAG-) ICAGEN INC.  
XX  
PI Jegla TJ;  
XX  
PI WPI; 2001-611467/70.  
DR

XX Polypeptides and polynucleotides of potassium channel KCNQ5 for  
PT identifying a compound modulating ion flux in eukaryotic cell or cell  
PT membrane expressing the protein, comprises KCNQ approximately alpha-subunits.  
XX  
PS Claim 5; Page 61-62; 78pp; English.

XX The invention relates to an isolated polypeptide comprising an alpha-  
subunit of a KCNQ potassium channel, with a subsequence having 65%  
sequence identity to amino acids 343-640 of hKCNQ5-1 amino acid sequence  
and forms a KCNQ potassium channel having the characteristic of voltage-  
gating with at least an additional KCNQ alpha-subunit. Also included in  
the scope of the invention are the nucleic acids encoding hKCNQ5  
(including splice variants encoding hKCNQ5-1 and hKCNQ5-2), expression  
vectors encoding them, antibodies against them, the use of 3-dimensional  
computer modelling to identify molecules that bind to a KCNQ containing  
potassium channel and modulate ion flux through the channel. The KCNQ  
polypeptide is useful for identifying a compound that increases or  
decreases ion flux through a potassium channel expressed in an eukaryotic  
host cell or cell membrane. The compound (and the KCNQ nucleic acid when  
used in gene therapy) is useful as a pharmaceutical agent for treating  
diseases involving abnormal ion flux, such as disorders of the central  
nervous system, such as epilepsy, migraines, hearing and vision problems,  
psychotic disorders, seizures, learning and memory disorders, stroke and  
pain. The antibodies are useful for detecting a KCNQ5 polypeptide in a  
human tissue and the use of a nucleotide sequence of KCNQ5 to search  
computer databases to find variants of the sequence which are associated  
with disease states, is useful for screening mutations of KCNQ5. The  
present sequence is a representative cDNA for hKCNQ5

SQ Sequence 3071 BP; 849 A; 734 C; 737 G; 750 T; 0 U; 1 Other;

## Alignment Scores:

Pred. No.:	0	Length:	3071
Score:	4533.50	Matches:	886
Percent Similarity:	98.89%	Conservative:	1
Best Local Similarity:	98.77%	Mismatches:	1
Query Match:	99.48%	Indels:	9
DB:	4	Gaps:	1

US-09-810-796-5 (1-888) x AAS14651 (1-3071)

Qy	1	MetLysAspValGluSerGlyArgGlyArgValLeuLeuAenSerAlaAlaAArgGly	20
Db	10	ATGAAGATGTGGAGTCGGCCGGGCGAGGCTGTCTGAACCTCGCAGCGCCGAGGCG	69
Qy	21	AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGly	40
Db	70	GACGGCTGTCTACTGTGGGACCCCGCGGCCACGCTTGTGGCGGGTGGCTG	129
Qy	41	ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer	60
Db	130	AGGAGAGCCCGCGGCGCAGCAGGCGCCGGATGAGCTGTGGGAGCCCTCTCT	189
Qy	61	TyrThrSerSerGlnSerCysArgAsnValLysTyrArgValGlnAenTyrLeu	80
Db	190	TACACGAGTAGCCAGAGCTGCCGCGCAAGCTCAAGTACCGCGGGTGCAGAACTACCTG	249
Qy	81	TyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu	100
Db	250	TACAACTGTGTGGAGACCCCGCGGCTGGCGGTTCATCTACCACTTTCGTTTTCTC	309
Qy	101	LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu	120
Db	310	CTTGTCTTTGGTTGCTTGATTTTGTCACTGTCTTCTACCATCCCTGAGCAGCAAAATTG	369
Qy	121	AlaSerSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe	140
Db	370	GCCTCAAGTTGCCTCTTGAATCTGGAGTTCGTGATGATTCGTCTTTGGTGGAGTTC	429
Qy	141	IleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu	160
Db	430	ATCATTCGAATCTGCTCGGGTTGCTGTGTTCGATATAGAGATGAGGAGGAGACTG	489

Qy	161	ArgPheAlaArgLysProPheCysValIleAspThrIleValleuIleAlaSerIleAla	180
Db	490	AGGTTTCTCGAAAGCCCTTCTGTGTATAGATACCAATCTGTCTTATCGCTCAATAGCA	549
Qy	181	ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg	200
Db	550	GTTGTCTTCGAAANAATCAGGGTAAATATTTTGCACGCTCTGCACATCAGAAGTCTCCGT	609
Qy	201	PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu	220
Db	610	TTCTCTACAGATCCTCCGCATGGTCGCATGGACCGAAGGGGAGGCACCTTGGAAATTACTG	669
Qy	221	GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu	240
Db	670	GGTTCACTGGTGTATAGTCTCAGCAAGGAATTAATCACAGCTTGGTATACATAGGATTTTGT	729
Qy	241	ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe	260
Db	730	GTTCTTATTTTTTTCGTTCTTCTTCCTGTCTCTCTGTGTGGAAAGGATGCCAATAAAGAGTTT	789
Qy	261	SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly	280
Db	790	TCTACATATGCAGATGCTCTCTGGTGGGCACAATTAATACATTGACAACTATTGGCTATGGA	849
Qy	281	AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly	300
Db	850	GACAAAACTCCCTTAACCTGGCTGGGAAGATTGCTTTCTCAGCGCTTTGCACCTCCTTGGC	909
Qy	301	IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln	320
Db	910	ATTTCTTTCTTTGGCACTTCTTCGCCGGCATTTCTTGGCTCAGGTTTGGATTTAAAGATACAA	969
Qy	321	GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln	340
Db	970	GAACAACACCGCCAGAAACACTTTTGAGAAAGAAAGGAACCCAGCTGCCAACCTCATTTCAG	1029
Qy	341	CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro	360
Db	1030	TGTTGTTGGCGTAGTTACGACGCTGATGAGAAATCTCTTTCCATTGCAACTCGGAAGCCA	1089
Qy	361	HisLeuLysAlaLeuHisThrCysSerProThr-----	371
Db	1090	CACTTGAAGGCCTTGCAACCTGCAGCCCTTACCAGAAAGAACACAGGGGAAGCATCMAGC	1149
Qy	372	AsnGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle	391
Db	1150	AGTCAAGAACTAAGTTTTTAAGACGCGAGTGCGCATGGCTAGCCCAAGCGGCCAGAGTATT	1209
Qy	392	LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu	411
Db	1210	AAGAGCCGACAAAGCCTCAGTAGGTGACAGAGAGTCCCAAGCACCGGCACATCAGCGCGAG	1269
Qy	412	GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro	431
Db	1270	GGCAGTCCCAACCAAGTGCAGAGAGCTGGAGCTTCAACGCCGAACCCGCTCCGGCCCC	1329
Qy	432	SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly	451
Db	1330	TCGCTGGCGCTCAAAAGTTCTCAGCCAAAACCCAGTAGATAGATGCTGACACAGAGCCCTTGGC	1389
Qy	452	ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr	471
Db	1390	ACTGATGATGATATGATGAAAAAGGATGCCAGTGTATGATGATGAGGAAGACCTCACC	1449
Qy	472	ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg	491
Db	1450	CCACCACTTAAATCTGTCATCTCGAGCTATCAGAAATTAGAAATTTCATGTTGCAAAACGG	1509
Qy	492	LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla	511
Db	1510	AAGTTTAAAGAAA CRTTACGTGCCATATGATGATAAAGATGTCATTGAACAAATATCTGCT	1569

Qy	512	GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu	531
Db	1570	GGTCATCTGCAGCATGTTGTGTAGAAATTAAGAAGCCTTCAAAACACGCTGTGATCAAAATTCCT	1629
Qy	532	GlyLysGlyGlnIleThrSerAspLysLysSerArgGlyLysIleThrAlaGluHisGlu	551
Db	1630	GGAAAAGGGCAATCACATCAGATAGAGAGCCGAGAGAAATATACAGCGAACAATCAG	1689
Qy	552	ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGlyLysGlnValGlnSer	571
Db	1690	ACCACAGCAGATCTCAGTATGCTCGGTGCGGTGAGTCAAGGTGTAAGAAACAGGTACAGTCC	1749
Qy	572	IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer	591
Db	1750	ATAGAATCCAAAGCTGGAGTCCTCCTACTAGACATCTATCAACAGGTCTCTTCGGAAGGCTCT	1809
Qy	592	AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer	611
Db	1810	GCCTCAGCCCTCGCTTGTGGCTTCATTCAGTTCACACTTCCACCTTTGATGTGAACAGACATCT	1869
Qy	612	AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys	631
Db	1870	GACTATCAAAAGCCCTGTGGATAGCAAAAGATCTTTTCGGGTTCCGCACAAAACAGTGGCTGC	1929
Qy	632	LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn	651
Db	1930	TTATCCAGATCAACTAGTGGCAACATCTCAGAGGCCCTGCAGTTTCATTTGACGCCAAAT	1989
Qy	652	GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln	671
Db	1990	GAGTTCTAGTGGCCAGACTTCTACGCCCTTAGCCCTACTATGCACAGTCAAGCAACACAG	2049
Qy	672	ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln	691
Db	2050	GTGCCAATTAGTCAAGGGATGGCTCAGCAGTGGCAGCCACCAACCACTTGCAAAACCAA	2109
Qy	692	IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro	711
Db	2110	ATAAATACGGCACCCCAAGCCAGCAGCAGCCCAACAACTTTTACAGATCCCACTCTCTCCCA	2169
Qy	712	AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu	731
Db	2170	GCCATCAAGCATCTGCCAGCCAGAAACTCTGCACCTTAACCTTGAGGCTTACAGGAA	2229
Qy	732	SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln	751
Db	2230	AGCATTTCTGACGTCAACACTGCCTGTTGGCTCCAAAGGAAATGTTTCAGTTGCACAG	2289
Qy	752	SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu	771
Db	2290	TCAAATCTCAACCAAGGACCGTTCTATCAGGAAAGACTTTGACATGGGAGAGAAACTCTG	2349
Qy	772	LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu	791
Db	2350	TTGTCTGTCTGTCATGTGGTCCGAGAGACTTTGGCAAAATCTTTTGTCTGTGCAAAACCTG	2409
Qy	792	IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg	811
Db	2410	ATCAGTGTCCAGGAGAACTGAATATACAACCTTCAGGGAGTGAGTCAAGTGGCTCCAGA	2469
Qy	812	GlySerGlnAspPheTyrProLysTyrArgGluSerLysLeuPheIleThrAspGluGlu	831
Db	2470	GGCAGCCAAAGATTTTATCCCCMAATGAGGGAAATCCAAATTTGTTTATAACTGATGAAGAG	2529
Qy	832	ValGlyProGluGluThrGluThrAspThrPheAspAlaalaProGlnProAlaArgGlu	851
Db	2530	GTGGGTCCCAAGAGACAGACAGACACTTTTGTATGCCGACCGCAGCTTGCAGGAA	2589
Qy	852	AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys	871
Db	2590	GCTGCCCTTGCATCAGACTCTCTAAGAGCTTGGAAAGTTCAGATCATCTCAGAGCATTTGT	2649
Qy	872	LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys	898

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Db      2650 AAGCGAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACACTGAAA 2700
|||||
RESULT 8
AAH49499
ID      AAH49499 standard; DNA; 3074 BP.
AC      AAH49499;
XX
DT      11-DEC-2001 (first entry)
XX
DE      Human KCNQ5 DNA.
XX
KW      KCNQ5; potassium channel protein; human; neurological; cardiovascular;
KW      anticonvulsant; excitability modulator; membrane potential; neuron;
KW      voltage-dependent KCNQ5 potassium channel; cardiomyocyte; epilepsy;
KW      screening; central nervous system disease; cardiovascular disease; ds.
XX
OS      Homo sapiens.
XX
PH      Key Location/Qualifiers
FT      CDS 110..2908
FT      /*tag= a
FT      /product= "KCNQ5"
XX
PN      DE10013732-A1.
XX
PD      27-SEP-2001.
XX
PF      21-MAR-2000; 2000DE-01013732.
XX
PR      21-MAR-2000; 2000DE-01013732.
XX
PA      (AVET ) AVENTIS PHARMA DEUT GMBH.
XX
PI      Steinmeyer K, Lerche C, Scherer C, Seebohm G, Busch AE;
XX
DR      WPI; 2001-571700/65.
XX
DR      P-PSDB; AAB86979.
XX
PT      New DNA sequence encoding potassium channel KCNQ5, useful in screening
PT      for specific modulators, potential agents for treating central nervous
PT      system and cardiovascular diseases.
XX
PS      Claim 2a; Page 9-10; 20pp; German.
XX
CC      This invention describes a novel DNA sequence (I) encoding: (i) a
CC      polypeptide (ii) with potassium channel KCNQ5 activity; (iii) a
CC      polypeptide with the amino acid (aa) sequence of KCNQ5. The products of
CC      the invention have neurological, cardiovascular and anticonvulsant
CC      activity and act as modulators of the voltage-dependent KCNQ5 potassium
CC      channel, a key regulator of membrane potential and modulator of
CC      excitability of electrically activated cells such as neurons and
CC      cardiomyocytes. KCNQ5 may be implicated in some forms of epilepsy. (II)
CC      are used to screen for compounds that modulate the activity of KCNQ5,
CC      potentially useful for treating central nervous system (e.g. epilepsy)
CC      and cardiovascular diseases. This sequence encodes the human potassium
CC      channel KCNQ5 protein described in the invention
XX
SQ      Sequence 3074 BP; 788 A; 784 C; 789 G; 713 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 3074
Score: 4513.50 Matches: 885
Percent Similarity: 98.77% Conservativeness: 1
Best Local Similarity: 98.66% Mismatches: 2
Query Match: 99.26% Indels: 9
DB: 4 Gaps: 1

US-09-810-796-5 (1-888) x AAH49499 (1-3074)

Qy      1 MetLysApValGluSerGlyArgGlyValLeuLeuAenSerAlaAlaAArgGly 20
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Db      215 ATGAAGGATGTGGAGTCGGGCGGCGGCGAGGTGCTGCTGAACCTCGGACGCGCGAGGGGC 274
Qy      21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeu 40
|||||
Db      275 GACGGCTGTCTACTGTCTGGGACCCGCGCGGCCACGCTTGGTGGCGCGGCGGTGGCGCTG 334
Qy      41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
|||||
Db      335 AGGAGAGCGCGCGGCGGCGAGCGGGGCGCGGATGAGCCCTGCTGGAGAGCGCGCTCTCT 394
Qy      61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAenTyrLeu 80
|||||
Db      395 TACACGAGTAGCAGAGCTGCGGCGCAACGCTCAAGTACCGCGGCGGTGCAGAACTACTCTG 454
Qy      81 TyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPheLeu 100
|||||
Db      455 TACAACGTGTGGAGAGACCCGCGCTGGCGGTTCATCTACCACGCTTTCGTTTTCTCTC 514
Qy      101 LeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120
|||||
Db      515 CTTGTCTTTGGTTGCTTGATTTTGTCAGTGTTTTTCTACCATCCTCGAGCACACAAAATTG 574
Qy      121 AlaSerSerCysLeuLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
|||||
Db      575 GCCTCAAGTTGCCTCTTGATCTCGAGTTCGTGATGATTCGTCTCTTTGGTTTGGAGTTC 634
Qy      141 IleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu 160
|||||
Db      635 ATCAATCGAATCTGGTCTGGGGTGTCTGTGTGATATAGATACCATTTCTTATCGCTTCAATAGCA 694
Qy      161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuLeuAlaSerIleAla 180
|||||
Db      695 AGGTTTGTCTGAAAGCCCTTCTGTGTTATAGATACCATTTCTTATCGCTTCAATAGCA 754
Qy      181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
|||||
Db      755 GTTGTCTTCTGCAAAACTCAGGGTAATATATTTTGGCCACGCTCTGCACCTCAGAAGTCTCCGT 814
Qy      201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTyrLysLeuLeu 220
|||||
Db      815 TTCTACAGATCTCTCCGATGGTGGCGATGGACCGAAGGGGAGGCATTTGAAATTTACTG 874
Qy      221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTyrIleGlyPheLeu 240
|||||
Db      875 GGTTCACTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTTG 934
Qy      241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAenLysGluPhe 260
|||||
Db      935 GTTCTTATTTTTCGTCCTTCTCTCTATCTGGTGGAAAAGGATGCGCAATAAAGAGTGT 994
Qy      261 SerThrTyrAlaAspAlaLeuTyrTyrGlyThrIleThrLeuThrThrIleGlyTyrGly 280
|||||
Db      995 TCTACATATGAGATGCTCTCTGGTGGGCGCAATTTACATTTGCACTATTTGGTATGGA 1054
Qy      281 AsplysThrProLeuThrTyrLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
|||||
Db      1055 GACAAAACCTCCCTAACTTGGCTGGGAAGATGCTTTCTCAGGCTTTTGCACCTCTTGGC 1114
Qy      301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
|||||
Db      1115 ATTTCTTTCTTTCGACTTCTCGCGGCATTTCTTGGCTCAGGTTTTTGCATTAATAAGTACAA 1174
Qy      321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAenLeuIleGln 340
|||||
Db      1175 GAACAACCGCCGCAAGAACTTTGAGAAAAGAGAACCCAGCTGCGCAACCTCATTTAG 1234
Qy      341 CysValTyrArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTyrLysPro 360
|||||
Db      1235 TGTGTTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTCCATTTGCAACCTCGAGGCCA 1294
Qy      361 HisLeuLysAlaLeuHisThrCysSerProThr----- 371
Db      1295 CACTTGAAGGCTTGCACACCTCGAGCCCTTACCAGAAAGAACAGAGGGGAGAGCATCAAGC 1354

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Db 1775 GGTCACTGGACATGTTGTAGAAATTAAGCCCTTCAACACACGGTGTGATCAAAATCTT 1834
Qy GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 551
Db 1835 GGAAGAAGGCAAAATCACATCAGATAAGAGAGCCGAGAGAAATAACACAGACATCAG 1894
Qy 552 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 571
Db 1895 ACCACAGACGATCTCAGTATGCTCGGTGGGTGGTCAAGGTTGAAAAACAGTACAGTCC 1954
Qy 572 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 591
Db 1955 ATAGAAATCAAGCTGAGCTGCTTCTAGACATCTATCAACAGGCTCTTCGGAAGGCTCT 2014
Qy 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProPheGluCysGluGlnThrSer 611
Db 2015 GCCTCAGCCCTCGCTTGGCTTCACTTCAGATCCCACTTTTGAATGTGAACAGACATCT 2074
Qy 612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
Db 2075 GACTATCAAGGCCCTGTGGATAGCAAAAGATCTTTCCGGTTCGGCAAAAACAGTGGCTGC 2134
Qy 632 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651
Db 2135 TTATCCAGATCACTAGTGCCAACTCTCGAGAGCCCTGCAGTTCTATCTGACGCCAAT 2194
Qy 652 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671
Db 2195 GAGTTCAAGTCCAGACACTTCTACGGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2254
Qy 672 ValProIleSerGlnSerAspGlySerAlaValAlaIleThrAsnThrIleAlaAsnGln 691
Db 2255 GTGCCAATTAGTCAAAAGGATGGCTTCAGCAGTGGCAGCCACCAACACCATTTGCAAAACAA 2314
Qy 692 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProLeuPro 711
Db 2315 ATAAATACGGACCCCAAGCCAGCAGCCCAACACTTTACAGATCCCACTCTCTCCCA 2374
Qy 712 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 731
Db 2375 GCCATCAAGCATCTGCCAGCCGAGAACTCTGCACCCCTAACCTTCAGGCTTACAGGA 2434
Qy 732 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 751
Db 2435 AGCAATTCAGTCAACCACTCCCTGCTGTGCTTCAAGGAAATGTTTCAGGTTGCACAG 2494
Qy 752 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 771
Db 2495 TCAAATCTCACCAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG 2554
Qy 772 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 791
Db 2555 TTGTCGTCTGTCCCATGTCGCGAAGGACTTGGGCAAACTTTCTGTCTGTGCAAAACCTG 2614
Qy 792 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 811
Db 2615 ATCAGTCGACCGAGGAACTGAATATACAACTTTTCAGGAGTGAAGTCAAGTGGCTCCAGA 2674
Qy 812 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 831
Db 2675 GGCACCCAAAGATTTTATCCCCAAATGGAGGGAAATCCAAATGTTTATTAACATGATGAAGAG 2734
Qy 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaIleProGlnProAlaArgGlu 851
Db 2735 GTGGTCCCGAAGACAGACAGACACACTTTTGTATGCGCACCCGACGCTGCCAGGAA 2794
Qy 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 871
Db 2795 GCTGCTTTTGCATCAGACTCTTAAGGACTGGAAGGTCAAGATCATCTCAGACGATTTGT 2854
Qy 872 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValIleLys 888
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Db 2855 AAGCAGAGAGAAAGTACAGATGCCCTCAGCTTGCTCATGTCAAACTGAAA 2905
RESULT 10
AAC64371
ID AAC64371 standard; cDNA; 3718 BP.
XX
AC AAC64371;
XX
DT 07-FEB-2001 (first entry)
XX
DE Human KCNQ5 (KCN6q) cDNA sequence SEQ ID NO:2.
XX
KW Human; KCNQ5; KCN6q; chromosome 6; voltage-gated potassium channel;
Stargardt-like macular dystrophy; cone-rod macular dystrophy;
Salla disease; ophthalmological; auditory; central nervous system;
cardioactive; anticonvulsant; gastrointestinal; muscular active;
age-related macular degeneration; macular degeneration; deafness;
epilepsy; neuropsychiatric disorder; heart disorder; muscle disorder;
gastrointestinal disorder; 88.
XX
OS Homo sapiens.
XX
PN WO200061606-A1.
XX
PD 19-OCT-2000.
XX
PF 10-APR-2000; 2000WO-US009587.
XX
PR 14-APR-1999; 99US-0129274P.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Petrukhin K, Caskey CT, Li W, Metzker ML;
DR WPI: 2000-647417/62.
XX
PT Voltage-gated potassium channel KCNQ5 DNA and protein, for identifying
inhibitors and activators which can treat e.g. Stargardt-like macular
dystrophy, cone-rod dystrophy, Salla disease, deafness, and epilepsy.
XX
PS Claim 3; Fig 2; 99pp; English.
XX
CC The present sequence encodes the human KCNQ5 (also called KCN6q) protein,
which is a voltage-gated potassium channel protein. Human KCNQ5 has
ophthalmological, auditory, central nervous system (CNS), cardioactive,
anticonvulsant, gastrointestinal and muscular active activities.
CC Sequences and methods from the present invention are useful for
identifying activators or inhibitors of KCNQ5 protein. These activators
and inhibitors are useful for treating Stargardt-like macular dystrophy,
cone-rod dystrophy, Salla disease, age-related macular degeneration,
other forms of macular degeneration, deafness, epilepsy, and different
forms of neuropsychiatric, heart, gastrointestinal, and muscle disorders.
CC Stargardt-like macular dystrophy and cone-rod dystrophies are located at
chromosome 6q
XX
SQ Sequence 3718 BP; 1054 A; 845 C; 866 G; 953 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0 Length: 3718
Score: 4346.50 Matches: 850
Percent Similarity: 98.84% Conservativeness: 1
Best Local Similarity: 98.72% Mismatches: 1
Query Match: 95.59% Indels: 9
DB: 3 Gaps: 1
US-09-810-796-5 (1-888) x AAC64371 (1-3718)
Qy 37 GlyGlyGlyLeuArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGly 56
Db 93 GCGCGTGCCTGAGGAGAGAGCCGCGGGAAGCAGGCGGCGGCGGCTGCTGGGG 152
Qy 57 LysProLeuSerTyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgVal 76
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Db 153 AAGCCGCTCTCTATACAGTAGCAGAGCTGCCGCGCAACGTCAGTAGCCGGCGGTG 212  
Qy 77 GlnAsnTyrLeuTyrAsnValLeuGluuArgProArgGlyTyrAlaPheIleTyrHisAla 96  
Db 213 CAGAACTACCTGTACAACTGCTGGAGAGACCCCGCGCTGGCGGTTTCATCTACCAGCT 272  
Qy 97 PheValPheLeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGlu 116  
Db 273 TTCGTTTTCCTCTGCTGCTTGGTTGCTGATTTGTTCAGTGTTCATCCATCCCTGAG 332  
Qy 117 HisThrLysLeuAlaSerSerCysLeuLeuLeuLeuGluPheValMetIleValPhe 136  
Db 333 CACACAAATTTGGCCCTCAAGTTGCCCTTGTGATCTCTGGAGTTCTGATGATTCGCTCTT 392  
Qy 137 GlyLeuGluPheIleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrp 156  
Db 393 GGTTCGGAGTTCATCATTCGAATCTGGTCTCGCGGTTGCTGTGCGATATAGAGGATGG 452  
Qy 157 GlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIle 176  
Db 453 CAAGGAAGACTCAGGTTTGTCTCGAAGCCCTTCTGTGTATAGATACCATTTCTTATC 512  
Qy 177 AlaSerIleAlaValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeu 196  
Db 513 GCTTCAATAGCAGTTGTTTCTGCAAAACTCAGGGTAATATTTTGGCCACGCTCTGCACTC 572  
Qy 197 ArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyThr 216  
Db 573 AGAAGTCTCCGTTTCTCTACAGATCTCCGATGGTGGCATGGACCGAAGGGGAGGCACT 632  
Qy 217 TrpLysLeuLeuGlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyr 236  
Db 633 TGGAAATTTACTGGGTTTCAAGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTAC 692  
Qy 237 IleGlyPheLeuValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAla 256  
Db 693 ATAGAAATTTTGGTTCTTATTTTTCGTTCTTCTGTCTATCTGTGGTGGAAAGAGTGCC 752  
Qy 257 AsnLysGluPheSerThrTyrAlaAspAlaLeuTrpTyrGlyThrIleThrLeuThrThr 276  
Db 753 AATAAAGAGTTTTCTACATATGCAGATGCTCTGTGGTGGGACAAATTTACATTTGACAACT 812  
Qy 277 IleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPhe 296  
Db 813 ATTGGCTATGGAGACAAAACTCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTT 872  
Qy 297 AlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAla 316  
Db 873 GCACCTCCTTGGCATTTCTTTTGCATCTCTGCGGCATTTCTTGGCTCAGGTTTGTGA 932  
Qy 317 LeuLysValGlnGluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAla 336  
Db 933 TTAAAGTACCAAGAACAAACACCGCCAGAAACACTTTGAGAAAGAAAGAACCCAGCTGCC 992  
Qy 337 AsnLeuIleGlnCysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAla 356  
Db 993 AACCTCATTCAGTGTGTTTGGGTAGTTACGACGCTGATGAGAAATCTGTTTCCATTGCA 1052  
Qy 357 ThrTrpLysProHisLeuLysAlaLeuHisThrCysSerProThr----- 371  
Db 1053 ACCTGGAAAGCCACACTTGAAGCCCTTGACACCTTCAGCCCTTACCAAGAAAGAAAGAGG 1112  
Qy 372 -----AsnGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArg 387  
Db 1113 GAAGCATCAAGCAGTCAGAGCTAAGTTTTAAGAGCGAGTGGCATGGCTAGCCCCAGG 1172  
Qy 388 GlyGlnSerIleLysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAsp 407  
Db 1173 GGCCAGAGTATTAAGAGCCGCAAGCCCTCAGTAGGTGACAGAGGTCCTCCCAAGCAGCGAC 1232  
Qy 408 IleThrAlaGluGlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThr 427

Db 1233 ATCACGCCGAGGCGAGTCCCAACAAAGTCAGAGAGCTGGAGCTTCAACAGCCGACACC 1292  
Qy 428 ArgPheArgProSerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAsp 447  
Db 1293 CGTTTCGGGCCCTCGCTGGCGCTCAAAAGTTTCTCAGCAAAACCGAGTGATAGATGCTGAC 1352  
Qy 448 ThrAlaLeuGlyThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerVal 467  
Db 1353 ACAGCCCTTGGCACTGATGATGATATATGATGAAAGAGTCCAGTAGTGTATGATCATCAGTG 1412  
Qy 468 GluAspLeuThrProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHis 487  
Db 1413 GAAGACCTCAACCCACCACTTAAACCTGATTCAGAGCTATCAGAAATATGAAATTTTCAT 1472  
Qy 488 ValAlaLysArgLysPheLysGluThrLeuArgProTyrAspValLysAspValIleGlu 507  
Db 1473 GTTCAAAACCGAAGTTTAAAGAAACATTCAGTCCATATGATGTAAGAAGATGTCATTGAA 1532  
Qy 508 GlnTyrSerAlaGlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgVal 527  
Db 1533 CAATATTTCTGCTGCTCATCTGGACATGTTGTGTAGAAATTAAGAGCCCTTCAACACAGTGTT 1592  
Qy 528 AspGlnIleLeuGlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThr 547  
Db 1593 GATCAAAATTTCTTGAAGAGGGCAAAATCACATCAGATAAGAGAGCCGAGAGAAATAACA 1652  
Qy 548 AlaGluHisGluThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLys 567  
Db 1653 GCAGAACATGAGACACAGACGATCTCAGTATGCTCGGTGGGTGGTCAAGTTTGAANA 1712  
Qy 568 GlnValGlnSerIleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeu 587  
Db 1713 CAGGTACAGTCCATAGAAATCCAAGCTGAGCTGCCTACTAGACATCTATCAACAGGTCCTT 1772  
Qy 588 ArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCys 607  
Db 1773 CGGAAAGGCTCTGCTCAGCCCTCGCTTTCGCTTCATTCAGATCCCAACCTTTTGAATGT 1832  
Qy 608 GluGlnThrSerAspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGln 627  
Db 1833 GAACAGACATCTGACTATCAAGCCCTGTGGATAGCAAGATCTTTCGGGTTCGACAA 1892  
Qy 628 AsnSerGlyCysLeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIle 647  
Db 1893 AACAGTGGCTGCTTATCCAGATCAACTAGTGCCAAACATCTCAGAGAGGCTCGAGTTCAT 1952  
Qy 648 LeuThrProAsnGluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSer 667  
Db 1953 CTGACGCCAAATGAGTTTCAGTGGCCAGACTTTCTACGCGCTTAGCCCTACTATGACAGT 2012  
Qy 668 GlnAlaThrGlnValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThr 687  
Db 2013 CAAGCAACACAGTGGCCATTTAGTCAAAAGGATGGCTCAGCAGTGGCAGCCACCAACACC 2072  
Qy 688 IleAlaAsnGlnIleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIlePro 707  
Db 2073 ATTCAAAACCAATAAATACGACCCCAAGCCAGCAGCCCAACCAACTTTACAGATCCCA 2132  
Qy 708 ProProLeuProAlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAla 727  
Db 2133 CCTCTCTCCAGCCATCAAGCATCTGCCAGGCCAGAAACTCTGCAACCCCTTAACCCCTGCA 2192  
Qy 728 GlyLeuGlnGluSerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnVal 747  
Db 2193 GGCTTACAGAAAGCATTTCTGAGTCAACCTGCTCTTGTTCCTCCAGGAAAATGTT 2252  
Qy 748 GlnValAlaGlnSerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGly 767  
Db 2253 CAGTTGCACAGTCAAAATCTCACCAAGGACCGTCTTATGAGGAAAAGCTTTGACATGGGA 2312  
Qy 768 GlyGluThrLeuLeuSerValCysProMetValProLysLeuGlyLysSerLeuSer 787  
Db 2313 GGAGAAACTCTGTTGTCTGTCTGTCCCATGGTGGCCGAGGACTTGGGCAATCTTTGTCT 2372





cardiovascular; disorder; ischaemia; aortic bending;  
vascular heart disease; endocarditis; atrial fibrillation; heart failure;  
angina; cardiomyopathy; cardiac death; gene; ds.  
Homo sapiens.

WO2003065984-A2.

14-AUG-2003.

29-JAN-2003; 2003WO-US002571.

01-FEB-2002; 2002US-0353224P.

15-MAR-2002; 2002US-0364529P.

19-APR-2002; 2002US-0373861P.

29-APR-2002; 2002US-0376287P.

12-JUN-2002; 2002US-0388080P.

24-JUN-2002; 2002US-0390971P.

03-JUL-2002; 2002US-0394130P.

10-JUL-2002; 2002US-0394797P.

21-AUG-2002; 2002US-0404904P.

23-AUG-2002; 2002US-0405450P.

04-SEP-2002; 2002US-0408070P.

06-NOV-2002; 2002US-0424300P.

05-DEC-2002; 2002US-0431042P.

05-DEC-2002; 2002US-0431079P.

(MILL-) MILLENNIUM PHARM INC.

Logan TJ, Chun M, Galvin KM, Healy A, Acton SL, Donaghue M;

Stagliano N, Perodin J, Rodrigue-Way A;

WPI; 2003-731468/69.

P-PSDB; ADE31699.

Identifying a compound capable of treating a cardiovascular disorder

(e.g. atherosclerosis) comprises assaying the ability of the compound to  
modulate the expression or activity of e.g. 1682, 6169 or 6193  
polypeptide or nucleic acid.

Disclosure; SEQ ID NO 55; 328pp; English.

The invention relates to a method for identifying a compound capable of  
treating a cardiovascular disorder. The present invention identifies the  
differential expression of 1682, 6169, 6193, 7771, 14395, 29002, 33216,  
43726, 69292, 21656, 32427, 2402, 7747, 1720, 9151, 60491, 1371, 7077,  
33207, 1419, 18036, 16105, 38650, 14245, 58848, 1870, 25856, 32394, 3484,  
345, 9252, 9135, 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912,  
2868, 283, 2554, 9464, 17799, 26866, 43848, 32135, 12208, 2914, 51130,  
19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474, 7992, 15400, 1452 or  
6585 genes in cardiovascular disease states. The methods are useful in  
diagnosing, preventing and treating cardiovascular disorders, such as  
atherosclerosis, cardiac hypertrophy, ischaemia, reperfusion injury,  
restenosis, arterial inflammation, vascular wall remodeling, coronary  
microembolism, tachycardia, bradycardia, pressure overload, aortic  
bending, coronary artery ligation, vascular heart disease, valvular  
disease, including but not limited to, valvular degeneration caused by  
calcification, rheumatic heart disease, endocarditis, or complications of  
artificial valves; atrial fibrillation, long-QT syndrome, congestive  
heart failure, sinus node dysfunction, angina, heart failure,  
hypertension, atrial fibrillation, atrial flutter, pericardial disease,  
including but not limited to, pericardial effusion and pericarditis;  
cardiomyopathies, e.g. dilated cardiomyopathy or idiopathic  
cardiomyopathy, myocardial infarction, coronary artery disease, coronary  
artery spasm, ischaemic disease, arrhythmia, sudden cardiac death and  
cardiovascular developmental disorders. The methods may also be used for  
identifying compounds that modulate cardiovascular disorders. Sequences  
given in ADE31644-ADE31769 represent the genes and proteins that may be  
regulated by a compound of the invention.

Sequence 2335 BP; 396 A; 812 C; 719 G; 408 T; 0 U; 0 Other;

Alignment Scores:

	Pred. No.:	9.35e-161	Length:	2335
Score:		2007.50	Matches:	434
Percent Similarity:		65.32%	Conservative:	82
Best Local Similarity:		54.94%	Mismatches:	133
Query Match:		44.15%	Indels:	141
DB:		10	Gaps:	16

US-09-810-796-5 (1-888) x ADE31698 (1-2335)

Qy	8	ArgGlyArgValLeuLeuAanSerAlaAlaAargGlyAspGlyLeuLeuLeuGly	27
Db	127	CGGGACGCCCCCGCGCGAGCTAGTGGCGCTCACGGC	165
Qy	28	ThrArgAlaAlaThrLeuGlyGlyGlyClyLeuArgGluSerArgArgGlyLys	47
Db	166	---CGTCAGAGCGAACAGGGCGAGCGGG	201
Qy	48	GlnGlyAla-ArgMetSerLeuLeuGlyLysProLeu	59
Db	202	CTCCCCCGCGCGCTCGGCTCTCTGGGAGCCCTCCGCGCGGGCGGCGCTCCCTGG	261
Qy	60	-----SerTyrThrSerSerGlnSerCysArgArgAanValLysTy	73
Db	262	GCCGGGCTCCGGCTCGGGCTCGGCTCGGCGCGAGCGCTCTCTCGGCGCGACAGCGCTA	321
Qy	73	rArgArgValGlnAanTyrLeuTyrAanValLeuGluArgProArgGlyTrpAlaPheI	93
Db	322	CCGCGCGCTCGAGAACTGGGTCTACAACTGCTGGAGCGCGCGCGCTGGGCTTGGT	381
Qy	93	eTyrHisAlaPheValPheLeuLeuValPheGlyCysLeuLeuLeuSerValPheSerTh	113
Db	382	CTACCAGCTCTTCATATTTTGTGGTCTTCAGCTGCTGGTGTGTGTGTGTGTGTGTGT	441
Qy	113	rIleProGluHisThrLysLeuAlaSerSerCysLeuLeuLeuLeuGluPheValMetI	133
Db	442	TATCCAGAGCACCCAGGAAGCTTGCACAGAGTGTCTCTCATCTTGGAAATTCGTGAT	501
Qy	133	eValValPheGlyLeuGluPheLeuLeuArgIleTrpSerAlaGlyCysCysArgTy	153
Db	502	CGTGGTTTCGGCTTGGAGTACATCGTCCGGGTGTGGTCCGCGGATGCTCTCGCGCTA	561
Qy	153	rArgGlyTrpGlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrI	173
Db	562	CCGAGGATGGCAGGTCGCTTCCGCTTTCGCAAGAGCCCTTCTGTGTCTATCGATTCAT	621
Qy	173	eValLeuIleAlaSerIleAlaValSerAlaLysThrGlnGlyAsnIlePheAlaTh	193
Db	622	CGTGTTCGTGGCTCGGTGGCGGTTCATCGCGCGGGTACCCAGGGCAACATCTTCGCC	681
Qy	193	rSerAlaLeuArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgAr	213
Db	682	GTCCGCGCTCGCAGCATCGCTTCTCTGAGATCCTCGCATGTGTGGCATGGACCGCG	741
Qy	213	gGlyGlyThrTrpLysLeuLeuGlySerValValTyrAlaHisSerLysGluLeuLeuTh	233
Db	742	CGCGCGCACCTCGGAAGCTGTGGGCTCAGTGTGTACGCGCATAGCAAGAGAGTATCAC	801
Qy	233	rAlaTrpTyrIleGlyPheLeuValLeuPheSerSerPheLeuValTyrLeuValI	253
Db	802	CGCTGTGTACATCGGTTCTGGTGTCTCACTTCGCTCTCTCTCTCTCTCTCTCTCTCT	861
Qy	253	uLysAspAlaAsnLysGluPheSerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleTh	273
Db	862	GAAGGACGCCAACTCCGACTTCTCTCTACCGCGACTCGCTCTGTGGTGGGAGCAGATTAC	921
Qy	273	rLeuThrThrIleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSe	293
Db	922	ATTGACACCAACATCGCTATGGTGTGACAGACACCCACACACATGGGTGGGCGGGTCTCGC	981
Qy	293	rAlaGlyPheAlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySe	313
Db	982	TGCTGGCTTGGCTTACTGGGCATCTCTTCTTTTGGCTGTGCTGGCGGATCTTAGGCTC	1041



QY 313 rGlyPheAlaLeuLysValGlnGlnHisArgGlnLysHisPheGluLysArgArgAs 333  
 Db 1042 CGGCTTTGCCCTGAAGGTCAGGAGCAGCAGCGGAGAGCATTCCGAGAGCGGAGAT 1101  
 QY 333 nProAlaAlaLeuLeuGlnCysValTrpArgSerTyrAlaAlaAsp----GluLysSe 352  
 Db 1102 GCCGCGACCAACCTCATCCAGGCTGCGCTGGCGCTGTACTCCACCGATATGAGCGGGC 1161  
 QY 352 rValSerIleAlaThrTrp----- 358  
 Db 1162 CTACCTGACAGCCACTGGTACTACTATGACAGATATCTCCATCTTCAGAGAGCTGGC 1221  
 QY 358 ----- 358  
 Db 1222 CCTCTGTTTGAGCAGCTGCAACGGCGCCGCAATGGGGGCTTACGGCCCTGGAGGTGCG 1281  
 QY 359 -----LysProHisIleLysAlaLeuHisTh 367  
 Db 1282 GGGGGCGCGGTACCCGAGGAGCACCTCCCGTTACCCCGCGTGGCCACTGCCACCG 1341  
 QY 367 r-----CysSerProThrAsnGlnLysLeuSerPheLysGluArgVa 381  
 Db 1342 GCCGGGAGCAGCTCTCTGCGCTGGGGAAGCAGCGGATGGCATCAAGACCGCAT 1401  
 QY 381 lArgMetAlaSerProArgGlyGlnSerIleLysSerArgGln-----AlaSerValGl 399  
 Db 1402 CGCATGGGAGCTCCAGCGCGGAGCGGGCTCTTCAAGCAGCAGCTGGCCACTCCCAAC 1461  
 QY 399 yAspArgArgSerProSerThrAspIleThrAlaGluGly---SerProThrLysValGl 418  
 Db 1462 AATGCCCACTCCCAAGCAGCAGCGAGGTGGGTGAGGCCACCGCCCAACCAAGGTGCA 1521  
 QY 418 nLysSerTrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerSe 438  
 Db 1522 AAAGAGCTGGAGCTTCATGACCGCAGCCCGCTTCGGGCATCTCTGAGACTC----- 1573  
 QY 438 rGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspValTyrAspGl 458  
 Db 1574 -----AAACCCCGCACCTCTGCTGAGGATGCC---CCCTCAGAGGAAGTAGCAGGA 1623  
 QY 458 uLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuLysThrValIl 478  
 Db 1624 GAAGAGCTACAGGTGTGAGCTCAGCGTGGAGCAGCATCATGCTGCTGTGAAGACAGTAT 1683  
 QY 478 eArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThrLeuAr 498  
 Db 1684 CGCTCCATCAGGATTCTCAAGTTCCTGCTGGCCAAAGAAATTCAGGAGACACTGCG 1743  
 QY 498 gProTyrAspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMetLeuCy 518  
 Db 1744 ACCGTACGACGTGAAGGACGTCATTGAGCAGTACTTCAGCAGGCCACCTGGACATGCTGG 1803  
 QY 518 sArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSe 538  
 Db 1804 CCGGATCAAGAGCTTGCAAACTCGGGTGGACCAATTTGGGTGGGGG-----CCCGG 1857  
 QY 538 rAspLysLysSerArgGlu-----LysIleThrAlaGluHisGluThrThrAspAs 555  
 Db 1858 GGACAGGAAGCCCGGAGAGAGGCGACAGGGGCCCTCCGACGGAGGTGGTGATGA 1917  
 QY 555 pLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSerIleGluSerLy 575  
 Db 1918 AATCAGCATGATGGAGCGCGTGGTCAAGGTGGAGAACGAGGTGAGTCCATCGAGCACA 1977  
 QY 575 sLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySerAlaSerAlaLe 595  
 Db 1978 GCTGACCTGCTGTGGGCTTCTATTCGCGTGGCTGCGCTGCGACCTCGGCC----- 2032  
 QY 595 uAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSerAspTyrGlnSe 615  
 Db 2033 -AGCTGGCGCGCGTGAAGTGGCGCTGTTCGACCCGACATCATCTCCGACTACCACAG 2091  
 QY 615 rProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSe 635

Db 2092 CCCTGTGGACACGAGGACATCTCGTCTCGCAGACAGCTCAGC---ATCTCCCGCTC 2148  
 QY 635 rThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAl 655  
 Db 2149 GGTGAGCAGCAACATGAGCTGAGG----- 2173  
 QY 655 aGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGlnValProIleSe 675  
 Db 2174 -----ACTTC 2178  
 QY 675 rGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAl 695  
 Db 2179 TCAGAGGAGGCGAGCACA-----CGGCCAGC 2205  
 QY 695 aProLysProAlaAlaProThrThrLeuGlnIleProProLeuProAlaIleLysH 715  
 Db 2206 CCGCGCGCTGGCGCTCCGACTGCCCTCGGAGCTCCGACTCCTCTCGTACTTGAAC 2265  
 QY 715 isLeuProArgProGluThrLeuHis 723  
 Db 2266 CACTCCCTCAGGCGAGAGACCCAC 2291  
 RESULT 13  
 ADS17851  
 ID ADS17851 standard; cDNA; 5595 BP.  
 AC ADS17851;  
 DT 02-DEC-2004 (first entry)  
 XX Rattus norvegicus KCNQ cDNA #2.  
 DE KCNQ; potassium channel; anxiety; insomnia; hyper-excitability disorder;  
 KW Alzheimer's disease; peripheral neuropathy; neurodegenerative disease;  
 KW neuroprotective; anticonvulsant; nootropic; tranquiliser; sedative;  
 KW norway rat; gene; ss.  
 XX Rattus norvegicus.  
 OS  
 FH Key Location/Qualifiers  
 FT CDS 1553..4111  
 FT /\*tag= a  
 FT /product= "KCNQ protein"  
 XX US2004175691-A1.  
 XX 09-SEP-2004.  
 XX 08-APR-2004; 2004US-00820307.  
 XX 03-DEC-1998; 98US-0110804P.  
 XX 03-DEC-1999; 99US-00454868.  
 XX (BROW)/ BROWN B S.  
 PA (MCKI)/ MCKINNON D.  
 XX Brown BS, Mckinnon D;  
 PI WPI; 2004-642119/62.  
 DR P-PSDB; ADS17852.  
 XX  
 PT Evaluating compound for utility in treating neurological disease such as  
 PT epilepsy and anxiety, involves contacting compound with cell co-  
 PT expressing KCNQ2 and KCNQ3 that form potassium channel, and measuring  
 PT activity of potassium channel.  
 XX Disclosure; SEQ ID NO 8; 38pp; English.  
 PS  
 CC The present invention relates to a method of evaluating a compound for  
 CC utility in treating neurological disease. The method involves contacting  
 CC a compound with a cell that co-expresses KCNQ2 and KCNQ3, where the KCNQ2  
 CC and KCNQ3 form a potassium channel and measuring the activity of the







Db 2301 GCGGACGACGACAGCTCCATCCATCCCGTCCGTG-----GACCACGAGGAGCTGGA 2354  
 Qy 799 nileGlnLeuSerGlySerGlnSerGlySerGlySerGlnAsp----- 815  
 Db 2355 GGGTCTTCACGGCTTCAGCATCTCCAGTCCAGGAGAACCTGGATGCTTCAACAG 2414  
 Qy 816 -PheTyrPro-LysTyrArg-----GlnSerLysLeuPheLeuThrAspGluGluV 832  
 Db 2415 CTGTACCGCGCGTGGCGCTTGTGCCAAGTCAAGCTCAGGATCGGAGGAGATC 2474  
 Qy 832 alGlyProGluThrGluThrAspThrPheAsp----- 843  
 Db 2475 AGACACCGACTCCGACCTCTGTACCCCGTGGCGGCCCGCCAGCTCGGCCACCGCGGA 2534  
 Qy 844 -----AlaAlaProGlnProAlaArgGluAlaAlaPheAlaSerA 857  
 Db 2535 GGGTCCCTTGTGTAGTGGCTGGCGCGGCCAGGAGTGAAGCGCGCTGGGC----- 2590  
 Qy 857 spSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCysLysAlaGly 874  
 Db 2591 -----CAGTGGACCGCGCGCGCTCTCTCAGCACGGTGCCTCCGAGGT 2635

## RESULT 15

ADB78685  
 ID ADB78685 standard; cDNA; 7407 BP.

AC ADB78685;

DT 04-DEC-2003 (first entry)

XX Human potassium channel subunit mutant cDNA SEQ ID NO:56.

XX ss; gene; mutant; ion channel; ion channel subunit; ICS; nootropic;  
 KW neuroprotective; inotropic; antipruritic; antiarrhythmic; antimigraine;  
 KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;  
 KW nephrotoxic; antidiabetic; ophthalmological; epilepsy;  
 KW ion channel dysfunction; human.

OS Synthetic.

OS Homo sapiens.

XX WO2003008574-A1.

XX 30-JAN-2003.

XX 08-JUL-2002; 2002WO-AU000910.

PR 18-JUL-2001; 2001AU-00006452.

PR 05-MAR-2002; 2002AU-00000910.

PR 13-MAY-2002; 2002AU-00002292.

XX (BION-) BIONOMICS LTD.

PA (WALL/) WALLACE R W.

XX Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;

PI Berkovic SF, Scheffer IE;

XX WPI; 2003-239332/23.

XX Identifying predisposition to an ion channel dysfunction, such as  
 PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,  
 PT schizophrenia, anxiety and depression, by detecting encoding-gene  
 PT mutation events.

XX Claim 6; SEQ ID NO 56; 106pp; English.

XX The invention relates to a novel method for identifying a subject  
 CC predisposed to a disorder associated with ion channel dysfunction. The  
 CC method comprises ascertaining if at least one of the genes encoding ion  
 CC channel subunits (ICS) has undergone a mutation event so that a cDNA  
 CC derived from the subject has any of 134 nucleotide sequences. The method  
 CC of the invention has nootropic, neuroprotective, inotropic, antipruritic,  
 CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,

CC neuroleptic, tranquiliser, analgesic, nephrotoxic, antidiabetic, and  
 CC ophthalmological activity. A polynucleotide of the invention acts as an  
 CC ion channel agonist, or ion channel antagonist. The methods, isolated  
 CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or  
 CC modulator of an ion channel, cells and genetically modified non-human  
 CC animal, are useful for the diagnosis and treatment of epilepsy and/or a  
 CC disorder associated with ion channel dysfunction, such as hyper- or hypo-  
 CC kalemic periodic paralysis, myotonias, malignant hyperthermia,  
 CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's  
 CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,  
 CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory  
 CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,  
 CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic  
 CC fibrosis, congenital stationary night blindness and total colour  
 CC blindness. The present sequence represents a mutant cDNA of the  
 CC invention. The sequence data for this patent is not represented in the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pat\_sequences.

XX Sequence 7407 BP; 1353 A; 2329 C; 2355 G; 1370 T; 0 U; 0 Other;

## Alignment Scores:

Pred. NO.: 4.73e-142 Length: 7407  
 Score: 1797.00 Matches: 411  
 Percent Similarity: 60.66% Conservative: 101  
 Best Local Similarity: 48.70% Mismatches: 182  
 Query Match: 39.52% Indels: 151  
 DB: 10 Gaps: 22

US-09-810-796-5 (1-888) x ADB78685 (1-7407)

Qy 17 AlaAlaArgGlyAspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGly 36  
 Db 142 TCCACCGCGGACGGGGCGCTGCTGATCGCGCTCCGAGGCCCCCAAG-----CGC 192  
 Qy 37 GlyGlyGlyLeuArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuGly 56  
 Db 193 GGCAGCATCTCTCAGCAAACTCGCGCGGGCGCGCGCGCC-----GGG 237  
 Qy 57 LysProLeuSerTyrThrSerSerGlnSerCysArgArgAlaValLysTyrArgVal 76  
 Db 238 AAGCCC-----CCCCAGCGCAACGCGCTTCTACCGCAAGCTG 273  
 Qy 77 GlnAsnTyrLeuTyrAsnValLeuGluArgProArgGlyTyrAlaPheLeuTyrHisAla 96  
 Db 274 CAGATTTCTCTACAACGTGCTGGAGCGCGCGCGCTGGGGCTTCATCACCACGCC 333  
 Qy 97 PheValPheLeuLeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGlu 116  
 Db 334 TAGCTGTTCCTCTGCTGTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 393  
 Qy 117 HisThrLysLeuAlaSerSerCysLeuLeuLeuLeuPheValMetIleValValPhe 136  
 Db 394 TATGAGAAGAGCTCGGAGGGGGCGCTCTACATCTGGAATCGTGACTATCGTGGTGT 453  
 Qy 137 GlyLeuGluPheLeuLeuArgLysPropheCysValIleLeuSerThrIleValLeu 156  
 Db 454 GCGTGGAGTACTTCGTGCGGATCTGGCGCGAGGCTGCTGCTGCTGCTGCTGCTGCTG 513  
 Qy 157 GlnGlyArgLeuArgPheAlaArgLysPropheCysValIleLeuSerThrIleValLeu 176  
 Db 514 AGGGCGCGCGCTCAAGTTTGGCCGGAACCGTCTCTGTGTGATGACATCATGCTGCTCATC 573  
 Qy 177 AlaSerIleAlaValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeu 196  
 Db 574 GCCTCCATTCGGTGTCTGGCGCGCGCTCCAGGGCAACGCTCTTGGCCATCATCTGCCCTC 633  
 Qy 197 ArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgGlyGlyThr 216  
 Db 634 CGGAGCGCTGCGCTTCCTGCGAGATTCGCGGATGATCGCATCGCATCGCGCGGGAGGCC 693  
 Qy 217 TrpLysLeuGlySerValValTyrAlaHisSerLysGluLeuLeuThrAlaTyrTyr 236

694	Db	TGG	AGAGCTGCTGGGCTCTGTGGTCTATGCCCCACAGCAAGGAGCTGGTCACTGCTCGTGATC	753
237	Qy	Ile	GlyPheLeuValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAla	256
754	Db	ATCGGCTTCCTTTGCTCTCATCTCGGCTCGTCTCTGGTGTTACTTGGCAGAGAGGGGGAG	813	
257	Qy	Asn	LysGluPheSerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThr	276
814	Db	AAGACCACTTTGACACTCAGCGGAGTGCACTCTGGTGGGCGCTGATCACTGCTGACCA	873	
277	Qy	Ile	GlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPhe	296
874	Db	ATTGGCTACGGGGACAAGTACCCCGACCTGGAAACGGCAGGCTCTTGGCGCAACCTTC	933	
297	Qy	Ala	LeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAla	316
934	Db	ACCTCATCGGTGCTCTCTTTTCGCGCTGCCTGCAGGCATCTTGGGGTCTGGGTTGCC	993	
317	Qy	Leu	LysValGlnGlnGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAla	336
994	Db	CTGAAGGTTTCAGGAGCAGCAGCAGCAAGCACTTTGAGAAGAGCGCGAAACCGGCGCA	1053	
337	Qy	Asn	LeuIleGlnCysValTrpArgSerTyrAlaAlaAsp-----	349
1054	Db	GGCTTGATCAGTCGGCTCGGCTGGAGATTCTACGCCACCACTCTGCGCCACAGACCTGCAC	1113	
350	Qy	-----	-----GluLysSerValSerIleAlaThrTrpLys-----ProHis	361
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362	Qy	Leu	LysAlaLeuHisThrCys-----	368
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369	Qy	-----	-----SerProThrAsnGlnLysLeuSerPheLysGluArgValArg	382
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1348	Db	AGCGGTGATCCACAGCGCCGACAGAGCTCGAGGACAGCCGCCAGCAAGGTGCCCAAGAGC	1407	
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1408	Db	TGGAGCTTCGGGGACCGCAGCGGGCAGCGCAGGCTTTCCGCATCAAGGGTGGCGGTCA	1467	
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GenCore version 5.1.6  
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Run on: April 3, 2005, 06:46:36 ; Search time 1190.47 Seconds  
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Searched: 5607317 seqs, 3026245999 residues  
Total number of hits satisfying chosen parameters: 11214634

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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11	4513.5	99.3	3074	9	US-09-813-148-1
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ALIGNMENTS

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; Sequence 3, Application US/09810796  
; Patent No. US20020102677A1  
; GENERAL INFORMATION:  
; APPLICANT: Jegla, Timothy James  
; APPLICANT: ICAGEN, Inc.  
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel  
; FILE REFERENCE: 018512-005010US  
; CURRENT APPLICATION NUMBER: US/09/810,796  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 60/190,954  
; PRIOR FILING DATE: 2000-03-21  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 2667  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:

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; OTHER INFORMATION: human outwardly rectifying, voltage-gated
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; OTHER INFORMATION: potassium channel KCNQ5-2 coding sequence
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; NAME/KEY: CDS
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; LOCATION: (1)..(2667)
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; OTHER INFORMATION: KCNQ5-2
US-09-810-796-3

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US-09-810-796-5 (1-888) x US-09-810-796-3 (1-2667)

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## RESULT 2

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; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kie, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020042505A1el Human Ion Channel Protein and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/09/825,147
; PRIORITY FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIORITY FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
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; TYPE: DNA
; ORGANISM: homo sapiens
US-09-825-147-1
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Score: 4547.00 Matches: 888
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
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US-09-810-796-5 (1-888) x US-09-825-147-1 (1-2772)

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Db 706 TTCTACAGATCTCCCGCATGTCGCGATGACCAAGGGAGGCACCTTGAAATTTACTG 765
Qy 221 GlySerValValTyrAlaHisSerLysGluLeuThrAlaTrpTyrIleGlyPheLeu 240
Db 766 GGTTCAGTGGTTTATGCTCACAGCAAGAAATTAATACAGCTTGGTACATAGGATTTTG 825
Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db 826 GTTCTTATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 885
Qy 261 SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
Db 886 TCTACATATGAGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 945
Qy 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300
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Db 946 GACAAACTCCCTAACTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACATCTCTTGGC 1005  
Qy 301 lIeSerPheAlaLeuProAlaGlyLeuGlySerGlyPheAlaLeuLysValGln 320  
Db 1006 ATTTCCTTTCTTGCACTTCCTGCGCGCATCTCTTGCTCAGGTTTGGCAATTAAGATACAA 1065  
Qy 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340  
Db 1066 GAACAACACCGCCAGAAACACTTTTGAGAAAGAGAGAACCCAGCTGCCAACCCTCATTCAG 1125  
Qy 341 CysValTrpArgSerTyAlaAlaAspGluLysSerValSerIleAlaLathTrpLysPro 360  
Db 1126 TGTGTTTGGCGTAGTACGCACTTCGAGCAATCTGTTTCCATTGCAACCTGGAAGCCA 1185  
Qy 361 HisLeuLysAlaLeuHisThrCysSerProThrArgGlnLysLeuSerPheLysGluArg 380  
Db 1186 CACTTGAAGGCTTTGCACACCTTCGAGCCTTACCATCAGAAGCTAAGTTTAAAGAGCGA 1245  
Qy 381 ValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAsp 400  
Db 1246 GTGGCATGGCTAGCCCCAGGGCCAGAGTATTAAAGCCGACCAAGCCTCAGTAGGTGAC 1305  
Qy 401 ArgArgSerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSer 420  
Db 1306 AGGAGGTCCCCAAGCAGCCGACATCACAGCCGAGGCGAGTCCCAACAAAGTGCAGAGAGC 1365  
Qy 421 TrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerSerGlnPro 440  
Db 1366 TGGAGCTTCAAGACCGAACCCTGCTCCGGCCCTCGCTGCGCCCTCAAAAGTTTCAGGCCA 1425  
Qy 441 LysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyAspGluLysGly 460  
Db 1426 AAACCAAGTATAGATGCTGACACAGCCCTTGGCACTGATGATGATATATGATGATAAGGA 1485  
Qy 461 CysGlnCysAspValSerValGluAspLeuThrProProLeuLysThrValIleArgAla 480  
Db 1486 TGCCAGTGTGATGATCATAGTGGAGACCTCACCCACCACCTTAAACACTGTCTATTCGAGCT 1545  
Qy 481 IleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThrLeuArgProTyr 500  
Db 1546 ATCAGATNTATGAATTTTCATGTTGCAAAACGGAAGTTTAAAGAAACATTAAGTCCATAT 1605  
Qy 501 AspValLysAspValIleGluGlnTySerAlaGlyHisLeuAspMetLeuCysArgIle 520  
Db 1606 GATGTAAAGATGTCAATGAACAATATCTGCTGCTCATCTGGACATGTTGTGTAGAAAT 1665  
Qy 521 LysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLys 540  
Db 1666 AAAAGCCCTTCAAAACACAGTGTGATCAAAATCTTGAAAAAGGGCAAAATCACATCAGATAAG 1725  
Qy 541 LysSerArgGluLysIleThrAlaGluHisGluThrThrAspAspLeuSerMetLeuGly 560  
Db 1726 AAGAGCCGAGAGAAATTAACAGCAGACATGAGACCAACAGATCTCAGTATGCTCGGT 1785  
Qy 561 ArgValValLysValGluLysGlnValGlnSerIleGluSerLysLeuAspCysLeuLeu 580  
Db 1786 CGGGTGGTCAAGTTGAAAAACAGTACAGTCCATAGAAATCCAAGTGGAGCTGCTACTA 1845  
Qy 581 AspileTyTrpGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPhe 600  
Db 1846 GACATCTATCAACAGGCTCTTCGAAAGGCTCTCGCTCAGCCCTCGCTTTGGCTTCATTC 1905  
Qy 601 GlnIleProProPheGluCysGluGlnThrSerAspTyTrpGlnSerProValAspSerLys 620  
Db 1906 CAGATCCACCTTTGATGTGACAGACATCTGACTATCAAGCCCTGTGGATAGCAAA 1965  
Qy 621 AspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIle 640  
Db 1966 GATCTTTCGGGTTCCGCACAAAACAGTGGCTGTCTTATCCAGATCAACTAGTGGCAACATC 2025  
Qy 641 SerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyAla 660  
Db 2026 TCGAGAGCCCTGCAGTTTCATCTGACGCCAAATGAGTTTCAGTGGCCAGACTTTCTACGCG 2085

Qy 661 LeuSerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySer 680  
Db 2086 CTTAGCCCTACTATGCACAGTCAAGCAACACAGGTGCCAATTAGTCAAGAGTGGCTCA 2145  
Qy 681 AlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAla 700  
Db 2146 GCAGTGGCAGCCACCAACACCATTTGCCAAACCAATTAATACGGCACCCACAGCAGGCC 2205  
Qy 701 ProThrThrLeuGlnIleProProLeuProAlaIleLysHisLeuProArgProGlu 720  
Db 2206 CCAACAACATTTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCAGGCCAGAA 2265  
Qy 721 ThrLeuHisProAsnProAlaGlyLeuGlnGlnSerIleSerAspValThrThrCysLeu 740  
Db 2266 ACTCTGCACCTTAACCTGAGGCTTACAGAAAGCAATTTCTGACGTACCACTGCGCTT 2325  
Qy 741 ValAlaSerLysGluAsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMet 760  
Db 2326 GTTGCCCTCCAAGGAAATGTTTCAGTTGCAAGTCAAAATCTCACCAAGGACCGTTCTATG 2385  
Qy 761 ArgLysSerPheAspMetGlyGlyGluThrLeuLeuSerValCysProMetValProLys 780  
Db 2386 AGGAAAAGCTTTGACATGGGAGGAGAACTCTGTTGTCTGTCTGCTCCATGGTCCGAAG 2445  
Qy 781 AspLeuGlyLysSerLeuSerValGlnAsnLeuIleArgSerThrGluGluLeuAsnIle 800  
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Qy 801 GlnLeuSerGlySerGluSerSerGlySerArgGlySerGlnAspPheTyTrpLysTrp 820  
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Qy 821 ArgGluSerLysLeuPheIleThrAspGluGluValGlyProGluGluThrGluThrAsp 840  
Db 2566 AGGGAATCCAATTTGTTTATACTGATGAAGAGTGGGTCCCGAAGAGACAGACAGAC 2625  
Qy 841 ThrPheAspAlaAlaProGlnProAlaArgGluAlaAlaPheAlaSerAspSerLeuArg 860  
Db 2626 ACTTTTGTATGCGGCACCGAGCTGCCAGGGAAGTGCCTTTGCATCAGACTCTCTAAGG 2685  
Qy 861 ThrGlyArgSerArgSerSerGlnSerIleCysLysAlaGlyGluSerThrAspAlaLeu 880  
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Qy 881 SerLeuProHisValLysLeuLys 888  
Db 2746 AGCTTGCCCTCATGTCAAACTGAAA 2769

## RESULT 3

US-10-803-268-1  
; Sequence 1, Application US/10803268  
; Publication No. US20040157259A1  
; GENERAL INFORMATION:  
; APPLICANT: Hu, Yi  
; APPLICANT: Kieke, James Alvin  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Nehls, Michael C.  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: Novel Human Ion Channel Protein and  
; FILE REFERENCE: LEX-0160-USA  
; CURRENT APPLICATION NUMBER: US/10/803,268  
; CURRENT FILING DATE: 2004-03-18  
; PRIOR APPLICATION NUMBER: US/09/825,147  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: US 60/194,255  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1

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; LENGTH: 2772
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-803-268-1

Alignment Scores:
Pred. No.: 0 Length: 2772
Score: 4547.00 Matches: 888
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-810-796-5 (1-888) x US-10-803-268-1 (1-2772)

Qy 1 MetLysAspValGluSerGlyArgGlyArgValLeuLeuAanSerAlaAlaAargGly 20
Db 106 ATGAAGGATGTGGAGTCGGCGCGGCGAGGTGCTGCTGAACTCGGAGCGCGCGAGGGC 165
Qy 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
Db 166 GACGGCTGCTACTGCTGGGACCCCGCGCGCCACGCTCGGTGGCGGGCGGTGGCTG 225
Qy 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
Db 226 AGGGAGAGCCCGCGGCGCAAGCGGGCGCCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 285
Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgValGlnAanTyrLeu 80
Db 286 TACACGAGTACCGAGAGTCCCGCGCGCAACGTCAGTACCGCGGGTGCGAGACTACCTG 345
Qy 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100
Db 346 TACACGCTGCTGGAGAGCCCGCGCGCTGGCGGCTTCATCTACCAACGCTTCGTTTTCTC 405
Qy 101 LeuValPheGlyCysLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120
Db 406 CTGTGCTTTGGTGTCTGATTTGTGAGTGTTCAGTGTTTCTACCATCCCTTGAGCACACAAATG 465
Qy 121 AlaSerSerCysLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
Db 466 GCCTCAAGTGTCTTCATCTCGAGTTCGTGATGATTGTCGTTCTTTGGTTGGAGTTC 525
Qy 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160
Db 526 ATCATTGAATCTGCTCTCGCGGTGCTGTTGTCGATATAGAGGATGCAAGGAGACTG 585
Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
Db 586 AGGTTTGTCTGAAAGCCCTTCTGTGTATAGATACCATTTGTTATCGCTTCAATAGCA 645
Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
Db 646 GTTGTTCCTGCAAAACTCAGGGTAAATATTTTGCACGCTGCACTCAGAACTCCGT 705
Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220
Db 706 TTCTACAGATCTCCGATGTCGCGCATGACCGAGGGAGGCACCTTGGAAATTAATCTG 765
Qy 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240
Db 766 GTTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTATAGGATTTTGT 825
Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
Db 826 GTTCTATATTTTTCGCTCTTCCTCTCTATCTGGTGGAAAGGATGCCAATAAGAGTTT 885
Qy 261 SerThrTyrAlaAspAlaLeuTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
Db 886 TCTACATATGAGATGCTCTCTGTTGGGGCACAAATACATTGACAACTATTGGCTATGGA 945
Qy 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300

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Db 946 GACAAAACCTCCCTAACTTGGCTGGGAAGATTGCTTTCTGCAGGCTTTGCACACTCCTTGGC 1005
Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
Db 1006 ATTTCTTTCTTTGTCACATTCCTCGCGGCATTTCTTGGCTCAGGTTTGTGATTAAGATGCAA 1065
Qy 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
Db 1066 GAACACACCGCCAGAAACACTTTTGAGAAAAGAAAGAACCCAGCTGCCAATCTCATTCAG 1125
Qy 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
Db 1126 TGTGTTTGGGTAGTTACGCAGCTGATGAGAAATCTGTTCCATTGCAACTGGAAGCCA 1185
Qy 361 HisLeuLysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPheLysGluArg 380
Db 1186 CACTTGAAGGCTTTGCACACTGCAGCCCTACCAATCAGAAGCTTAAGTTTTTAAGAGAGCGA 1245
Qy 381 ValArgMetAlaSerProArgGlyGlnSerLysSerArgGlnAlaSerValGlyAsp 400
Db 1246 GTGGCATGGCTAGCCCGGCGCCAGAGTATTNAGAGCCGCAAGGCTCAGTAGGTGAC 1305
Qy 401 ArgArgSerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSer 420
Db 1306 AGGAGTTCCTCAAGACCGACATCACAGCCGAGGCGAGTCCCAACAAAGTCGAGAGAGC 1365
Qy 421 TrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerSerGlnPro 440
Db 1366 TGGAGCTTCAACGACCGAAACCGCTTCGGGCCCTCGCTGGCCCTCAAAAGTTCTCAGCCA 1425
Qy 441 LysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyrAspGluLysGly 460
Db 1426 AAACAGTGTATGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1485
Qy 461 CysGlnCysAspValSerValGluAspLeuThrProLeuLysThrValIleArgAla 480
Db 1486 TGCCAGTGTGATGTATCAGTGGAGAGCTCACCCACCACCTTAAACATGTCTATTCGAGCT 1545
Qy 481 IleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThrLeuArgProTyr 500
Db 1546 ATCAGAATATGAAATTTTCATGTTGCAAAACGGAAGTTTAAAGAAACATTAACGTCATAT 1605
Qy 501 AspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMetLeuCysArgIle 520
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Qy 521 LysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSerAspLys 540
Db 1666 AAAAGCCTTCAACACAGCTGTTGATCAATTTCTTGGAAAAGGCGCAATCACATCAGATAAG 1725
Qy 541 LysSerArgGluLysIleThrAlaGluHisGluThrThrAspAspLeuSerMetLeuGly 560
Db 1726 AAGAGCCGAGAGAAAATAACAGCAGAGACATGAGACCACAGACGATCTCAGTATGCTCGGT 1785
Qy 561 ArgValLysValGluLysGlnValGlnSerIleGluSerLysLeuAspCysLeuLeu 580
Db 1786 CGGTGTGTCAAGTTGAAAACAGGTACAGTCCATAGAAATCCAAGCTGGAGCTGCCTACTA 1845
Qy 581 AspileTyrGlnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPhe 600
Db 1846 GACATCTATCAACAGGTCTCTCGGAAGGCTCTGCCTCAGCCCTCGCTTGGCTTCATTC 1905
Qy 601 GlnIleProPheGluCysGluGlnThrSerAspTyrGlnSerProValAspSerLys 620
Db 1906 CAGATCCACCTTTTGAATGTGAACAGACATCTGACTATCAAGCCCTGTGGATAGCAAA 1965
Qy 621 AspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIle 640
Db 1966 GATCTTTGGGTTCGCGACAAAACAGTGGCTGCTTATCCAGATCAACTAGTAGGCCAACATC 2025
Qy 641 SerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAla 660
Db 2026 TCGAGAGCCCTGCGAGTTCAITCTCGACCCCAANTGAGTTCACTGCGCCAGACTTTCTACGG 2085

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QY 661 LeuSerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySer 680
Db 2086 CTTAGCCCTTACTATGCAAGTCAAGCAACACAGGTGCCAATTAGTCAAAAGCGATGGCTCA 2145
QY 681 AlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAla 700
Db 2146 GCAGTGGCAGCCACCAACACCATTCGAAACCAATAAATACGACACCAAGCCAGCAGCC 2205
QY 701 ProThrThrLeuGlnIleProProProProLeuProAlaIleLysHisLeuProArgProGlu 720
Db 2206 CCAACAACCTTACAGATCCACCTCTCTCCAGCCATCAAGCATCTGCCAGGCCAGAA 2265
QY 721 ThrLeuHisProAsnProAlaGlyLeuGlnGlnSerIleSerAspValThrThrCysLeu 740
Db 2266 ACTCTGACCCCTTAACCTTCGAGGCTTACAGAAAGCAATTCCTGAGTCACCACTGGCTT 2325
QY 741 ValAlaSerLysGluAsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMet 760
Db 2326 GTTGCTCCAAAGAAATGTTTCAGGTGCACAGTCAAAATCTCACCAAGGACCGTTCTATG 2385
QY 761 ArgLysSerPheAspMetGlyGlyLeuThrLeuLeuSerValCysProMetValProLys 780
Db 2386 AGGAAAGCTTTGACATCGGAGGAGAAACTCTGTGTCTGTCTGTCTGTCTGTCTGTCTGT 2445
QY 781 AspLeuGlyLysSerLeuSerValGlnAsnLeuIleArgSerThrGluGluLeuAsnIle 800
Db 2446 GACTTGGGCAAACTTTCTGTGTGCAAAACCTGATCAGTGCACCGAGGAACCTGAATATA 2505
QY 801 GlnLeuSerGlySerGluSerSerGlySerArgGlySerGlnAspPheTyrProLysTrp 820
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QY 821 ArgGluSerLysLeuPheIleThrAspGluGluValGlyProGluGluThrGluThrAsp 840
Db 2566 AGGGAATCCAAATGTTTATTAACATGAAGAGGTGGTCCCGAAGACAGACAGACAGAC 2625
QY 841 ThrPheAspAlaAlaProGlnProAlaArgGluAlaAlaPheAlaSerAspSerLeuArg 860
Db 2626 ACTTTGATGCGCACCCGACGCTGCCAGGAGTGGCTTGTGATCAGATCTCTTAAG 2685
QY 861 ThrGlyArgSerArgSerSerGlnSerIleCysLysAlaGlyGluSerThrAspAlaLeu 880
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## RESULT 4

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US-09-825-147-3
; Sequence 3, Application US/09825147
; Patent No. US20020042505A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Kieke, James Alvin
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael C.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020042505A1el Human Ion Channel Protein and
; FILE REFERENCE: LEX-0160-USA
; CURRENT APPLICATION NUMBER: US/09/825,147
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,255
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3111
; TYPE: DNA
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; ORGANISM: homo sapiens

US-09-825-147-3

## Alignment Scores:

Pred. No.:	0	Length:	3111
Score:	4547.00	Matches:	888
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-810-796-5 (1-888) x US-09-825-147-3 (1-3111)

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QY 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
Db 225 GACGGCTGTCTACTGTGGGCACCCGCGGCCACGCTCGGTGGCGGCGGTGGCTG 284
QY 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
Db 285 AGGAGAGCCCGCGGGCAAGCAGGGGGCCGGGATGAGCCTGTGCTGGGGGAAAGCCGCTCTCT 344
QY 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80
Db 345 TACACAGAGTGCACAGACTGCGCGGCGCAAGCTCAAGTACCGCGGGTGCAGACTACTCTG 404
QY 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100
Db 405 TACAACGTGTGGAGAGACCCCGCGGTGGCGGTTCATCTACCAACGCTTTCGTTTTCTC 464
QY 101 LeuValPheGlyCysLeuIleLeuSerValPheSerThrIleProGluHisThrLysLeu 120
Db 465 CTTGTCTTTGGTGTGATTTTGTACAGTGTCTTCTACCATCCCTGAGCAGCAGCAAAATTG 524
QY 121 AlaSerSerCysLeuLeuLeuLeuGluPheValMetIleValValPheGlyLeuGluPhe 140
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QY 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160
Db 585 ATCAATCGAATCTGGTCTGGGGTGTGTTGTTCGATATAGAGGATGCAAGGAAAGACTG 644
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QY 261 SerThrTyrAlaAspAlaLeuThrTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
Db 945 TCTACATATGAGATGCTCTCTGTTGGGGCACAATTAACATTAATGACATTAATGGCTATGGA 1004
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Db 1005 GACAAAACCTCCCTTAACCTTGGCTGGGGAAGATGCTTTTCTGCAGGCTTTGCACTCTTGGC 1064
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i ORGANISM: homo sapiens  
US-10-803-268-3

## Alignment Scores:

Pred. No.: 0 Length: 3111  
Score: 4547.00 Matches: 888  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 18 Gaps: 0

US-09-810-796-5 (1-888) x US-10-803-268-3 (1-3111)

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QY 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
DB 225 GACGGCTGTACTGTGGCACC CGCGCCACGCTCGGTGGCGGGTGGCTG 284
QY 41 ArgGluSerArgArgGlyGlyGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60
DB 285 AGGGAGAGCGCGGGGCAAGCAGGGCGCCCGGATGAGCCCTGTGGGAAAGCCGCTCTCT 344
QY 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgValGlnAsnTyrLeu 80
DB 345 TACAGGATGCCAGAGCTGCGGGCGCAACGTCAAGTACCGGGGTGCAGACTACCTG 404
QY 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100
DB 405 TACACGTGTCTGGAGAGACCGCGCGCTGGCGCTTCACTACACGCTTTCGTTTTCTC 464
QY 101 LeuValPheGlyCysLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120
DB 465 CTGTGCTTGGTGTGATTTGTTCAGTGTTCCTACCATCCCTTGACACACAAAAATTG 524
QY 121 AlaSerSerCysLeuLeuLeuPheValMetIleValValPheGlyLeuGluPhe 140
DB 525 GCCTCAAGTGTCTCTGATCTGGAGTTCGTGATGATGTGCTTGTGTTGGAGTTC 584
QY 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160
DB 585 ATCATTCGAATCTGTGCTGCGGGTGTGTTGTGCGATATAGAGGATGCAAGGAGACTG 644
QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180
DB 645 AGTTTGTCTGAAAGCCCTTCGTGTTATAGATACATTTGTTATCGCTTCAATAGCA 704
QY 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200
DB 705 GTTGTCTTCTGCAAAACTCAGGTAATATTTTTCACAGTCTGCACTCAGAACTCCGT 764
QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220
DB 765 TTCTACAGATCCTCCGATGTGGCGCATGACCGAGGGGAGGCACTTGGAAATTTACTG 824
QY 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTyrIleGlyPheLeu 240
DB 825 GGTTCAGTGGTTATGCTCACAGCAGGAATTAATCAACAGCTTGTGATAGGATTTTGT 884
QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260
DB 885 GTTCTATATTTTCTGCTTCTCTGCTATCTGTGGAAAGGATGCCAATAAAGAGTTT 944
QY 261 SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280
DB 945 TCTACATATGAGATGCTCTCTGTGGGGCAATATTAATCAATGCAACTATTGGGTATGGA 1004
QY 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuGly 300
DB 1005 GACAAACTCCCTTAACCTTGGCTGGGAGATTTGCTTCTGACGGCTTTCCTCTGCGC 1064

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QY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320
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QY 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
DB 1125 GAACAACACGCCAGAAACACTTTTGAGAAAAGAGGAACCCAGCTGCCAACCTCATTCAG 1184
QY 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
DB 1185 TGTGTTTGGCGTAGCTTACGACAGCTGATGAGAAATCTGTTCATTGCAACCTGGAAGCCA 1244
QY 361 HisLeuLysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPheLysGluArg 380
DB 1245 CACTTGAAGGCTTGGCACCTCGACCTTACCCTTACCAATCAGAAAGCTTAAGTTTTAAGAGCGA 1304
QY 381 ValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAsp 400
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QY 401 ArgArgSerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSer 420
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QY 421 TrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerSerGlnPro 440
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QY 461 CysGlnCysAspValSerValGluAspLeuThrProLeuLysThrValIleArgAla 480
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QY 541 LysSerArgGluLysIleThrAlaGluHisGluThrThrAspAspLeuSerMetLeuGly 560
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QY 561 ArgValLysValGluLysGlnValGlnSerIleGluSerLysLeuAspCysLeuLeu 580
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QY 581 AspIleTyrGlnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLysPhe 600
DB 1905 GACATCTATCAACAGGTCTTCGAAAGGCTCTGCGCTCAGCCCTCGCTTTGGCTTCATTC 1964
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DB 1965 CAGATCCACCTTTTGAATGTGAACAGACATCTGACTATCAAAAGCCCTGTGGATAGCAAA 2024
QY 621 AspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIle 640
DB 2025 GATCTTTTCGGGTTCGCGACAAAACAGTGGCTGTCTTATCCAGATCACTAGTGGCAACATC 2084
QY 641 SerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyrAla 660
DB 2085 TCGAGAGGCTTCAGTTCATCTTCAGCGCCAAATAGTTCAGTGCACAGACTTTCTACGGC 2144
QY 661 LeuSerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySer 680

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Qy 701 ProThrThrLeuGlnIleProProLeuProLeuProAlaIleLysHisLeuProArgProGlu 720  
Db 2265 CCAACAACTTTTACAGATCCCACTCTCTCCAGCCATCAAGCATCTGCCAGCCAGAA 2324  
Qy 721 ThrLeuHisProAsnProAlaGlyLeuGlnGlnSerIleSerAspValThrCysLeu 740  
Db 2325 ACTCTGACCTTACCTTGAGGCTTACAGAAAGCAATTTCTGAGTCACCACTGCCCTT 2384  
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Db 2385 GTTGCTCCAAAGGAAATGTTTCAGGTTGCACAGTCAATCTCACCAAGGACCGTTCATG 2444  
Qy 761 ArgLysSerPheAspMetGlyGlyLeuThrLeuLeuSerValCysProMetValProLys 780  
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Qy 801 GlnLeuSerGlySerGluSerSerGlySerArgGlySerGlnAspPheThrProLysTrp 820  
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Qy 861 ThrGlyArgSerArgSerSerGlnSerIleCysLysAlaGlyGluSerThrAspAlaLeu 880  
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Qy 881 SerLeuProHisValLysLeuLys 888  
Db 2805 AGCTTGCCCTCATGTCAAACTGAAA 2828

## RESULT 6

US-09-866-020-1  
; Sequence 1, Application US/09866020  
; Publication No. US20020040000A1  
; GENERAL INFORMATION:  
; APPLICANT: DWORETZKY, STEVEN I  
; APPLICANT: RAMANATHAN, CHANDRA S  
; APPLICANT: TROJNACKI, JOANNE T  
; APPLICANT: BOISSARD, CHRISTOPHER G  
; APPLICANT: GRIEBOFF, VALENTIN K  
; TITLE OF INVENTION: HUMAN KCNQ5 POTASSIUM CHANNEL METHODS AND COMPOSITIONS  
; FILE REFERENCE: THEREOF  
; FILE REFERENCE: 3053-4091US1  
; CURRENT APPLICATION NUMBER: US/09/866,020  
; CURRENT FILING DATE: 2001-05-24  
; PRIOR APPLICATION NUMBER: 60/207,389  
; PRIOR FILING DATE: 2000-05-26  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 2694  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-020-1  
Alignment Scores:

Pred. No.: 0 Length: 2694  
Score: 4527.50 Matches: 887  
Percent Similarity: 99.00% Conservative: 1  
Best Local Similarity: 98.89% Mismatches: 0  
Query Match: 99.57% Indels: 9  
DB: 9 Gaps: 1  
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Qy 1 MetLysAspValGluSerGlyArgValLeuLeuAsnSerAlaAlaAaArgGly 20  
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Qy 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeu 40  
Db 61 GACGGCTGTCTACTGTGGGCACCCGGCGGCCACGCTTGGTGGCGGGCGGTGGCGCTG 120  
Qy 41 ArgGluSerArgArgGlyLysGlnGlyValArgMetSerLeuLeuGlyLysProLeuSer 60  
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Qy 61 TyrThrSerGlnSerCysArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80  
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Qy 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100  
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Db 301 CTGTGCTTTGGTGTCTGTGATTTTGTCTAGTGTCTTCTACCATCTCTGAGCACAAAAATG 360  
Qy 121 AlaSerCysLeuLeuIleLeuGluPheValMetIleValValPheGlyLeuGluPhe 140  
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Qy 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160  
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Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180  
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Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200  
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Qy 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240  
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Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260  
Db 721 GTTCTTATTTTCT 780  
Qy 261 SerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280  
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Qy 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300  
Db 841 GACAAAACCTCCCTAACTTGGCTGGGGAAGATGCTTTTTCGAGGCTTTTGCACCTCTTGGC 900  
Qy 301 IleSerPheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320  
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Qy 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340
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Qy 341 CysValTrpArgSerTyAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360
Db 1021 TGTGTTTGGCGTAGTTAGCGAGCTGATGAGAAATCTGTTTCATTTGCAACCTGGAAGCCA 1080
Qy 361 HisLeuLysAlaLeuHisThrCysSerProThr----- 371
Db 1081 CACTTGAAGGCTTGCACACCTGCGAGCCTACCAGAAAGAACAGGGAAGCATCAAGC 1140
Qy 372 AsnGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 391
Db 1141 AGTCAGAGCTAAGTTTAAAGAGCGAGTGGCGATGGCTAGCCCCAGGGGCCAGAGTATT 1200
Qy 392 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 411
Db 1201 AAGAGCCGACAAAGCCTCAGTAGGTGACAGGAGGTCCCCAAGCAGCATCACAGCCGAG 1260
Qy 412 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 431
Db 1261 GCGAGTCCCAACCAAGTCAGAGAGCTGGAGCTTCAACGACCGAACCCGCTTCGGGCC 1320
Qy 432 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 451
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Qy 452 ThrAspAspValTyArgGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 471
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Qy 472 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaIleArg 491
Db 1441 CCACCACTTAACACTGCTATTCGAGCTATCAGAAATTATGAATTTTCATGTGCAAAACGG 1500
Qy 492 LysPheLysGluThrLeuArgProTyArgValLysAspValIleGluGlnTySerAla 511
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Qy 532 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 551
Db 1621 GGAAAGGCGCAATCACATCAGATAGAAAGAGCCGAGAGAAATAACACGACACATGAG 1680
Qy 552 ThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSer 571
Db 1681 ACCACAGACGATCTCAGTATGCTCGGTGGGTGTCAGGTGTAAGGTTGAAACACAGGTACAGTCC 1740
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Db 1741 ATAGAGTCCAGCTGGAGCTGCTACTAGACATCTATCAACAGGTCCTTCGGAAGGCTCT 1800
Qy 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 611
Db 1801 GCCTCAGCCCTCGCTTGGCTTCATTCAGATCCACCTTTTGAATGTGAACACACATCT 1860
Qy 612 AspTyArgGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631
Db 1861 GACTATCAAGCCCTGTGGATAGCAAGATCTTTCGGGTTCGACACAAAACAGTGGCTGC 1920
Qy 632 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651
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Qy 652 GluPheSerAlaGlnThrPheTyArgAlaLeuSerProThrMetHisSerGlnAlaThrGln 671
Db 1981 GAGTTCAGTCCGACGACTTCTACGCGCTTAGCCCTACTATGCACAGTCAGCAACACAG 2040
Qy 672 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 691
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Qy 752 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 771
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Qy 772 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 791
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Qy 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 851
Db 2521 GTGGTCCCGAGAGACAGACAGACACATTTTGTATGCCGACCGCAGCTGCCAGGGAA 2580
Qy 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 871
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RESULT 7
US-09-810-796-2
; Sequence 2, Application US/09810796
; Patent No. US20020102677A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy James
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: KCN05, a No. US20020102677A1el Potassium Channel
; FILE REFERENCE: 018512-005010US
; CURRENT APPLICATION NUMBER: US/09/810,796
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/190,954
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human outwardly-rectifying, voltage-gated
; OTHER INFORMATION: potassium channel KCNQ5-1 coding sequence
; NAME/KEY: CDS
; LOCATION: (1)..(2694)
; OTHER INFORMATION: KCNQ5-1
US-09-810-796-2

Alignment Scores: 0 Length: 2694
Pred. No.: 4527.50 Matches: 887
Score:
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Db 1081 CACTTGAAGGCGCTTGACACCTCGACGCGCTTACCAAGAAAGAAACAAGGGAAGCATCAAGC 1140
Qy 372 AsnGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 391
Db 1141 AGTCAGAGAGCTAAAGTTTAAAGAGCGAGTGCGCATAGCTAGCCCGACGAGGCGCAGATATT 1200
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Qy 412 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 431
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Qy 432 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 451
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Qy 632 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651
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Qy 752 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 771
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Db 2401 ATCAGTTCGACCGAGGAACTGAAATATACAATTTTCAGGAGTGAGTCAAGTGGCTCCAGA 2460
Qy 812 GlySerGlnAspPheTyProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 831
Db 2461 GGCAGCCCAAGATTTTACCCCAATGAGGGAATCCAAATTTGTTATAACTGTATCAAGAG 2520
Qy 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaIleProGlnProAlaArgGlu 851
Db 2521 GTGGGTCCCAAGAGACAGACAGACACTTTTGATCCGACCCAGCCCTGCCAGGGAA 2580
Qy 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerGlnSerIleCys 871
Db 2581 GCTGCCCTTGCATCAGACTCTCTAAGGACTTGAAGGTCAAGATCATCTCAGAGCATTTGT 2640
Qy 872 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 888
Db 2641 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACCTGAAA 2691
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## RESULT 9

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US-10-661-629-1
; Sequence 1, Application US/10661629
; Publication No. US20040180405A1
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNELS AND GENES ENCODING THESE POTASSIUM CHANNELS
; FILE REFERENCE: 2815-0236P
; CURRENT APPLICATION NUMBER: US/10/661,629
; CURRENT FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3137
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2691)
US-10-661-629-1
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## Alignment Scores:

Pred. No.:	0	Length:	3137
Score:	4527.50	Matches:	887
Percent Similarity:	99.00%	Conservative:	1
Best Local Similarity:	98.89%	Mismatches:	0
Query Match:	99.57%	Indels:	9
DB:	18	Gaps:	1

US-09-810-796-5 (1-888) x US-10-661-629-1 (1-3137)

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Qy 1 MetLysAspValGluSerGlyArgGlyArgValLeuLeuAsnSerAlaAlaArgGly 20
Db 1 ATGAAGATGTGAGTGGGCGGCGGAGGTGTGTGTAACCTCGGACGCCCGCCAGGGGC 60
Qy 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40
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Db ||||| 61 GACGGCTGTACTGCTGGGCAACCGCGGCACGCTCGTGGCGGGCGGTGGCCTG 120  
Qy 41 ArgGluSerArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60  
Db 121 AGGAGAGCCCGGGGCAAGCAGGGGGCCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 180  
Qy 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80  
Db 181 TACACGAGTAGCCAGAGCTGCCGGCGCAACGTCAGATACCGGGGGTGCAGNACTACCTG 240  
Qy 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100  
Db 241 TACAAACGCTGCTGGAGAGACCCCGCGCTGGCGGTCATCTACACGCTTCGTCTTC 300  
Qy 101 LeuValPheGlyCysLeuLeuSerValPheSerThrIleProGluHisThrIysLeu 120  
Db 301 CTGTGCTTTGGTGTCTGATTTGTGAGTGTTCCTACCATCCCTGGAGCACACAAATTTG 360  
Qy 121 AlaSerSerCysLeuLeuLeuPheValMetIleValValPheGlyLeuGluPhe 140  
Db 361 GCCTCAAGTTGCTCTTCATCTGGAGTTCGTGATGATGTCTTCCTTTGGTGGAGTTC 420  
Qy 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160  
Db 421 ATCATTCGAATCTGCTGCGGGTGTCTGTTCGATATAGAGGATGGCAAGGAAGACTG 480  
Qy 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIleAla 180  
Db 481 AGGTTTGTCTGNAAGCCCTTCGTGTTATAGATACCATTTGTTCTTCCTGCTTCATAGCA 540  
Qy 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200  
Db 541 GTTGTTCCTGCAAAACTCAGGTAATATTTTGGCACGCTCGCACTCAGAACTCCGT 600  
Qy 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220  
Db 601 TTCTTACAGATCTCTCGATGTCGCATGGACCGAAGGGGAGGCACCTTGGAAATTTACTG 660  
Qy 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240  
Db 661 GGTTCAAGTGGTTATGCTCACAGCAGGAATTAATCACAGCTTGTGATAGGATTTTGT 720  
Qy 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260  
Db 721 GTTCTTAITTTTCTGCTCTCTGCTATCTGGTGGGCAATATACATTTGCAACTATTTGGCTATGGA 780  
Qy 261 SerThrTyrAlaAspAlaLeuTrpGlyThrIleThrLeuThrIleGlyTyrGly 280  
Db 781 TCTCATATGAGATGCTCTCTGGTGGGCAATATACATTTGCAACTATTTGGCTATGGA 840  
Qy 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300  
Db 841 GACAAACTCCCTTAACCTTGGCTGGGAGATGCTTCTCGAGGCTTTGCACTCTCTGGC 900  
Qy 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320  
Db 901 ATTTCTTTCTTGGACTTCTGCGGCATCTCTGGCTCAGGTTTTTGCATTTAAAGTACAA 960  
Qy 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340  
Db 961 GAACAACACCCCGAGAAACATTTGAGAAAGAGAGAACCCAGCTGGCCAACTCATTTGAG 1020  
Qy 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360  
Db 1021 TGTGTTGGCTGAGTACGAGCTGATGAGAAATCTGTTTCATTTGCNACCTGGAAGCCA 1080  
Qy 361 HisLeuLysAlaLeuHisThrCysSerProThr----- 371  
Db 1081 CACTTGAAGGCTTGCAACCTGCGAGCCCTACCAAGAAAGAAACCAAGGGAAGCATCAAGC 1140  
Qy 372 AsnGlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 391  
Db :|||

Db 1141 AGTCAGAGCTAAAGTTTAAAGAGCGAGTGGCATGGCTAGCCCCAGGGGCCAGAGTATT 1200  
Qy 392 LysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu 411  
Db 1201 AAGAGCCGACAAGCCTCAGTAGGTGACAGGAGGTCCCAAGCACCGCATCACAGCCGAG 1260  
Qy 412 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgTrpArgPheArgPro 431  
Db 1261 GGCAAGTCCCAACCAANGTGCAGAGAGCTGGAGCTTCAACGACCGAAACCGGCTTCGGGCC 1320  
Qy 432 SerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 451  
Db 1321 TCGCTGGCGCTCAAAAGTTCTCAGCCAAACACCAAGTATAGATGTGACACAGCCCTTGGC 1380  
Qy 452 ThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 471  
Db 1381 ACTGATGATGATATGATGAAAGAGTGCAGTGTGATGTATCAGTGGAGAGACTCACC 1440  
Qy 472 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 491  
Db 1441 CCACCACCTTAAACCTGTTCATTCGAGCTATCAGAATTTATGAAATTTTCATGTTGCAACGG 1500  
Qy 492 LysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAla 511  
Db 1501 AAGTTTAAAGGAAACATTTACGTCCATATGATGATAAGATGTTCATTTGAACAATATTCGT 1560  
Qy 512 GlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 531  
Db 1561 GGTCACTCGACATGTTGTAGATTTAAAGCCCTTCAAAACACGTGTGATCAAAATTCCT 1620  
Qy 532 GlyLysGlyGlnIleThrSerAspLysSerArgGluLysIleThrAlaGluHisGlu 551  
Db 1621 GGAAGAGGCAATCATCAGATAAGACGCGAGAGAAATAACACAGACAACATGAG 1680  
Qy 552 ThrThrAspAspLeuSerMetLeuGlyArgValLysValGluLysGlnValGlnSer 571  
Db 1681 ACCACAGACGATCTCAGTATGCTCGGTGGGTGGTCAAGGTTGAAAAACAGGTACAGTCC 1740  
Qy 572 IleGluSerLysLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySer 591  
Db 1741 ATAGATCCAAGCTGGACTGCTACTAGACATCTATCAACAGGTCTTCGGAAGGCTCT 1800  
Qy 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 611  
Db 1801 GCCTCAGCCCTCGCTTTGGCTTCATTCAGATCCACATCCCATTTTGAATGTGAACAGACATCT 1860  
Qy 612 AspTyrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631  
Db 1861 GACTATCAAAAGCCCTGTGGATAGCAAGATCTTTGGGGTTCCGCACAAAAACAGTGGCTGC 1920  
Qy 632 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651  
Db 1921 TTATCCAGATCAACTAGTGCCAACTCTCGAGAGGCTCGAGTTTCATCTGACGCCAAAT 1980  
Qy 652 GluPheSerAlaGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671  
Db 1981 GAGTTCAAGTCCAGACTTTCTACGGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2040  
Qy 672 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 691  
Db 2041 GTGCCAATTAGTCAAGCGATGCTCAGCAGTGGCAGCCACCAACCATTTGCAAAACCAA 2100  
Qy 692 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro 711  
Db 2101 ATAAATACGCCACCCAGCCAGCAGCCCAACAACTTTACAGATCCACCTCTCTCTCCA 2160  
Qy 712 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 731  
Db 2161 GCCATCAAGCATCTGCGCAGGCAGAACTCTGCACCTAACCTGACGCTTACAGGAA 2220  
Qy 732 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 751  
Db 2221 AGCATTTCTGACGTCAACCTGCTTTGTCCTCCAAAGGAAATGTTTCAGGTTGACAG 2280



QY 752 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 771  
DB 2281 TCAAATCTCACCAGGACCGTTCTATGAGGAAAGCTTTGACATGGGAGGAGAACTCTG 2340  
QY 772 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 791  
DB 2341 TTGCTGTCTGTCCCATGGTCCGGAAGACTTGGCAAAATCTTTGTCTGTGCAAAACCTG 2400  
QY 792 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGlySerSerGlySerArg 811  
DB 2401 ATCAGGTCCGAGGAACTGAATATACAACTTTTCAGGAGTGAGTCAAGTGGCTCCAGA 2460  
QY 812 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 831  
DB 2461 GGCAGCCCAAGATTTTACCCCAATGGAGGAAATCCAAATTTGTTTATTAACATGATGAGAG 2520  
QY 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaAProGlnProAlaArgGlu 851  
DB 2521 GTGGTCCCGAAGACAGACAGACACTTTTGAATGCCGACCCGACCTGCCAGGGA 2580  
QY 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 871  
DB 2581 GCTGCTTTGCATCAGACTCTCTAAGGACTGGAAGGTCAAGTCACTCATCTCAGAGCATTTGT 2640  
QY 872 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 888  
DB 2641 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAA 2691

## RESULT 10

US-09-810-796-1  
; Sequence 1, Application US/09810796  
; Patent No. US20020102677A1  
; GENERAL INFORMATION:  
; APPLICANT: Jega, Timothy James  
; APPLICANT: ICAGEN, Inc.  
; TITLE OF INVENTION: KCNQ5, a No. US20020102677A1el Potassium Channel  
; FILE REFERENCE: 018512-005010US  
; CURRENT APPLICATION NUMBER: US/09/810,796  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 60/190,954  
; PRIOR FILING DATE: 2000-03-21  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 3071  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human outwardly rectifying, voltage-gated  
; OTHER INFORMATION: potassium channel KCNQ5-1  
; NAME/KEY: CDS  
; LOCATION: (10)..(2703)  
; OTHER INFORMATION: KCNQ5-1  
US-09-810-796-1

## Alignment Scores:

Pred. No.:	0	Length:	3071
Scores:	4523.50	Matches:	886
Percent Similarity:	98.89%	Conservative:	1
Best Local Similarity:	98.77%	Mismatches:	1
Query Match:	99.48%	Indels:	9
DB:	9	Gaps:	1

US-09-810-796-5 (1-888) x US-09-810-796-1 (1-3071)

QY 1 MetLysAspValGluSerGlyArgValLeuLeuAsnSerAlaAlaArgGly 20  
DB 10 ATGAAGGATGTGGAGTCGGCGCGGAGGTGCTGCTGAACTCGGCAGCGCCAGGGGC 69  
QY 21 AspGlyLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40  
DB 70 GACGGCCTGCTACTGCTGGGCAACCCGCGGCCACGCTTGGTGGCGGGGGTGGCCTG 129

QY 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysPheLeuSer 60  
DB 130 AGGAGAGCCCGCGGCGCAAGCAGGGGCGCGGATGAGCCTGCTGGGGAAGCCGCTCTCT 189  
QY 61 TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyrLeu 80  
DB 190 TACACAGAGTACCCAGAGCTGCCGCGCAACGTCAAGTACCGCGGCGGTGCAGACTACCTG 249  
QY 81 TyrAsnValLeuGluArgProArgGlyTrpAlaPheIleTyrHisAlaPheValPheLeu 100  
DB 250 TACAACGTGCTGGAGAGACCCCGCGCTGGCGGTTTCATCTACCAACGCTTCGTTTTCTC 309  
QY 101 LeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeu 120  
DB 310 CTTGCTCTTGGTTGCTTGAATTTGTCAGTGTTTCTTACCATCCCTGAGCACACAAATG 369  
QY 121 AlaSerSerCysLeuLeuLeuGlnPheValMetIleValValPheGlyLeuGluPhe 140  
DB 370 GCCTCAAGTTCGCTTCATCCTCGAGTTCGTGATGATTCGTCCTTTGGTTTGGAGTTC 429  
QY 141 IleIleArgIleTrpSerAlaGlyCysCysArgTyrArgGlyTrpGlnGlyArgLeu 160  
DB 430 ATCATTGCAATCTGCTCGCGGTTGCTGTTGTCGATATAGAGGATGCAAGGAAGACTG 489  
QY 161 ArgPheAlaArgLysProPheCysValIleAspThrIleValLeuLeuAlaSerIleAla 180  
DB 490 AGGTTGCTCGAAAGCCCTTCTGTGTTATAGATACCATTTGTTTATCGCTTCAATAGCA 549  
QY 181 ValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeuArg 200  
DB 550 GTTGTTCGCAAAACCTCAGGGTAATATTTTGCACGCTGCAAGTCTCCGT 609  
QY 201 PheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTrpLysLeuLeu 220  
DB 610 TTCTTACAGATCCTCCGATGTCGTCATGACCGAAGGAGGACACTTGGAAATTAATG 669  
QY 221 GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTrpTyrIleGlyPheLeu 240  
DB 670 GGTTCAGTGGTTTATGCTCACAGCAAGGAATTAATCACAGCTTGGTACATAGGATTTG 729  
QY 241 ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe 260  
DB 730 GTTCTTATTTTTCGTTCTTCTTCCTGTCATCTGGTGGAAAGGATGCCAAATAAGAGTT 789  
QY 261 SerThrTyrAlaAspAlaLeuTrpGlyThrIleThrLeuThrThrIleGlyTyrGly 280  
DB 790 TCTACATATGCAGATGCTCTCTGGTGGGCAACAATTACATTGACAACTATTGGCTATGA 849  
QY 281 AspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGly 300  
DB 850 GACAAACTCCCTAACTTGGCTGGGAAGATTGCTTCTGCAAGGCTTTGCACTCTCTGCG 909  
QY 301 IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln 320  
DB 910 ATTTCTTTCTTTGCACTTCCTCGCGGCATCTTGGCTCAGGTTTGGCAATTAAGATACA 969  
QY 321 GluGlnHisArgGlnLysHisPheGluLysArgArgAsnProAlaAlaAsnLeuIleGln 340  
DB 970 GAACAACACCCGACAGAAACACTTTGAGAAAGAGAGAACCCAGCTGCCAACCCTCATTC 1029  
QY 341 CysValTrpArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysPro 360  
DB 1030 TGTGTTGGCGTAGTTACGCAGCTGATGAGAAATCTGTTTCCATTGCAACCTGGAAGCA 1089  
QY 361 HisLeuLysAlaLeuHisThrCysSerProThr----- 371  
DB 1090 CACTTGAAGGCTTTGCACACCTGACGCTGAGGAAAGAACCAAGGGAAGCATCAAGC 1149  
QY 372 AsnGlnLysLeuSerPhePheLysGluArgValArgMetAlaSerProArgGlyGlnSerIle 391  
DB 1150 AGTCAGAGACTAAGTTTAAAGAGGAGTGGCATGGCTAGCCCCCAGGGGCCAGATATT 1209

Qy 392 LysSerArgGlnAlaSerValGlyAspArgSerProSerThrAspIleThrAlaGlu 411  
Db 1210 AAGAGCCGACAAAGCTCAGTAGGTGACAGGAGGTCCCAAGCACCAGCATCACAGCCGAG 1269  
Qy 412 GlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgPro 431  
Db 1270 GGCAAGTCCCAAGTGCAGAAAGAGTGGAGCTTCAACGACCGAACCCGCTTCGGGCC 1329  
Qy 432 SerLeuArgLeuLysSerGlnProLysProValIleAspAlaAspThrAlaLeuGly 451  
Db 1330 TCGTGGCCCTCAAAAGTTCTCAGCCAAACAGTAGATAGTGTGACACAGCCCTTGGC 1389  
Qy 452 ThrAspAspValThrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThr 471  
Db 1390 ACTGATGATGATATGATGATAAAGAGTGCAGTGTGATGATCAGTGGAAAGACTCAC 1449  
Qy 472 ProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArg 491  
Db 1450 CCACCACTTAAACCTGCTCATTGAGCTATCAGAAATTATGAAATTTCATGTTGCCAAACGG 1509  
Qy 492 LysPheLysGluThrLeuArgProThrAspValLysAspValIleGluGlnIleThrSerAla 511  
Db 1510 AAGTTTAAGGAAACRTTACGTCCATATGATGATAAAGATGTCATTTGAACAATATCTGCT 1569  
Qy 512 GlyHisLeuAspMetLeuLysArgIleLysSerLeuGlnThrArgValAspGlnIleLeu 531  
Db 1570 GGTCACTCGGACATGTTGTGTAGAAATTAAGAGCTTCAACACAGCTGTGTGATCAAAATCTT 1629  
Qy 532 GlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluHisGlu 551  
Db 1630 GGAAAGAGGCAAAATCACATCAGTAAGAAGAGCCGAGAGAAATAAACAAGCAGACATGAG 1689  
Qy 552 ThrThrAspAspLeuSerMetLeuGlyArgValLysValLysValGluLysGlnValGlnSer 571  
Db 1690 ACCACAGACATCTCAGTATGCTGGTGGGTGTCAAGTTTGAAACAGAGTACAGTCC 1749  
Qy 572 IleGluSerLysLeuAspCysLeuAspIleThrGlnGlnValLeuArgLysGlySer 591  
Db 1750 ATAGAATCCAAGCTGGAGCTACTACATCATCATCAACAGGTCTTCGGAAGGCTCT 1809  
Qy 592 AlaSerAlaLeuAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSer 611  
Db 1810 GCCTCAGCCCTCGCTTGGCTTCATTCAGTTCCTCCACCTTTTGAATGGAACACAGATCT 1869  
Qy 612 AspThrGlnSerProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCys 631  
Db 1870 GACTATCAAGCCCTGTGATAGCAAGATCTTTCCGGTTCGACACAAACAGTGGCTGC 1929  
Qy 632 LeuSerArgSerThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsn 651  
Db 1930 TTATCCAGATCAACTAGTGCCCAACATCTCGAGAGCCCTGCAAGTTCAATTCGACGCCAAAT 1989  
Qy 652 GluPheSerAlaGlnThrPheThrAlaLeuSerProThrMetHisSerGlnAlaThrGln 671  
Db 1990 GAGTTCAAGTCCAGACTTCTAGCGCTTAGCCCTACTATGCACAGTCAAGCAACACAG 2049  
Qy 672 ValProIleSerGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGln 691  
Db 2050 GTGCCAATTAGTCAAGCGATGGCTCAGCAGTGGCAGCCACCAACACCATTTGCAACCAA 2109  
Qy 692 IleAsnThrAlaProLysProAlaAlaProThrThrLeuGlnIleProProProLeuPro 711  
Db 2110 ATAAATACGGCACCACCAAGCCAGCAGCCCAACAACTTTACAGATCCCACTCTCTCCCA 2169  
Qy 712 AlaIleLysHisLeuProArgProGluThrLeuHisProAsnProAlaGlyLeuGlnGlu 731  
Db 2170 GCCATCAGCAATCTGCCAGCCGCAAAACTCTGCACCCCTAACCTTCGAGGCTTACAGGAA 2229  
Qy 732 SerIleSerAspValThrThrCysLeuValAlaSerLysGluAsnValGlnValAlaGln 751  
Db 2230 AGCATTTCTGACGTCAACCACTGCTTGTTCCTCCCAAGGAAATGTTTCAGTTGTCACAG 2289  
Qy 752 SerAsnLeuThrLysAspArgSerMetArgLysSerPheAspMetGlyGlyGluThrLeu 771

Db 2290 TCAAATCTCAAGGACCGTTCTATGAGGAAAAGCTTTGACATGGGAGGAGAACTCTG 2349  
Qy 772 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 791  
Db 2350 TTGTCTGTCTGTCCATGGTGGCCGAGGACTTGGGCAAACTTTTGTCTGTGCAAAACCTG 2409  
Qy 792 IleArgSerThrGluGluLeuAsnIleGlnLeuSerGlySerGluSerSerGlySerArg 811  
Db 2410 ATCAGGTGAGCCGAGGAGTGAATATACACTTTCAGGAGTGAGTCAAGTGGCTCCAGA 2469  
Qy 812 GlySerGlnAspPheThrProLysTrpArgGluSerLysLeuPheIleThrAspGluGlu 831  
Db 2470 GGCAGCCAAAGATTTTACCCCAATGGAGGAAATCCAAATTTGTTTATAACTGTATGAAGAG 2529  
Qy 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaProGlnProAlaArgGlu 851  
Db 2530 GTGGGTCCCAAGAGACAGACAGACACTTTTATGCCGACCCGAGCCCTGCCAGGGAA 2589  
Qy 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 871  
Db 2590 GCTGCCCTTGCATCAGACTCTTAAGGACTGGAAGGTCAAGATCATCTCAGAGCATTTGT 2649  
Qy 872 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 888  
Db 2650 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCCTCATGTCAAACTGAAA 2700

## RESULT 11

US-09-813-148-1

; Sequence 1, Application US/09813148

; Patent No. US20020076809A1

; GENERAL INFORMATION:

; APPLICANT: STEINMEYER, Klaus

; APPLICANT: LERCHE, Christian

; APPLICANT: SCHERER, Constanze

; APPLICANT: SEEBOHM, Guiscard

; APPLICANT: BUSCH, Andreas E.

; TITLE OF INVENTION: POTASSIUM CHANNEL PROTEIN KCNQ5, A NEW TARGET FOR DISEASES OF CEN

; FILE REFERENCE: 38005-119

; CURRENT APPLICATION NUMBER: US/09/813,148

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: DE 100 13 732.6

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: US 60/194,041

; PRIOR FILING DATE: 2000-04-03

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 3074

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-813-148-1

## Alignment Scores:

Pred. No.:	0	Length:	3074
Score:	4513.50	Matches:	885
Percent Similarity:	98.77%	Conservative:	1
Best Local Similarity:	98.66%	Mismatches:	2
Query Match:	99.26%	Indels:	9
DB:	9	Gaps:	1

US-09-810-796-5 (1-888) x US-09-813-148-1 (1-3074)

Qy 1 MetLysAspValGluSerGlyArgGlyValLeuLeuAsnSerAlaAlaArgGly 20  
Db 215 ATGAAGATGTGGAGTGGGCCGGGGGAGGTGCTGTGAACTCGGACGCCGAGGGGC 274  
Qy 21 AspGlyLeuLeuLeuLeuGlyThrArgAlaAlaThrLeuGlyGlyGlyGlyLeu 40  
Db 275 GACGGCTGTACTGTCTGGGACCCCGCGCCACGCTTGTGTGGCGCGGTGGCTG 334  
Qy 41 ArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeuLeuGlyLysProLeuSer 60



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Qy 772 LeuSerValCysProMetValProLysAspLeuGlyLysSerLeuSerValGlnAsnLeu 791
Db 2555 TTGCTGTCTGTCCTCCATGTCGCGAGAGACTTGGCAAAATCTTTGTCTGTGCAAAACCTG 2614
Qy 792 IleArgSerThrGluLeuAsnLeuGlnLeuSerGlySerGluSerSerGlySerArg 811
Db 2615 ATCAGTTCGACCGAGGAACTGAATATACAACTTTTCAGGGAGTGAGTCAAGTGGCTCCAGA 2674
Qy 812 GlySerGlnAspPheTyrProLysTrpArgGluSerLysLeuPheIleThrAspGlu 831
Db 2675 GCGACCCAGATTTTACCCCAATGAGGGAATCCAAATTTGTTATTAACATGATGAAGAG 2734
Qy 832 ValGlyProGluGluThrGluThrAspThrPheAspAlaAlaProGlnProAlaArgGlu 851
Db 2735 GTGGGTCCGAGAGACAGACACACTTTTGATGCCGACCCACCCATGCTCCAGGAA 2794
Qy 852 AlaAlaPheAlaSerAspSerLeuArgThrGlyArgSerArgSerSerGlnSerIleCys 871
Db 2795 GCTGCTTTGCATCAGACTCTCTAAGGACTGGAAGTCAAGATCATCTCAGAGCATTTGT 2854
Qy 872 LysAlaGlyGluSerThrAspAlaLeuSerLeuProHisValLysLeuLys 888
Db 2855 AAGCAGGAGAAAGTACAGATGCCCTCAGCTTGCTCCTCATGTCAAACTGAAA 2905

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## RESULT 12

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US-10-353-690-55
; Sequence 55, Application US/10353690
; Publication No. US20030215840A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyoung
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Healy, Aileen
; APPLICANT: Acton, Susan L.
; APPLICANT: Donoghue, Mary
; APPLICANT: Stagliano, Nancy
; APPLICANT: Perodin, Jacqueline
; APPLICANT: Rodrigue-Way, Amelie
; TITLE OF INVENTION: Methods and compositions for treating
; cardiovacular disease using 1882, 6169, 6193, 7771, 14395,
; 29002, 33216, 43726, 69292, 26156, 32427, 2402, 7747, 1720,
; 9151, 60491, 1371, 7077, 33207, 1419, 18036, 16105, 38650,
; 14245, 58848, 1870, 25856, 32394, 3484, 345, 9252, 9135,
; 10532, 18610, 8165, 2448, 2445, 64624, 84237, 912, 2868,
; 283, 2554, 9464, 17799, 26696, 43848, 32135, 12208, 2914,
; 51130, 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474,
; 9792, 15400, 1452 of 6585 molecules
; FILE REFERENCE: MPI02-018PIRNMNIM
; CURRENT APPLICATION NUMBER: US/10/353,690
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 60/353,224
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/364,529
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: 60/373,861
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/376,287
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 60/388,080
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: 60/390,971
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/394,130
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/394,797
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/404,904
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 60/405,450
; PRIOR FILING DATE: 2002-08-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 126

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 2335
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-353-690-55
Alignment Scores:
Pred. No.: 5,64e-198 Length: 2335
Score: 2007.50 Matches: 434
Percent Similarity: 65.32% Conservative: 82
Best Local Similarity: 54.94% Mismatches: 133
Query Match: 44.15% Indels: 141
DB: 17 Gaps: 16
US-09-810-796-5 (1-888) x US-10-353-690-55 (1-2335)
Qy 8 ArgGlyArgValLeuLeuAsnSerAlaAlaAlaArgGlyAspGlyLeuLeuLeuGly 27
Db 127 CGGGGACGCCCCCGCGCGGAGCTAGTGGCGCTCACGGC----- 165
Qy 28 ThrArgAlaAlaThrLeuGlyGlyGlyGlyGlyLeuArgGluSerArgArgGlyLys 47
Db 166 ---CGTGCAGAGCGAACAGGGCGGAGCGGG-----CGGGGCGG 201
Qy 48 GlnGlyAla-ArgMetSerLeuLeuGlyLysProLeu----- 59
Db 202 CTCCCCCGCGCGCTCGGCTCTTGGGCAGCCCTCCCGCGGGCGCGCCCTCCCTGG 261
Qy 60 -----SerTyrThrSerSerGlnSerCysArgArgAsnValLysTy 73
Db 262 GCGGGGCTCCGGCTCGGGCTCCGCTCGCGCCAGCGCTCTCGCGCGCGCACAGCGCTA 321
Qy 73 rArgArgValGlnAsnTyrLeuTyrAsnValLeuGluArgProArgGlyTrpAlaPheI 93
Db 322 CCGCCGCTCGAGAACTGGGTCTACACAGTGTGAGCGCGCGCGCGCTTGGCTTCGT 381
Qy 93 eTyrHisAlaPheValPheLeuLeuValPheGlyCysLeuLeuLeuSerValPheSerTh 113
Db 382 CTACCAGCTCTTATATTTTGTGTCTTCAGCTGCTGTGTGTGTGTGTGTGTGTGTGTGT 441
Qy 113 rIleProGluHisThrLysLeuAlaSerSerCysLeuLeuLeuGluPheValMetI 133
Db 442 TATCCAGGAGCACAGGAACTTGCACAGAGTGTCTCTCATCTTGGAAATTCGTGATGAT 501
Qy 133 eValValPheGlyLeuPheIleAlaGlleTrpSerAlaGlyCysCysArgTy 153
Db 502 CGTGGTTCGCGCTTGGAGTACATCGTCCGGGTCTGTGTCCGGGATGCTGTGTCCGCTA 561
Qy 153 rArgGlyTrpGlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrI 173
Db 562 CCAGGATGACAGGTCGCTTCGCTTTCGAGAAAGCCCTTCTGTGTCTATCGACTTCAT 621
Qy 173 eValLeuIleAlaSerIleAlaValSerAlaLysThrGlnGlyAsnIlePheAlaTh 193
Db 622 CGTGTTCGTCGCTCGGTGCGCTCATCGCGCGGGGTACCCAGGCAACATCTTCGCGCAC 681
Qy 193 rSerAlaLeuArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArg 213
Db 682 GTCGCGCTCGGAGATGCGCTTCCTGCAGATCTCGGCATGCTGCGCATGGTGGCATGCCCG 741
Qy 213 gGlyGlyThrTrpLysLeuLeuGlySerValValTyrAlaHisSerLysGluLeuIleTh 233
Db 742 CGCGCGCACCTGGAAGCTGTGGGCTCAGTGGTCTACGGCGCATAGCAAGGAGCTGATCAC 801
Qy 233 rAlaTrpTyrIleGlyPheLeuValLeuIlePheSerSerPheLeuValTrpLeuValGI 253
Db 802 CGCTGTGTATCATCGGTTCCTGTGTGTCTATCTTCGCTCTCTCTGTGTGTGTGTGTGTGT 861
Qy 253 uLysAspAlaAsnLysGluPheSerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleTh 273
Db 862 GAAGGAGCCCACTCCGACTTCTCTCTACGCGGACTCGCTGTGTGTGTGTGTGTGTGTGTGT 921

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Qy	273	rLeuThrThrIleGlyTyrGlyAspLysThrProLeuThrTriPleuGlyArgLeuLeuSe	293
Db	922	ATTGACAAACCATCGGCTATGCTGACAAAGACACCGCACACATGCTGGCAGGCTCCTGGC	981
Qy	293	rAlaGlyPheAlaLeuLeuGlyIleSerPheAlaLeuProAlaGlyIleLeuGlySe	313
Db	982	TGCTGGCTTCGCCTTACTGGGCATCTCTTTCTTGGCTCGCTCGCGCATCTTAGCTC	1041
Qy	313	rGlyPheAlaLeuLysValGlnGlnHisArgGlnLysHisPheGluLysArgArgAs	333
Db	1042	CGGCTTTGCCCTGAAGTCCAGGAGCAGCACCGCAGAACCACTTCGAGAAGCGGAGGAT	1101
Qy	333	nProAlaAlaAsnLeulleGlnCysValTrpArgSerTyrAlaAlaAsp---GluLysSe	352
Db	1102	GCGCGCAGCAACCTCATCCAGGCTGCTGCGCGCTGTACTCCACCGATATGAGCGCGGC	1161
Qy	352	rValSerIleAlaThrTrp-----	358
Db	1162	CTACCTGACAGCCACCTGGTACTACTATGACAGTATCCTCCCATCCTTCAGAGAGTGGC	1221
Qy	358	-----	358
Db	1222	CCTCTTTGTGAGCACGTGCAACGGGCCCGCAATGGGGCTACGGCCCTCGAGGTGGC	1281
Qy	359	-----LysProHisLeuLysAlaLeuHisTh	367
Db	1282	GCGGGCCCGGTACCCGACGAGCACCTCCCGTTACCCCGCGTGTGCCACCTGCCACCG	1341
Qy	367	r-----CysSerProThrAsnGlnLysLeuSerPheLysGluArgVa	381
Db	1342	GCGGGCAGCACCTCTTCTGCCCTGGGAAAGACGCGGATGGGCATCAAGACCGCAT	1401
Qy	381	lArgMetAlaSerProArgGlyGlnSerIleLysSerArgGln-----AlaSerValGl	399
Db	1402	CCGCATGGCAGCTCCACGCGCGGACGGTCTCTCAAGCAGCAGCTGGCCTCCAAC	1461
Qy	399	yAspArgArgSerProSerThrAspIleThrAlaGluGly---SerProThrLysValGl	418
Db	1462	AATGCCACCTCCCAAGCAGCAGCAGGTGGGTGAGGCCACCAAGGTGCA	1521
Qy	418	nLysSerTrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerSe	438
Db	1522	AAAGAGCTGGAGCTTCAATACGCCACCCCGCTCCCGGCGATCTCTGAGACTC-----	1573
Qy	438	rGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyrAspGl	458
Db	1574	-----AAACCCCGCAGCTCTGCTAGGATGCC---CCCTCAGAGAAAGTAGCAGGGA	1623
Qy	458	uLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuLysThrValIl	478
Db	1624	GAAGAGCTACCCAGTGTGAGCTCACCGTGGACACATCATGCTGCTGTGAAGACAGTCTAT	1683
Qy	478	eArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThrLeuAr	498
Db	1684	CCGCTCATCAGGATCTCAAGTTCTTGGTGGCCAAAGAAATTCGAAGAGACACTGGC	1743
Qy	498	gProTyrAspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuAspMetLeuCy	518
Db	1744	ACCGTAGACGTGAAGACAGTCTATTGACAGTACTCAGCAGGCCACCTGACATGCTGGG	1803
Qy	518	sArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyLysGlyGlnIleThrSe	538
Db	1804	CCGGATCAAGACCTGCAAACTCGGGTGGACCAATTTGGTTCGGTTCGGGG-----CCCGG	1857
Qy	538	rAspLysLysSerArgGlu-----LysIleThrAlaGluHisGluThrThrAspAs	555
Db	1858	GGACAGAAAGGCCCGGAGAGAGCGCAAGAGGGGCCCTCCGACGCGGAGGTGGTGATGA	1917
Qy	555	pLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSerIleGluSerLy	575
Db	1918	AATCAGCATGATGGACCGGTGGTCAGGTGGAGAGCAGGTGCAGTCCATTCAGCAACA	1977
Qy	575	sLeuAspCysLeuLeuAspIleTyrGlnGlnValLeuArgLysGlySerAlaSerAlaLe	595

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Db 1978 GCTGGACCTGCTGTGGCGCTTATTGCGCGCTGCCTCGCTCTGGCACCCTCGGCC----- 2032
Qy 595 uAlaLeuAlaSerPheGlnIleProProPheGluCysGluGlnThrSerAspTyrGlnSe 615
Db 2033 -AGCTGGGCGCGCTGCAAGTGGCGCTGTTGCGACCCGACATCACCTCCGACTACCACAG 2091
Qy 615 rProValAspSerIysAspLeuSerGlySerAlaGlnAAsnSerGlyCysLeuSerArgSe 635
Db 2092 CCCTGTGGACCAAGGAGACATCTCCGTCTCGCAGACAGCGCTCAGC---ATCTCCCGCTC 2148
Qy 635 rThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAl 655
Db 2149 GGTGAGCACCACATGAGCTAGGG----- 2173
Qy 655 aGlnThrPheTyrAlaLeuSerProThrMetHisSerGlnAlaThrGlnValProIleSe 675
Db 2174 -----ACTTC 2178
Qy 675 rGlnSerAspGlySerAlaValAlaThrAsnThrIleAlaAsnGlnIleAsnThrAl 695
Db 2179 TCAGAGCGAGGGCAGCACA-----CGGCCAGC 2205
Qy 595 aProIysProAlaAlaProThrThrLeu-GlnIleProProProLeuProAlaIleIysH 715
Db 2206 CCCGCGCGCTGGCGCTCCGACTGCCCTCTGAGGCTCCGAGCTCCTCTCGTACTTGAAC 2265
Qy 715 isLeuProArgProGluThrLeuHis 723
Db 2266 CACTCCCTCAGGGGAGAGAGACCAC 2291

RESULT 13
US-10-850-928-1
; Sequence 1, Application US/10850928
; Publication No. US20050037460A1
; GENERAL INFORMATION:
; APPLICANT: JENTSCH, Thomas J.
; TITLE OF INVENTION: POTASSIUM CHANNELS AND GENES ENCODING THESE
; FILE OF INVENTION: POTASSIUM CHANNELS
; FILE REFERENCE: 2815-127PUS2
; CURRENT APPLICATION NUMBER: US/10/850,928
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: 09/492,361
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2335
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(2335)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (83)..(2170)
US-10-850-928-1

Alignment Scores:
Pred. No.: 5.64e-198 Length: 2335
Score: 2007.50 Matches: 434
Percent Similarity: 65.32% Conservative: 82
Best Local Similarity: 54.94% Mismatches: 133
Query Match: 44.15% Indels: 141
DB: 19 Gaps: 16

US-09-810-796-5 (1-888) x US-10-850-928-1 (1-2335)
Qy 8 ArgGlyArgValLeuLeuAAsnSerAlaAlaArgIysAspGlyLeuLeuLeuGly 27
Db 127 CGGGAGACCCCGCGGGAGCTAGTGGCGCTCAGGC----- 165
Qy 28 ThrArgAlaAlaThrLeuLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 47

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Db 166 ---CGTGAGAGCAAGAGCGAGCGGG-----CGGGCGG 201  
Qy 48 GlnGlyAla-ArgMetSerLeuLeuGlyLysProLeu----- 59  
Db 202 CTCCTCCGCGCGCTCGGCTCTCTGGGAGCCCTCGCGCGCGCGCTCCCTCGG 261  
Qy 60 -----SerTyThrSerSerGlnSerCysArgArgAsnValLysTy 73  
Db 262 GCCGGCTCCGGCTCGGCTCGGCGGCGAGCGCTCTCGGCGCGGCAAGCGCTA 321  
Qy 73 rArgArgValGlnAsnTyLeuTyAsnValLeuGluArgProArgGlyTyrAlaPheII 93  
Db 322 CGCGCGCTCGAGAACTGGGTCTCAACGCTGTGGAGCGCGCGCGCTGGCTCGT 381  
Qy 93 eTyHisAlaPheValPheLeuLeuValPheGlyCysLeuLeuLeuSerValPheSerTh 113  
Db 382 CTACACGCTCTCATATTTTGTGTCTTCTCAGCTGCTGTGTGTGTGTGTGTGTGT 441  
Qy 113 rIleProGluHisThrLysLeuAlaSerSerCysLeuLeuLeuLeuGluPheValMetII 133  
Db 442 TATCAGAGCACCGAGAACTTGCACAGAGTGTCTCTCATCTTGGAAATTCGTGATGAT 501  
Qy 133 eValValPheGlyLeuGluPheIIeIleArgIleTrpSerAlaGlyCysCysArgTy 153  
Db 502 CGTGGTTTTCGGCTTGGAGTACATCGTCCGGTCTGGTCCGCGGATGCTGCTCCGCTA 561  
Qy 153 rArgGlyTrpGlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAspThrII 173  
Db 562 CCGAGATGGCAGGTCGCTTCGCTTTCGCGAGAAAGCCCTTCTGTGTATCATCATCAT 621  
Qy 173 eValLeuIleAlaSerIleAlaValSerAlaLysThrGlnGlyAsnIlePheAlaTh 193  
Db 622 CGTGTTCGTGGCTCGGTGGCGTATCGCGCGGGTACCCAGGCAACATCTTCGCCAC 681  
Qy 193 rSerAlaLeuArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAspArgAr 213  
Db 682 GTCCGCGCTGGCGAGCATCGCTTCTGCAGATCTCGCATCTGTGGCATGTGTGGACCGCG 741  
Qy 213 gGlyGlyThrTrpLysLeuLeuGlySerValValTyAlaHisSerLysGluLeuIleTh 233  
Db 742 CGCGCGCACTTGGAGCTGTGGGCTCAGTGGTCTACCGCATGACGAGGAGCTGATCAC 801  
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Db 802 CGCTGTGTATCATCGGTTCTGTGTCTCATCTTCGCTCTCTTCTGTGTCTACCTGGCGGA 861  
Qy 253 uLysAspAlaAsnLysGluPheSerThrTyAlaAspAlaLeuTrpTrpGlyThrIleTh 273  
Db 862 GAAGAGCCCAACTCCGACTTCTCTCTACCGCGACTCGCTCTGTGGGGGAGCATTAC 921  
Qy 273 rLeuThrThrIleGlyTyArgLysPheThrProLeuThrTrpLeuGlyArgLeuLeuSe 293  
Db 922 ATTGACAACTATCGCTATGTGTGACAGACACCGACACATGTGGTGGGCGGGTCTGGG 981  
Qy 293 rAlaGlyPheAlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySe 313  
Db 982 TGCTGGCTTCGCTTACTGGGCATCTCTTTCTTGGCTGTGCTGGCGCATCTTAGGCTC 1041  
Qy 313 rGlyPheAlaLeuLysValGlnGluHisArgGlnLysHisPheGluLysArgArgAs 333  
Db 1042 CGGCTTTTCCTGAAGGTTCAGAGGACGACCGCGAGAACACTTCGAGAGCGGAGGAT 1101  
Qy 333 nProAlaAlaAsnLeuIleGlnCysValTrpArgSerTyrrAlaAlaAsp---GluLysSe 352  
Db 1102 GCCGGCAGCCAACTCATCCAGGCTGCTGGCTGTACTTCCACCATATGACCGCGGC 1161  
Qy 352 rValSerIleAlaThrTrp----- 358  
Db 1162 CTACTGACAGCCACTGGTACTACTATGACAGTATCTCCCATCTTCAGAGAGCTGGC 1221  
Qy 358 ----- 359

Db 1222 CCTCTTCTTTGAGCACGTGCACCGGCGCGCAATGGGGGCTACGGCCCTGGAGGTGCG 1281  
Qy 359 -----LysProHisLeuLysAlaLeuHisTh 367  
Db 1282 GCGGGCGCGGTACCCGACGAGACACCTCCGCTTACCCTCCGCGCTTCCCTCCACCG 1341  
Qy 367 r-----CysSerProThrAsnGlnLysLeuSerPheLysGluArgVa 381  
Db 1342 GCCGGGAGCACCTCTCTTCTGCTGGGAAAGAGCGCGGATGGGCATCAAGACCGCAT 1401  
Qy 381 lArgMetAlaSerProArgGlyGlnSerIleLysSerArgGln-----AlaSerValGI 399  
Db 1402 CCGCATGGGAGCTCCCGACGCGGACGGTCTTCAAGCAGCAGCTGGCACCTCCAAC 1461  
Qy 399 yAspArgArgSerProSerThrAspIleThrAlaGluGly---SerProThrLysValGI 418  
Db 1462 AATGCCACCTCCCAAGCAGCAGGAGGTGGGTGAGGCCACCGACCCCAAGAGGTGCA 1521  
Qy 418 nLysSerTrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLysSerSe 438  
Db 1522 AAGAGCTGGAGCTTCAATGACCGCACCCGCTTCGGGGCATCTGTGAGCTC----- 1573  
Qy 438 rGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyArgGI 458  
Db 1574 -----AAACCCCGCACCTCTGTGAGGATGCC---CCCTCAGAGGAAGTAGCAGGA 1623  
Qy 458 uLysGlyCysGlnCysAspValSerValGluAspLeuThrProLeuLysThrValII 478  
Db 1624 GAAGAGCTACAGGTGAGCTCAGGTGGACGACATCATGCTGCTGTGAAGCAGTCAT 1683  
Qy 478 eArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThrLeuAr 498  
Db 1684 CGCTCCATCAGGATCTCAAGTTCCTGGTGGCCAAAGAAATTCAGGAGACACTGCG 1743  
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Db 1744 ACCGTACAGCTGAAGACGTCATGTAGCAGTACTCAGCAGGCCACCTGGACACTGCTGG 1803  
Qy 518 sArgIleLysSerLeuGlnThrArgValAspGlnIleLeuGlyGlyGlnIleThrSe 538  
Db 1804 CCGATCAAGAGCTCGAAACTCGGTGGACCAAAATGTGGTGGGGG-----CCCGG 1857  
Qy 538 rAspLysLysSerArgGlu-----LysIleThrAlaGluHisGluThrThrAspAs 555  
Db 1858 GCACAGGAAGCGCGGAGGAAGCGGCAAGAGGCGCTCCGACGCGAGGTGGTGATGA 1917  
Qy 555 pLeuSerMetLeuGlyArgValLysValGluLysGlnValGlnSerIleGluSerLy 575  
Db 1918 AATCAGCATGATGGGCGCGTGTCAAGGTGGAGAACAGCAGTGCAGTCCATCGAGCAAA 1977  
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Db 1978 GCTGGACTCTGTGGGCTTCTATTCGCGCTGCTGCTGCTGCGACCTCGGCC----- 2032  
Qy 595 uAlaLeuAlaSerPheGlnIleProPheGluCysGluGlnThrSerAspTyrrGlnSe 615  
Db 2033 -AGCTGGGCGCGTCAAGTGGCTGTTCGACCCCGACATCACCTCCGACTACCACAG 2091  
Qy 615 rProValAspSerLysAspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSe 635  
Db 2092 CCCTGTGGACACGAGGACATCTCCGCTCCGACACAGCTCAGC---ATCTCCGCTC 2148  
Qy 635 rThrSerAlaAsnIleSerArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAl 655  
Db 2149 GGTACGACCAACATGACTGAGG----- 2173  
Qy 655 aGlnThrPheTyrrAlaLeuSerProThrMetHisSerGlnAlaThrGlnValProIleSe 675  
Db 2174 -----ACTTC 2178  
Qy 675 rGlnSerAspGlySerAlaValAlaAlaThrAsnThrIleAlaAsnGlnIleAsnThrAl 695  
Db 2179 TCAGGAGCGGCGAGCACA-----CGGCCAGC 2205









Db 2338 CGTGGACCACGAGAGCTGGAGGTTCTTTCAGCGCTTCAGCATCTCCCAAGGA 2397  
Qy 796 uGluleuAen 799  
Db 2398 GAACCTGGAT 2407

Search completed: April 3, 2005, 17:28:47  
Job time : 1261.47 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 3, 2005, 02:34:27 ; Search time 6829.39 Seconds  
(without alignments)  
4949.353 Million cell updates/sec

Title: US-09-810-796-5

Perfect score: 4547

Sequence: 1 MKDVESGRVLLNSAARG.....SICKAGESTDALSLPHVKLK 888

Scoring table:

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Ygapop 10.0			0.5
Fgapop 6.0			7.0
Delop 6.0			7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO_spool/US09810796/runat_31032005_141121_18209/app query.fasta_1.2126
-DB_EST_QFMT=fastap -SUFFIX=rst -MINMATCH=0 -IOPCL=0 -LOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09810796 @CGN 1 1 7935 @runat_31032005_141121_18209 -NCPU=6
-NO_MMAP -LARGQUERY -NEG SCORE=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database : EST:\*  
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2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4529	99.6	2733	9 AY407013	AY407013 Homo sapi
2	4221.5	92.8	2729	9 AY407015	AY407015 Mus muscu
3	3099	68.2	2014	9 AY407014	AY407014 Pan trogl
4	2655.5	58.4	2276	3 AK033079	AK033079 Mus muscu
5	1525.5	33.5	1571	3 AK040190	AK040190 Mus muscu
6	1258.5	27.7	997	2 BB609854	BB609854 BB609854
7	1171.5	25.8	797	6 CD629762	CD629762 55049367J
8	1121.5	24.7	864	7 CK772601	CK772601 961159 MA
9	1105.5	24.3	732	6 CD629756	CD629756 55049343J

10	1099	24.2	658	2	BE158938
c 11	1088.5	23.9	742	6	CD629754
12	1080	23.8	744	6	CB244389
c 13	1073	23.6	628	5	EX917798
c 14	1051.5	23.1	717	6	CD629766
c 15	1050.5	23.1	691	6	CD629755
c 16	1043.5	22.9	679	2	BB647997
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18	1038	22.8	1766	9	AY404832
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28	953	21.0	624	6	CD629751
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c 33	905	19.9	737	6	CD629764
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36	892	19.6	914	2	BF312386
37	864	19.0	908	2	BF240146
c 38	858	18.9	659	5	BX926684
c 39	854.5	18.8	920	2	BF317072
c 40	849	18.7	659	5	BX919587
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#### ALIGNMENTS

RESULT 1  
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DEFINITION Homo sapiens KCNQ5 gene, VIRTUAL TRANSCRIPT, partial sequence,  
ACCESSION AY407013  
VERSION AY407013.1 GI:39762984  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2733)  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,  
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferrerira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.  
TITILE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 2733)  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,  
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferrerira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.  
TITILE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
FEATURES  
Location/Qualifiers  
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## ORIGIN

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 Query Match: 99.60% Indels: 0  
 DB: 9 Gaps: 0

US-09-810-796-5 (1-888) x AY407013 (1-2733)

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Db	127	GACGGCTGCTACTGCTGGGACCCCGCGCCACGCTCGGTGGCGGGGGTGGCGTG	186
Qy	41	ArgGluSerArgGlyGlyGlyGlyGlyAlaArgMetSerLeuLeuGlyLysProLeuSer	60
Db	187	AGGGAGACCGCGGGCGGAGCAGGGGGCGCGGATGAGCCTGCTGGGGAAGCCGCTCTCT	246
Qy	61	TyrThrSerSerGlnSerCysArgArgAsnValLysTyrArgValGlnAsnTyrLeu	80
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Db	307	TACACGTCGTGGAGAGACCCCGCGGCTGGGGCTTCATCTACCGCGCTTCGTTTTCTC	366
Qy	101	LeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrLysLeu	120
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Qy	141	IleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArgLeu	160
Db	487	ATCATTCGAATCTGGTCTGGGGTGTGCTGATATAGGATGGCAAGGAGACTG	546
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Qy	201	PheLeuGlnIleLeuArgMetValArgMetAspArgGlyGlyThrTyrLysLeuLeu	220
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Qy	221	GlySerValValTyrAlaHisSerLysGluLeuIleThrAlaTyrTyrIleGlyPheLeu	240
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Qy	241	ValLeuIlePheSerSerPheLeuValTyrLeuValGluLysAspAlaAsnLysGluPhe	260
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Qy	261	SerThrTyrAlaAspAlaLeuTyrTyrGlyThrIleThrLeuThrThrIleGlyTyrGly	280
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Qy	301	IleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGln	320
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Qy	341	CysValTyrArgSerTyrAlaAlaAspGluLysSerValSerIleAlaThrTyrLysPro	360
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Qy	401	ArgArgSerProSerThrAspIleThrAlaGluLysSerProThrLysValGlnLysSer	420
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Qy	581	AspIleTyrGlnGlnValLeuArgLysGlySerAlaSerAlaLeuAlaLeuAlaSerPhe	600
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Qy	621	AspLeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIle	640
Db	1927	GATCTTTGGGTTCCGACAAAACAGTGGCTGCTTATCCAGATCAACTAGTGCACATC	1986

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 ACCESSION AY407015.1 GI:39762986  
 VERSION  
 KEYWORDS  
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 2729)  
 REFERENCE  
 AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,  
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
 Adams, M.D. and Cargill, M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302

REFERENCE 2 (bases 1 to 2729)  
 AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,  
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
 Adams, M.D. and Cargill, M.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering  
 them based on alignment.  
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Alignment Scores:  
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US-09-810-796-5 (1-888) x AY407015 (1-2729)

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## RESULT 3

AY407014

LOCUS

DEFINITION

Pan troglodytes KCMQ5 gene, VIRTUAL TRANSCRIPT, partial sequence,

genomic survey sequence.

ACCESSION

AY407014

VERSION

AY407014.1 GI:39762985

KEYWORDS

GSS.

SOURCE

Pan troglodytes (chimpanzee)



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ORGANISM Pan troglodytes
REFERENCE 1 (bases 1 to 2014)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2014)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
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 KEYWORDS  
 HTC; Cap trapper.  
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 Mus musculus (house mouse)  
 ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1  
 Carninci, P. and Hayashizaki, Y.  
 TITLE  
 High-efficiency full-length cDNA cloning  
 JOURNAL  
 Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE  
 99279253  
 PUBMED  
 10349636  
 2  
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 TITLE  
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL  
 Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE  
 20499374  
 PUBMED  
 11042159  
 3  
 Shibata, K., Itoh, M., Aizawa, K., Nagasaka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 TITLE  
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
 JOURNAL  
 Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE  
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 PUBMED  
 11076861  
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 TITLE  
 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
 JOURNAL  
 Nature 409, 685-690 (2001)  
 MEDLINE  
 11076861  
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AUTHORS  
 TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
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 JOURNAL  
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 REFERENCE  
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 ORIGIN  
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The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
 Functional annotation of a full-length mouse cDNA collection  
 Nature 409, 685-690 (2001)  
 5  
 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 6 (bases 1 to 2276)  
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission  
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome.gsc.riken.jp/  
 URL: http://fantom.gsc.riken.jp/.  
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 ORGANISM Mus musculus  
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 REFERENCE 1  
 AUTHORS Carninci, P. and Hayashizaki, Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636  
 REFERENCE 2  
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

TITLE Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
 Genome Res. 10 (10), 1617-1630 (2000)  
 20495374  
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 Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M.,  
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
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 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer  
 Genome Res. 10 (11), 1757-1771 (2000)  
 20530913  
 11076861

## JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

4 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 Functional annotation of a full-length mouse cDNA collection  
 Nature 409, 685-690 (2001)  
 5

## JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

6 The FANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.  
 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 6 (bases 1 to 1571)

## JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T.,  
 Kato, H., Kawai, O., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,  
 Koya, S., Kurahara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohashi, N.,  
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
 Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A.,  
 Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission

## JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp).  
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,  
 Fax: 81-45-503-9216

## JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome.gsc.riken.jp/  
 URL: http://fantom.gsc.riken.jp/  
 Location/Qualifiers  
 1..1571  
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CDS

## ORIGIN

Alignment Scores:  
 Pred. No.: 7,48e-138 Length: 1571  
 Score: 1525.50 Matches: 308  
 Percent Similarity: 69.51% Conservative: 59  
 Best Local Similarity: 58.33% Mismatches: 70  
 Query Match: 33.55% Indels: 91  
 DB: 3 Gaps: 9

US-09-810-796-5 (1-888) x AK040190 (1-1571)

Qy 35 GlyGlyGlyGlyLeuArgGluSerArgArgGlyLysGlnGlyAlaArgMetSerLeu 54

Db 42 GGGGGGGGGGGCTTCGGCGT-----CGCCTCGGCGTT 74

Qy 55 LeuGlyLysProLeu----- 59

Db 75 CTGGGAGCCCTTCGGCGGGCGGGCTCCCTCGGGCGGGCTCCGGCTCGGCTCC 134

Qy 60 SerTyrThrSerGlnSerCysArgArgAsnValLysTyrArgArgValGlnAsnTyr 79

Db 135 GCCTCGGGCGGGCGGCTCTCCGGCGGGCGGAGCGCTACCGCGCTGCAGACTGG 194

Qy 80 LeuTyrAsnValLeuGluArgProArgGlyTyrAlaPheIleTyrHisAlaPheValPhe 99

Db 195 GTCTACCAACGAGTGTCTCTTATCTTGGAAATTCGTGATGATTCTTTGGCTTGGAG 374

Qy 100 LeuLeuValPheGlyCysLeuLeuLeuSerValPheSerThrIleProGluHisThrLys 119

Db 255 TTCTAGTCTTTCAGCTGCTTGGTGTCTGTCTGTTCTCCACCATCAGGAGCACCGAA 314

Qy 120 LeuAlaSerSerCysLeuLeuLeuLeuGluPheValMetIleValValPheGlyLeuGlu 139

Db 315 CTTGCCAACGAGTGTCTCTTATCTTGGAAATTCGTGATGATTCTTTGGCTTGGAG 374

Qy 140 PheIleIleArgIleTyrSerAlaGlyCysCysArgTyrArgGlyTyrGlnGlyArg 159

Db 375 TATATATCCGTGCTGGTGGCGCGGATGCTGTGTTCGTCTACGATTCATCGTGTGGGCTCGTG 494

Qy 160 LeuArgPheAlaArgLysProPheCysValIleAspThrIleValLeuIleAlaSerIle 179

Db 435 TTTGCGCTTCGCCAGGAAACCTTCTGTGTATCATCATCTTATCGTGTGGGCTCGTG 494

Qy 180 AlaValValSerAlaLysThrGlnGlyAsnIlePheAlaThrSerAlaLeuArgSerLeu 199

Db 495 GCAGTGATAGTCCGGGCGCACAAAGGCAACATCTTTTGTACGTCCCGTTCGCGAGTATG 554

Qy 200 ArgPheLeuGlnIleLeuArgMetValArgMetAspArgArgGlyGlyThrTyrLysLeu 219

Db 555 CGTTCTCTACAGATCTCGGCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 614

Qy 220 LeuGlySerValTyrAlaHisSerLysGluLeuIleThrAlaTyrTyrIleGlyPhe 239

Db 615 TTGGATCCGTGCTATGCGCACAGTACAGGAGCTATCACCGCTTGTACATCGGCTTC 674

Qy 240 LeuValLeuIlePheSerPheLeuTyrLeuValGluLysAspAlaSerLysGlu 259

Db 240 LeuValLeuIlePheSerPheLeuTyrLeuValGluLysAspAlaSerLysGlu 259

Qy 240 LeuValLeuIlePheSerPheLeuTyrLeuValGluLysAspAlaSerLysGlu 259

Db 240 LeuValLeuIlePheSerPheLeuTyrLeuValGluLysAspAlaSerLysGlu 259

Qy 240 LeuValLeuIlePheSerPheLeuTyrLeuValGluLysAspAlaSerLysGlu 259



Score: 1258.50 Matches: 237  
Percent Similarity: 87.42% Conservative: 27  
Best Local Similarity: 78.48% Mismatches: 33  
Query Match: 27.68% Indels: 5  
DB: 2 Gaps: 2

US-09-810-796-5 (1-888) x BB609854 (1-997)

QY 72 LysTyrArgArgValGlnAsnTyrAsnValLeuGluArgProArgGlyTrpAla 91  
Db 36 CGCTACCGCGCTCGAGAACTGGGTCTACACAGTGTGGAGCGCCCGGGGGGCC 95

QY 92 PheLeuTyrHisAlaPheValPheLeuValPheGlyCysLeuLeuLeuSerValPhe 111  
Db 96 TTCTGCTACACGCTTTCATATTTTGTAGTCTTTCAGCTGCTGCTGCTGCTACTG 155

QY 112 SerThrIleProGluHisThrLysLeuAlaSerSerCysLeuLeuLeuGluPheVal 131  
Db 156 TCCACATCCAGGACACAGAACTTGCACACAGAGTGTCTCTTATCTTGGATTCGTG 215

QY 132 MetIleValValPheGlyLeuGluPheLeuLeuArgIleTyrSerAlaGlyCysCys 151  
Db 216 ATGATGTGTCTTTGGCTTGGAGTATATATCCGTGTCTGCGCGAGTCTGTGT 275

QY 152 ArgTyrArgGlyTrpGlnGlyArgLeuArgPheAlaArgLysProPheCysValIleAsp 171  
Db 276 CGCTACAGAGTAGCGAGGACGCTTTCGCTTCGCGAGAAACCTTCTGTGTCTATCGAC 335

QY 172 ThrIleValLeuLeuAlaSerIleAlaValValSerAlaLysThrGlnGlyAsnIlePhe 191  
Db 336 TTCATCGTGTCTCGTGGCTTGGTGGAGTATATATCCGTGTCTGCGCGAGTCTGTGT 395

QY 192 AlaThrSerAlaLeuArgSerLeuArgPheLeuGlnIleLeuArgMetValArgMetAsp 211  
Db 396 GCTACGTCCGCGTTCGCGAGTATGCGCTTCTACAGATCCCTGCGCATGCTGCTATGGAT 455

QY 212 ArgArgGlyGlyThrTrpLysLeuLeuGlySerValValTyrAlaHisSerLysGluLeu 231  
Db 456 CGCCGCGTGGCACCTGGAAGCTGTGGGATCCGTGTCTATGCGCACAGTAAGAGCTG 515

QY 232 IleThrAlaTrpTyrIleGlyPheLeuValLeuIlePheSerSerPheLeuValTyrLeu 251  
Db 516 ATCACCGCTGTATCATCGGTTCCTGTGTCTCAFCITTTGCTCTTCTCTGCTACTCTG 575

QY 252 ValGluLysAspAlaAsnLysGluPheSerThrTyrAlaAspAlaLeuTrpTrpGlyThr 271  
Db 576 GCTGAGAAGGATGCCAATCTGACTTCTCTCTCTATGCGACTGCTGCTGCTGGGGACG 635

QY 272 IleThrLeuThrIleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeu 291  
Db 636 ATCACACTGACGACCATTTGGCTATGCTGACAGAGCGCCACATACATGCTGGCGAGGTT 695

QY 292 LeuSerAlaGlyPheAlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeu 311  
Db 696 CTGGCTCGCGCTTTCGCTTACTGGGCACTCTCTTCTTGTCCCTGCTGCGGATCTCTG 755

QY 312 GlySerGlyPheAlaLeuLysValGlnGlnHisArgGlnLysHisPheGluLysArg 331  
Db 756 GGCTCTGGCTTTGCTCCTGAAGTCCAGGAGCAGCACAGGAGAGACGCTTGAGAGCGC 815

QY 332 ArgAsnProAlaAlaAsnLeuIleGln---CysValTrpArgSerTyrAlaAlaAspGlu 350  
Db 816 AGGATGCCAGCAGCTAATCTCATTTCCAGGCTGCGTCTGCTGCTGCTGCTGCTGCTG 875

QY 351 LysSerValSerIleAlaThr-----TrpLysProHisLeuLysAlaLeuHis 366  
Db 876 CGGGCATATTTGAGCGCACTCGTATTATACATGACAGCATCTCCATCTTCAAGAGTGGC 935

QY 367 ThrCys 368  
Db 936 TCTTGT 941

RESULT 7

CD629762/c  
LOCUS CD629762 797 bp mRNA linear EST 12-JAN-2004  
DEFINITION 5504936701 FLP Homo sapiens cDNA, mRNA sequence.  
ACCESSION CD629762  
VERSION CD629762.1 GI:40278028  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
TITLE Fu.G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.  
JOURNAL Circular rapid amplification of cDNA ends for high-throughput  
COMMENT extension cloning of partial genes  
Genomics 84 (1), 205-210 (2004)  
Contact: Fu GK  
Incyte Genomics, Inc.  
3160 Porter Dr., Palo Alto, CA 94304, USA  
Tel: 6508454102  
Email: gfu@incyte.com

FEATURES  
source  
1..797  
/organism="Homo sapiens"  
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/clone\_lib="FLP"  
/note="Vector: pDrive Cloning Vector"

ORIGIN

Alignment Scores:  
Pred. No.: 1.15e-103 Length: 797  
Score: 1171.50 Matches: 238  
Percent Similarity: 94.90% Conservative: 4  
Best Local Similarity: 93.33% Mismatches: 3  
Query Match: 25.76% Indels: 11  
DB: 6 Gaps: 1

US-09-810-796-5 (1-888) x CD629762 (1-797)

QY 330 LysArgArgAsnProAlaAlaAsnLeuIleGlnCysValTrpArgSerTyrAlaAlaAsp 349  
Db 764 GAAAGAAAGAGCCAGCTGCCAATCTTCACTCACTGTGTTTG-CGTAGTTACGCGATTGAT 706

QY 350 GluLysSerValSerIleAlaThrTrpLysProHisLeuLysAlaLeuHisThrCysSer 369  
Db 705 GAGAAATCTGTTTCCATTGCAACTGGAAGCCACACTTGAAGCCCTTGCACACTGCGAC 646

QY 370 -ProThr-----AsnGlnLysLeuSerPheLysGluAr 380  
Db 645 CCCTACCAAGAAAGCAAGGGGAAGCATCAAGCAGTCAAGAGCTAAGTTTAAAGGAGCG 586

QY 380 gValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSerValGlyAs 400  
Db 585 AGTGGCATGGCTTAGCCCCAGGGCCAGAGTATTAAAGAGCCGACACACCTCAGTAGTGA 526

QY 400 pArgArgSerProSerThrAspIleThrAlaGluGlySerProThrLysValGlnLysSe 420  
Db 525 CAGAGGTCCCCAAGCACCCGACATCACGCCGAGGGCAGTCCACCACCAAGTGCAGAGAG 466

QY 420 rTrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSerSerGlnPr 440  
Db 465 CTGGAGCTTCAACGACGGAACCCGCTTCGCGCCCTCGCTGCGCTCANAAGTTCTCAGCC 406

QY 440 oLysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTyrAspGluLysGI 460  
Db 405 AAAACAGATGATAGTGTGACACAGCCCTTGGCATGTGATGTATATATGATGATAAAGG 346

QY 460 YCysGlnCysAspValSerValGluAspLeuThrProProLeuLysThrValIleArgAl 480  
Db 345 ATGCCAGTGTGATGTATCAGTGGAGACCTCACCCACCACTTAAACCTGTCATTCGAGC 286

QY 480 alleArgIleMetLysPheHisValAlaLysArgLysPheLysGluThrLeuArgProTy 500





JOURNAL  
COMMENT

extension cloning of partial genes  
Genomics 84 (1), 205-210 (2004)  
Contact: Fu GK  
Incyte Genomics, Inc.  
3160 Porter Dr., Palo Alto, CA 94304, USA  
Tel: 6508454102  
Email: gfu@incyte.com.

## FEATURES

source  
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Location/Qualifiers  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
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## ORIGIN

Alignment Scores:  
Pred. No.: 2,91e-97 Length: 732  
Score: 1105.50 Matches: 230  
Percent Similarity: 93.88% Conservativity: 0  
Best Local Similarity: 93.88% Mismatches: 4  
Query Match: 24.31% Indels: 13  
DB: 6 Gaps: 1

US-09-810-796-5 (1-888) x CD629756 (1-732)

QY 339 ileGlnCysValTrpArgSer-TyrAlaAlaAspGluLysSerValSerIleAlaThrTr 358  
Db 731 ATTCACTGTGTTGGCGTAGTTAACCGACGTCATGAGAATCTGTTTCATTCGCACTG 672  
QY 358 pLysProHisLeuLysAlaLeuHisThrCysSerProThrAsn----- 372  
Db 671 GAAGCACACCTTGAAGGCGCTTCACACCTCGACCGCTACCCCA-AGAAAGAACAGGGGGA 613  
QY 373 -----GlnLysLeuSerPheLysGluArgValArgMetAlaSerProArgG1 388  
Db 612 AGCATCAACGACGTCAGAGCTAAGTTTAAAGAGCGAGTGCATGCTAGCCCGAGGG 553  
QY 388 yGlnSerIleLysSerArgGlnAlaSerValGlyAspArgSerProSerThrAspI1 408  
Db 552 CCAGAGTATTAAAGCCGACAGCCTCAGTAGTGCAGAGGAGTCCCAACGACCGACAT 493  
QY 408 eThrAlaGluLysSerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrAr 428  
Db 492 CACAGCCGAGGCGAGTCCCAAGAGTGCAGAGAGTGCAGAGTTCACAGCCCGAACCCG 433  
QY 428 gPheArgProSerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspTh 448  
Db 432 CTTCCGGCCCTCGCTCGCCTCAGAAAGTTCTCAGCCAAACCACTGATGATGCTGACAC 373  
QY 448 tAlaLeuGlyThrAspAspValTyrAspGluLysGlyCysGlnCysAspValSerValG1 468  
Db 372 AGCCCTTGGCACTGATGATGATATATGATGATAAGAGGATGCCAGTGTGATGATCAGTGA 313  
QY 468 uAspLeuThrProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisVa 488  
Db 312 AGACCTCACCCCACTTAAACTGTTCATTCGAGCTATCAGAAATTATGAATTTCATGT 253  
QY 488 lAlaLysArgLysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluG1 508  
Db 252 TGCAGAAAGGAGTTTAAAGAAACATTACGTCCTATATGATGATAAGAGATGCTATTGAACA 193  
QY 508 nTyrSerAlaGlyHisLeuAspMetLeuLysArgGlyIleLysSerLeuGlnThrArgValAs 528  
Db 192 ATATTCCTGCTGCTCATCTGGACATGTTGTGTAGAAATTAAAGCCCTTCAAAACAGCTGTGA 133  
QY 528 pGlnIleLeuGlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAl 548  
Db 132 TCAAAATCTTGAAAGGCGCAATACATCAGATAAGAGCGGAGGAGAAATACAGC 73  
QY 548 aGluHisGluThrThrAspAspLeuSerMetLeuGlyArgValValLysValGluLysG1 568  
Db 72 AGAATGAGACACACGACGATCTCAGTATGCTCGGTCCGGTGGTCTCAG-GTTGAAAGACA 14

QY 568 nValGlnSerIle 572  
Db 13 GGTACAGTCCATA 1

## RESULT 10

BE158938

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BE158938 658 bp mRNA linear EST 21-JUN-2000  
MRO-HT0404-210200-001-c04 HT0404 Homo sapiens cDNA, mRNA sequence.  
BE158938  
EST  
BE158938.1 GI:8621659  
Homo sapiens (human)

Homosapiens

Homosapiens

Homosapiens

Homosapiens

Homosapiens

Homosapiens

Homosapiens

Homosapiens

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## ORIGIN

Alignment Scores:

Pred. No.: 1,06e-96 Length: 658

Score: 1099.00 Matches: 211

Percent Similarity: 99.53% Conservativity: 1

Best Local Similarity: 99.06% Mismatches: 1

Query Match: 24.17% Indels: 0

DB: 2 Gaps: 0

US-09-810-796-5 (1-888) x BE158938 (1-658)

QY 278 GlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAla 297

Db 18 GGCTATGGAGACAAACCTCCCTAACTTGGCTGGGAGATTGCTTCTGCAGGCTTTCGA 77

QY 298 LeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGlyPheAlaLeu 317

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Db      78 CTCTTGGCATTCTTTCTTGGCACTTCTCTCCGCGCATCTTGGCTCAGGTTTGGCATTA 137
Qy      318 LysValGlnGlnHisArgGlnLysHisPheGlnLysArgArgAsnProAlaAlaAsn 337
Db      138 AAAGTACAAGAACACACCGCCAGAACACATTTTGAGAAAGAGAACCCAGCTGCCAAC 197
Qy      338 LeuLeuGlnCysValTrpArgSerTyrAlaAlaSerGluLysSerValSerIleAlaThr 357
Db      198 CTCAATTCAGTGTGTGGCGTAGTACGACGATGAGAAATCTGTTTCCATTGCCAAC 257
Qy      358 TrpLysProHisLeuLysAlaLeuHisThrCysSerProThrAsnGlnLysLeuSerPhe 377
Db      258 TGGAGCCACACTTGAAGGCTTGGACACCTTGCAGCCCTTACCAATCAGAACTAAGTTT 317
Qy      378 LysGluArgValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGlnAlaSer 397
Db      318 AAGGAGCGAGTGCATGGCTAGCTAGCCAGGCGCCAGAGTATTAAAGCCGACAGCCCTCA 377
Qy      398 ValGlyAspArgArgSerProSerThrAspIleThrAlaGluGlySerProThrLysVal 417
Db      378 GTAGGTGACAGAGTCCCAAGCAGCCAGCTCAGCCGAGGCGAGTCCCAACCAAGTG 437
Qy      418 GlnLysSerTrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLysSer 437
Db      438 CAGAAGAGCTGGAGCTTCACGACCGAACCCTTCCGCGCTTCCGCGCTCAGAAAGT 497
Qy      438 SerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspValTyrAsp 457
Db      498 TCTCAGCCAAACAGTATAGATGCTGACACAGCCCTTGGCACTGATGATGATATGAT 557
Qy      458 GluLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuLysThrVal 477
Db      558 GAAAAGAGTATCCAGTGTGTATCAGTGTGAAGACCTCACCCACCACTTAAACCTGTC 617
Qy      478 IleArgAlaIleArgIleMetLysPheHisValAlaLys 490
Db      618 ATTCAGCTATCAGAAATATGAAATTTCTTGTGGCAAA 656

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RESULT 11
CD629754/c
LOCUS      CD629754      742 bp      mRNA      linear      EST 12-JAN-2004
DEFINITION 55049327J1 FLP Homo sapiens cDNA, mRNA sequence.
ACCESSION  CD629754
VERSION     CD629754.1  GI:40278020
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens

```

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REFERENCE   1  (bases 1 to 742)
AUTHORS    Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
TITLE      Circular rapid amplification of cDNA ends for high-throughput
           extension cloning of partial genes
JOURNAL     Genomics 84 (1), 205-210 (2004)
COMMENT     Contact: Fu GK
           Incyte Genomics, Inc.
           3160 Porter Dr., Palo Alto, CA 94304, USA
           Tel: 6508454102
           Email: gfu@incyte.com.

```

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FEATURES             source
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## ORIGIN

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Alignment Scores:
Pred. No.:      1.38e-95      Length:      742
Score:          1088.50      Matches:      229
Percent Similarity: 93.12%      Conservative: 1

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Best Local Similarity: 92.71%      Mismatches: 5
Query Match:          23.94%      Indels: 13
DB:                   6          Gaps: 1

```

US-09-810-796-5 (1-888) x CD629754 (1-742)

```

Qy      340 GlnCysValTrpArgSerTyrAlaAlaAspGlnLysSerValSerIleAlaThrTrpLys 359
Db      740 CAGTGTGTGTTCCTCCGTAT-TAGCGCAGCTGATGAGAAATCTGTTTCCATTGCCAAC 682
Qy      360 ProHisLeuLysAlaLeuHisThrCysSerProThr----- 371
Db      681 CCACACTTGAAGGCTTGCACACCTGCGCCCTACCAAGAAAGAACCCAGGGAGCATC 622
Qy      372 ----AsnGlnLysLeuSerPheLysGlu-ArgValArgMetAlaSerProArgGlyGlns 390
Db      621 AAGCAGTCAAGCTAAGTTTAAAGGAGCCGAGTGCAGTGCCTAGCTAGCCAGGGGCCAGA 562
Qy      390 erlleLysSerArgGlnAlaSerValGlyAspArgArgSerProSerThrAspIleThrA 410
Db      561 GTATTAAAGCCGACAAAGCCTCAGTAGGTGACAGGAGGTCCCAAGCACCCACATCACAG 502
Qy      410 laGluGlySerProThrLysValGlnLysSerTrpSerPheAsnAspArgThrArgPheA 430
Db      501 CCGAGGCGAGTCCCAACCAAGTGCAGAGAGCTGGAGCTTCAACGACCGAACCCGCTTCC 442
Qy      430 rgProSerLeuArgLeuLysSerSerGlnProLysProValIleAspAlaAspThrAlaL 450
Db      441 GGCCCTCGCTCGGCTCAAAAGTTCTCAGCCAAACCCAGTGTATGATGCTGACACAGGCC 382
Qy      450 euGlyThrAspAspValTyrAspGlnLysGlyCysGlnCysAspValSerValGluAspL 470
Db      381 TTGCACTGATGATGATATATGATGAAAAGAGATGCCAGTGTGATGATCAGTGAAGACC 322
Qy      470 euThrProProLeuLysThrValIleArgAlaIleArgIleMetLysPheHisValAlaL 490
Db      321 TCACCCCAACCACTTAAACCTGTCTATTCAGCTATCAGAAATATGAAATTTTCATGTTG 262
Qy      490 ysArgLysPheLysGluThrLeuArgProTyrAspValLysAspValIleGluGlnTyrS 510
Db      261 AACGGAAGTTTAAATAAACATTACGTCCATATGATGATAAAGATGTCAATTGAACAATAT 202
Qy      510 erAlaGlyHisLeuAspMetLeuCysArgIleLysSerLeuGlnThrArgValAspGlnI 530
Db      201 CTGCTGTGTCATCTGGACATGTGTGTAGAAATTAAGAGCCCTTCAACACACGTTGATCAA 142
Qy      530 leLeuGlyLysGlyGlnIleThrSerAspLysLysSerArgGluLysIleThrAlaGluH 550
Db      141 TTCTTGGAAAAGGCAANTCACATCAGATAAGAGAGCCGAGAGAAATAACAGCAGAAC 82
Qy      550 isGluThrThrAspAspLeuSerMetLeuGlyArgVal-VallysValGluLysGlnVal 569
Db      81 ATGAGACACACAGACGATCTCAGTATGTCGTCGGTGGTGGTCAAGGTTGAAAACACAGG 22
Qy      570 GlnSerIleGluSer 574
Db      21 CAGTCCATAGATCC 7

```

## RESULT 12

CD6244389

LOCUS

DEFINITION

IMAGE:6832924 5', mRNA sequence.

ACCESSION

CD244389

VERSION

CD244389.1

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

AUTHORS

TITLE

CB244389 744 bp mRNA linear EST 09-JUL-2003  
 UI-M-PY0-cdq-c-03-0-UI.r1 NIH\_BMAP\_FY0 Mus musculus cDNA clone  
 IMAGE:6832924 5', mRNA sequence.

CB244389  
 CB244389.1 GI:28366033  
 EST.  
 Mus musculus (house mouse)

Mus musculus  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 744)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL  
COMMENT

Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cga@rs@mail.nih.gov  
Tissue Procurement: Dr. Jim Lin, University of Iowa  
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP)

Seq primer: pYX-5.

## FEATURES

source

Location/Qualifiers  
1..744  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:6832924"  
/tissue\_type="whole brain"  
/dev\_stage="embryo 13.5, 14.5, 16.5, 17.5 dpc"  
/lab\_host="DH10B (T1 phage resistant)"  
/clone\_lib="NIH-BMAP\_FY0"  
/note="Organ: Brain; Vector: pYX-Asc; Site\_1: Ecor I;  
Site\_2: Not I; The library was constructed according  
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. Denatured RNA was size fractionated on a 1% agarose  
gel. First strand cDNA synthesis was primed with oligo-dT  
primer containing a Not I site. Double strand cDNA was  
size selected according to mRNA size fraction, ligated  
with Ecor I adaptor, digested with NotI and then cloned  
directionally into pYX-Asc vector. The library tag  
sequence located between the Not I site and the polyA tail  
is AGCAGACAG. This library was created for the University  
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the  
Developing Mouse Nervous System', supported by National  
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,  
program coordinator."

## ORIGIN

## Alignment Scores:

Pred. No.: 9,396-95 Length: 744  
Score: 1080.00 Matches: 216  
Percent Similarity: 91.46% Conservative: 9  
Best Local Similarity: 87.80% Mismatches: 21  
Query Match: 23.75% Indels: 0  
DB: 6 Gaps: 0

US-09-810-796-5 (1-888) x CB244389 (1-744)

QY 622 LeuSerGlySerAlaGlnAsnSerGlyCysLeuSerArgSerThrSerAlaAsnIleSer 641  
DB 7 CTGCTGGCTCAGCACAAACAGCGGCTGTTTAAACAGAGTCCAGCAGTCCCAATCTCA 66  
QY 642 ArgGlyLeuGlnPheIleLeuThrProAsnGluPheSerAlaGlnThrPheTyAlaLeu 661  
DB 67 AGAGCCCTGCAGTTCATCCTTAACCAACCAATGAGTTCAGTGTCTCAGACTTTCTATGCGCTT 126  
QY 662 SerProThrMetHisSerGlnAlaThrGlnValProIleSerGlnSerAspGlySerAla 681  
DB 127 AGCCCTACTATGCACAGCCAGACTACCAGTAGTACCATGAGTCAAAATGACGGCTCTCC 186  
QY 682 VallalaThrAsnThrIleAlaAsnGlnIleAsnThrAlaProLysProAlaAlaPro 701  
DB 187 GTGTAGTACCAATAACATTGCAAAACCAATAAGCGCGCACCAAGCCAGCAGCCCA 246  
QY 702 ThrThrLeuGlnIleProProLeuProAlaIleLysHisLeuProArgProGluThr 721  
DB 247 ACAATTTCAGATCCCTCTCTCTCGGCCATCAGACATGTCTCAGCGCCAGAACCT 306  
QY 722 LeuHisProAsnProAlaGlyLeuGlnGluSerIleSerAspValThrThrCysLeuVal 741

DB 307 CTGCTCTCAAAACCCACCGCTTACAGAGAGTATTTCTGATGTACACACCTGCTGTTT 366  
QY 742 AlaSerLysGluAsnValGlnValAlaGlnSerAsnLeuThrLysAspArgSerMetArg 761  
DB 367 GCCTCCAAAGGAAGTGTTCAGTTTTCAGTCAAACTGACCAAGGACCGTTCCTGAGG 426  
QY 762 LysSerPheAspMetGlyGlyGluThrLeuLeuSerValCysProMetValProLysAsp 781  
DB 427 AAAAGTTTCGACATGGGAGGAGAACTCTGTGTCTGTCGCGCCCATGGTGCCCAAGAT 486  
QY 782 LeuGlyLysSerLeuSerValGlnAsnLeuIleArgSerThrGluGluLeuAsnIleGln 801  
DB 487 TTGGGCAAAATCTCTGTCTGTACAAACCTGATCAGTTCGACAGAGAACTGAACTTACAG 546  
QY 802 LeuSerGlySerGluSerSerGlySerArgGlySerGlnAspPheTyProLysThrArg 821  
DB 547 TTTTCAGGCGACGAGTCAAGCGCTCTCGAGGCGAGTCAAGATTTTATCCCAAGTGAGA 606  
QY 822 GluSerLysLeuPheIleThrAspGluGluValGlyProGluGluThrGluThrAspThr 841  
DB 607 GAATCCANATTGTTTATTAATGATGAGGAGTCTGTCGAGGAGAGAGAGAGAGAGTACT 666  
QY 842 PheAspAlaProGlnProAlaArgGluAlaPheAlaSerAspSerLeuThr 861  
DB 667 TTTGACGCGCACCCACCGCTCTGCGGGGAGGCTGCTTCTCATCAGACTCTCTAGGACT 726  
QY 862 GlyArgSerArgSerSer 867  
DB 727 GGAAGGTTCACGGTCACTCT 744

## RESULT 13

BX917798/c

## LOCUS

BX917798

DEFINITION

scan0033d.1.06 5prim, mRNA sequence.

ACCSSION

BX917798

VERSION

BX917798.1

KEYWORDS

EST.

SOURCE

Sus scrofa (pig)

ORGANISM

Sus scrofa

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

## FEATURES

source

1..628

Location/Qualifiers

/organism="Sus scrofa"

/mol\_type="mRNA"

/db\_xref="taxon:9823"

/clone="scan0033d.1.06"

/tissue\_type="mixed"

/dev\_stage="from embryos to adults"

/clone\_lib="Sus Scrofa library (scan)"

/notes="tissues: adipose tissue, brain, kidney, liver,

muscle, ovary, testis, heart, hypothalamus, pancreas,

skin, spleen, thymus, placenta, pituitary gland, seminal

vesicle, small intestine, uterus, adrenals, bulbo uretral

gland, cerebral trunk, epididymis, female gonad,

sequence.

Plate: 0033 row: 1 column: 6.

gall-bladder, hippocampus, large intestine, male gonad,  
melanocytes, stomach, udder"

## ORIGIN

Alignment Scores:  
Pred. No.: 3,44e-94 Length: 628  
Score: 1073.00 Matches: 207  
Percent Similarity: 99.52% Conservative: 1  
Best Local Similarity: 99.04% Mismatches: 1  
Query Match: 23.60% Indels: 0  
DB: 5 Gaps: 0

US-09-810-796-5 (1-888) x BX917798 (1-628)

```
QY 195 AlaLeuArgSerLeuArgPheLeuGlnLeuArgMetValArgMetAspArgGly 214
DB 628 GCACCTGCGAAGTCTCCGCTTCTTGACAGATCTCCGATGCTGCGCATGGACCGCGAGGG 569
QY 215 GlyThrTrpLysLeuLeuGlySerValValTyrAlaHisSerLysGluLeuIleThrAla 234
DB 568 GGCACCTGGAAGTTACTGGGCTCCGCTGTTATGCTCACAGCAAGGAATTAATCACAGCG 509
QY 235 TrpTyrIleGlyPheLeuValLeuIlePheSerSerPheLeuValTyrLeuValGluLys 254
DB 508 TGGTACATAGAGATTTTGGTCTTATTTTTCATCTTCTTCTTATCTGGTGAAGAAG 449
QY 255 AspAlaAsnLysGluPheSerThrTyrAlaAspAlaLeuTrpTrpGlyThrIleThrLeu 274
DB 448 GATGCAATAAGGAGTTTCTACATATGACAGATGCTCTGCTGGGGCACAATAACATTG 389
QY 275 ThrThrIleGlyTyrGlyAspLysThrProLeuThrTrpLeuGlyArgLeuLeuSerAla 294
DB 388 ACAACGATTGGCTATGAGACAAAACCCCTGACTTGGCTGGGAAGGCTGCTCTGCA 329
QY 295 GlyPheAlaLeuLeuGlyIleSerPhePheAlaLeuProAlaGlyIleLeuGlySerGly 314
DB 328 GGCCTTGACATCTCTGGCATTTCTTCTTCTTCTTCTTCTGACGAGCATTTCTTGGCTCAGGT 269
QY 315 PheAlaLeuLysValGlnGlnHisArgGlnLysHisPheGluLysArgArgAsnPro 334
DB 268 TTTGCAATTAAGATGCAAGAACAGCACCGCCAGAACACACTTTGAGAAAGAAAGAACCCG 209
QY 335 AlaAlaAsnLeuIleGlnCysValTrpArgSerTyrAlaAlaAspGluLysSerValSer 354
DB 208 GCTGCCAACCTTATTCAGTGGCTTTGGCGGAGTTATGACGCGCAGCAAAATCTGCTGCC 149
QY 355 IleAlaThrTrpLysProHisLeuLysAlaLeuHisThrCysSerProThrAsnGlnLys 374
DB 148 ATTGCAACTGGAAGCCACACTGAAGGCTTGACACCTGACGAGCCCAACCAATCAGAAG 89
QY 375 LeuSerPheLysGluArgValArgMetAlaSerProArgGlyGlnSerIleLysSerArg 394
DB 88 CTCAGCTTTAAGGAGCGGTGGCATGCCAGCCACCGGGCCAGCATTAAGAGCAGA 29
QY 395 GlnAlaSerValGlyAspArgSer 403
DB 28 CAAGCTTAAGTGGGTGACAGGAGGTCC 2
```

RESULT 14  
CD629766/C  
LOCUS CD629766 717 bp mRNA linear EST 12-JAN-2004  
DEFINITION 55049391J1 FLP Homo sapiens cDNA, mRNA sequence.  
ACCESSION CD629766  
VERSION CD629766.1 GI:40278032  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 717)

AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.  
TITLE Circular rapid amplification of cDNA ends for high-throughput  
extension cloning of partial genes

JOURNAL  
COMMENT

Genomics 84 (1), 205-210 (2004)  
Contact: Fu GK  
Incyte Genomics, Inc.  
3160 Porter Dr., Palo Alto, CA 94304, USA  
Tel: 6508454102  
Email: gfu@incyte.com.

## FEATURES

source  
1..717  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_lib="FLP"  
/note="Vector: pDrive Cloning Vector"

## ORIGIN

Alignment Scores:  
Pred. No.: 5,47e-92 Length: 717  
Score: 1051.50 Matches: 218  
Percent Similarity: 92.95% Conservative: 6  
Best Local Similarity: 90.46% Mismatches: 4  
Query Match: 23.13% Indels: 13  
DB: 6 Gaps: 1

US-09-810-796-5 (1-888) x CD629766 (1-717)

```
QY 345 SerTyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysProHisLeuLysAla 364
DB 715 AGTTACGACGCTGATGAGAAATCTGTGCCATTTGCACCTGGAGGCCACACTTGAAGGCT 656
QY 365 LeuHisThrCysSerProThr-----AsnGlnLysLeu 375
DB 655 TTGCACACCTGCAGCCCTTACCAAGAAAGAACAGAGGGAAGCATCAAGCAGTCAGAAAGCTA 596
QY 376 SerPhe-LysGluArgValArgMetAlaSerProArgGlyGlnSerIleLysSerArg-G 395
DB 595 AGTTATTAAAGAGCGAGTGCCGATGGCTAGCCCCAGGGGCGGAGTATTAAAGAGCCGAC 536
QY 395 InAlaSerValGlyAspArgSerProSerThrAspIleThrAlaGluLysSerProT 415
DB 535 AAGCTCTAGTAGTGACAGGAGTCCCCAAGCAGCAGCATCACAGCCGAGGCGAGTCCCA 476
QY 415 hrLysValGlnLysSerTrpSerPheAsnAspArgTrpArgPheArgProSerLeuArgL 435
DB 475 CCAAGTGCGAAGAGCTGGAGCTTCAACAGACCCGCTTCGCGCCCTCGCTCGCC 416
QY 435 euLysSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspAspV 455
DB 415 TCAAAAGTTCTCAGCCAAACACAGTATAGTGTGACACAGCCCTTGGCACTGATGATG 356
QY 455 alTyrAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuL 475
DB 355 TATATGATGAAAAAGGATGCCAGTGTGATGATCAGTGGAAAGACCTCACCCACCACTTA 296
QY 475 ysThrValIleArgAlaIleArgIleMetLysPheHisValAlaLysArgLysPheLysG 495
DB 295 AAATGTCATTCGAGCTATCAGAAATTGAATTTTCATGTTGCAAAACGGAAGTTTAAGT 236
QY 495 luThrLeuArgProTyrAspValLysAspValIleGluGlnTyrSerAlaGlyHisLeuA 515
DB 235 AAACATTACGCTCCATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 176
QY 515 spMetLeuCysArgIleLysSerIleuGln-ThrArgValAspGlnIleLeuGlyLysGly 534
DB 175 ACATGTTGTGTAGAAATTAAGAACCTTCAATAACACGCTGTGTGATCAAAATTCCTTGG 116
QY 535 GlnIleThrSerAspLysLys-SerArgGluLysIleThrAlaGluHisGluThrThrAs 554
DB 115 CAATCATCATCAGATAGAAGACGAGCCGAGAGAAATAATACAGCAGAACATGAGACCA 56
QY 554 pAspLeuSerMetLeuGlyArgValValLysValGluLysGlnValGlnSerIle 572
DB 55 CGATCTCACTATGCTCGGTGGTCAAGGTTGTAAGAGGTTGTAAGAGGTTGTAAGGTTG 1
```

## RESULT 15

CD629755 691 bp mRNA linear EST 12-JAN-2004  
 LOCUS 55049343H1 FLP Homo sapiens cDNA, mRNA sequence.  
 DEFINITION CD629755  
 ACCESSION CD629755.1 GI:40278021  
 VERSION CD629755.1  
 KEYWORDS EST.

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 691)  
 AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.  
 TITLE Circular rapid amplification of cDNA ends for high-throughput  
 extension cloning of partial genes

JOURNAL Genomics 84 (1), 205-210 (2004)

## COMMENT

Contact: Fu GK  
 Incyte Genomics, Inc.  
 3160 Porter Dr., Palo Alto, CA 94304, USA  
 Tel: 6508454102  
 Email: gfu@incyte.com.

## FEATURES

Location/Qualifiers

1..691  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone\_lib="FLP"  
 /note="Vector: pDrive Cloning Vector"

## ORIGIN

## Alignment Scores:

Pred. No.: 6.44e-92 Length: 691  
 Score: 1050.50 Matches: 215  
 Percent Similarity: 93.94% Conservative: 2  
 Best Local Similarity: 93.07% Mismatches: 4  
 Query Match: 23.10% Indels: 12  
 DB: 6 Gaps: 1

US-09-810-796-5 (1-888) x CD629755 (1-691)

QY 266 AlaLeuTTPTrpGlyThrIleThrLeuThrThrIleGlyTyrGlyAspLysThrProLeu 285  
 Db 1 GCTCTCTGGTGGGGGCAATACATGACACTATTGGCTATGGAGACAAACCTCCCTA 60  
 QY 286 ThrTrpLeuGlyArgLeuLeuSerAlaGlyPheAlaLeuLeuGlyIleSerPheAla 305  
 Db 61 ACTTGGCTGGGAAGATTGCTTTCTGACGGCTTTCACCTCTTGGCACTTCTTTCTTGA 120  
 QY 306 LeuProAlaGlyIleLeuGlySerGlyPheAlaLeuLysValGlnGlnHisArgGln 325  
 Db 121 CTTCCTGCGCGCATTCCTTGGCTCAGGTTTGCATTAAAGTACAAGAACACACCGCCAG 180  
 QY 326 LysHisPheGluLysArgArgAsnProAlaAlaLeuIleGlnCysValTrpArgSer 345  
 Db 181 AAACACTTTGAGAAAGAGAACCCAGCTGCCAACCTCATTCAGTGTGTTGGCGTAGT 240  
 QY 346 TyrAlaAlaAspGluLysSerValSerIleAlaThrTrpLysProHisLeuLysAlaLeu 365  
 Db 241 TACGAGCTGATGAGAAATCTGTTTCCATTGCACTGGAAGCCACACTTGAAGGCTTG 300  
 QY 366 HisThrCysSerProThr-----AsnGlnLysLeuSer 376  
 Db 301 CACACCTGCAGCCCTTACCAGAAAGACAGGGGAAGCATCAAGCAGTCAGAGCTAAGT 360  
 QY 377 PheLysGluArgValArgMetAlaSerProArgGlyGlnSerIleLysSerArgGlnAla 396  
 Db 361 TTTAAGGAGCGAGTGGCGATGGCTAGCCCCAG-GGCCAGAGTATTAGAGCCGACAGCC 419  
 QY 397 SerValGlyAspArgArgSerProSerThrAspIleThrAlaGlu-GlySerProThrLy 416  
 Db 420 TCAGTAGGTGACGAGAGTCCCAAGCAGCCGACATCACGCGAGGGGCGAGTCCCAACAA 479  
 QY 416 sValGlnLysSerTrpSerPheAsnAspArgThrArgPheArgProSerLeuArgLeuLy 436

Db 480 AGTCAGAAAGAGCTGGAGCTTCAACGGCCGAAACCGCTTCCGGCCCTCGCTGCGCCTCAA 539  
 QY 436 sSerSerGlnProLysProValIleAspAlaAspThrAlaLeuGlyThrAspAspValTy 456  
 Db 540 AAGTTCTCAGCCAAACCCAGTGATAGATGCTGACACAGCCCTTGGCACTGATGATGATA 599  
 QY 456 rAspGluLysGlyCysGlnCysAspValSerValGluAspLeuThrProProLeuLysTh 476  
 Db 600 TGATCAAAAAGGATGCCAGTGTGATGATCATCATGTGAAGAAGACTCACCCCCACACTTAA-AC 658  
 QY 476 rValIleArgAlaIleArgIleMetLysPhe 486  
 Db 659 TGTCAATTCGAGCTATCAGAAATTTATGAATTC 689

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 Job time : 6853.39 secs